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PCA-DRIVEN MULTISTAGE-MULTISCALE FUSION FRAMEWORK FOR BREAST HISTOPATHOLOGY IMAGE CLASSIFICATION

Sunil Kureel[1], Vijayshri Chaurasia[1*], Vivek Patel[1,2*], Jai Kumar Chaurasia[3]

[1]Department of Electronics and Communication Engineering, MANIT, Bhopal, Madhya Pradesh, 463003, India
[2]School of Artificial Intelligence, Amrita Vishwa Vidyapeetham, Delhi NCR Campus, Faridabad, 121002, India
[3]Department of Pathology and Lab Medicine, AIIMS, Bhopal, Bhopal, Madhya Pradesh, 462003, India

ABSTRACT
Breast cancer is worldwide existing one of the critical diseases among the women. This is spreading quite drastically and many people facing with this disease. Early diagnosis, prognosis and treatment are only the way with which we can fight and overcome this and also save the life of someone. There are different diagnosis systems already developed and also being developed to diagnose breast cancer at early stage, but the performance of these systems is a major concern. Developing a lightweight and more efficient diagnosis system with is quite difficult. To improve the performance, we have proposed a principal component analysis (PCA) with attention based Deep Convolutional Neural Network (DCNN). There is PCA driven feature extraction approach is adopted. The input image is directly feeded to the base Deep network model after performing augmentation and extracted features at every stage are concatenated then PCA reduce the features maps with more significant feature adaptation, finally these features are enhanced to put more discrimination through the attention network. The proposed model is reporting a superior accuracy of 97.68% as that of existing state of the methods.

KEYWORDS: Breast cancer; Deep CNN; Histopathology Image; Feature Fusion; PCA

INTRODUCTION

Cancer is the second most common cause of death worldwide and a major global public health issue. According to World Health Organization (WHO) reports the total number of cancer cases increased from 10 million in 2000 to 19.3 million in 2020, about 50% comparative growth [1], [2]. The WHO Global Breast Cancer Initiative (GBCI) targeted to prevent 2.5 million breast cancer mortalities worldwide between 2020 and 2040 [2]. There are 684,996 deaths from breast cancer worldwide in 2020 only [2], [3]. In 2021, the ratio of breast cancer among women is 1 to 8, while it was 1 to 11 in 1975 as per National Breast Cancer Coalition [3]. In order to administer the treatments that are currently known to be effective, the plans for improving breast cancer outcomes depend on the core health system being strengthened [2], [4]. These is crucial thing for the treatment of further malignancies as well as other non-communicable non-malignant disorders (NCDs). Breast cells that are isolated and proliferate out of control cause breast cancer. Threats can arise from malignant cells because they can damage the tissues around them, multiply, and spread. Channels within lobules are where in-situ carcinoma first appears [5]. The tissues are stained for increasing the clarity in observation and analysis, using Hematoxylin and Eosin (H&E). As a result, Computer Aided Diagnosis (CAD) can speed up the work of pathologists, add reproducibility, and lower observer subjectivity, all of which can improve the confidence as well [6]. Many breast cancer detection techniques such as: radiology based and histopathology based among th ese X-Ray, Ultrasound, Magnetic Resonance Imaging (MRI), Computed Tomography (CT) etc. are radiology based while Histopathology Imaging based techniques help to diagnose the breast cancer with cumbersome work for the pathologist [7].

Artificial Intelligence (AI) techniques are frequently employed in the detection and classification tasks of breast histopathology images in order to increase the precision and objectivity in it [5]. The scientific community is currently paying more attention to deep approaches like deep neural networks (DNN) because of better performance on massive datasets. Many researchers have devoted lots of efforts on versatile data augmentation techniques to enhance the generalizability in available HI datasets. CNN is able to extract more discriminative features when compared to machine learning techniques [8]. Two essential features for differentiating one image from another are shape and texture. Shapes and textures are also quite helpful for discriminating between biopsy images [9]. Deep convolutional neural networks (DCNN) are capable to discriminate the shape and features between images. There are different deep networks are developed such as VGGNets, ResNets, and DenseNets etc. which are widely used for the medical image analysis [10].

The ResNet and DenseNet architectures are widely used to avoid the vanishing gradient problem as compared to the networks that do not have skip connections in their architecture. Due to the unavailability of a bulk of breast cancer datasets, it is a smart approach to adapt the transfer learning technique to train the base networks being used in the model [11]. Attention modules have been added by several researchers to the field of computer visio [12],

[13]. The attention network becomes a highly deep, trainable network and simultaneously learns additional significant features [14].
PCA is the multivariate statistical tool which works along the maximum variation with feature reduction. This is a powerful tool to reduce the number of features while preserving most significant features optimally. Singular value decomposition (SVD) is followed to find the transformation matrix, responsible for reducing the features [15], [16].

MATERIALS AND METHODS

The most current deep learning innovation has enormous potential to boost application performance. This development drew our keen and attention, which sparked our investigation and development of an effective deep learning method to address a practical issue in the processing of medical data [10]. A convolutional neural network (CNN) takes an input image and models the most representative features to achieve high accuracy [17]. A deep hybrid attention network for the classification of breast cancer histopathology images public dataset, test out method, and gets about 96% accuracy [18]. F. Shahidi et.al [19] have proposed Inception-ResNet-V2 based image classification method and reported accuracy of 97.5% using ICIAR 2018 database. Full Training CNNs for Medical Image Analysis is beneficial for image classification [20]. Y. Song et al., in 2017, [21] have employed fisher vector method for feature extraction and attained good classification accuracy using pretrained model. The CNN networks with adequate fine tuning overcome the cumbersome training of network from scratch. Explainability of DCNN models are limited and possesses diverse possibility of layer wise modification M. Z. Alom et al., 2019 [11]. The channel attention (CA) is used to strengthen the most relevant information and by redistributing the channel feature responses. The spatial attention (SA) learns more representative features through combining multiscale information of high- and low-level stages, method suggested by T. Shan and J. Yan, 2021 [22]. A deep multiple instance based CNN approach is suggested by A. Das et al. [23]. Another work is proposed by Rachapudi et al. [24] to classify the breast cancer images. M.Gour [25] has suggested a method to explore the spatial feature more significantly and to classify breast cancer. S. Dabeer and his team proposed a CNN-based method to classify breast cancer [26]. In the year of 2023 R. Mahadeva and co-researchers proposed residual concatenated feature based deep learning system to classify the breast cancer from the histopathology images [27].

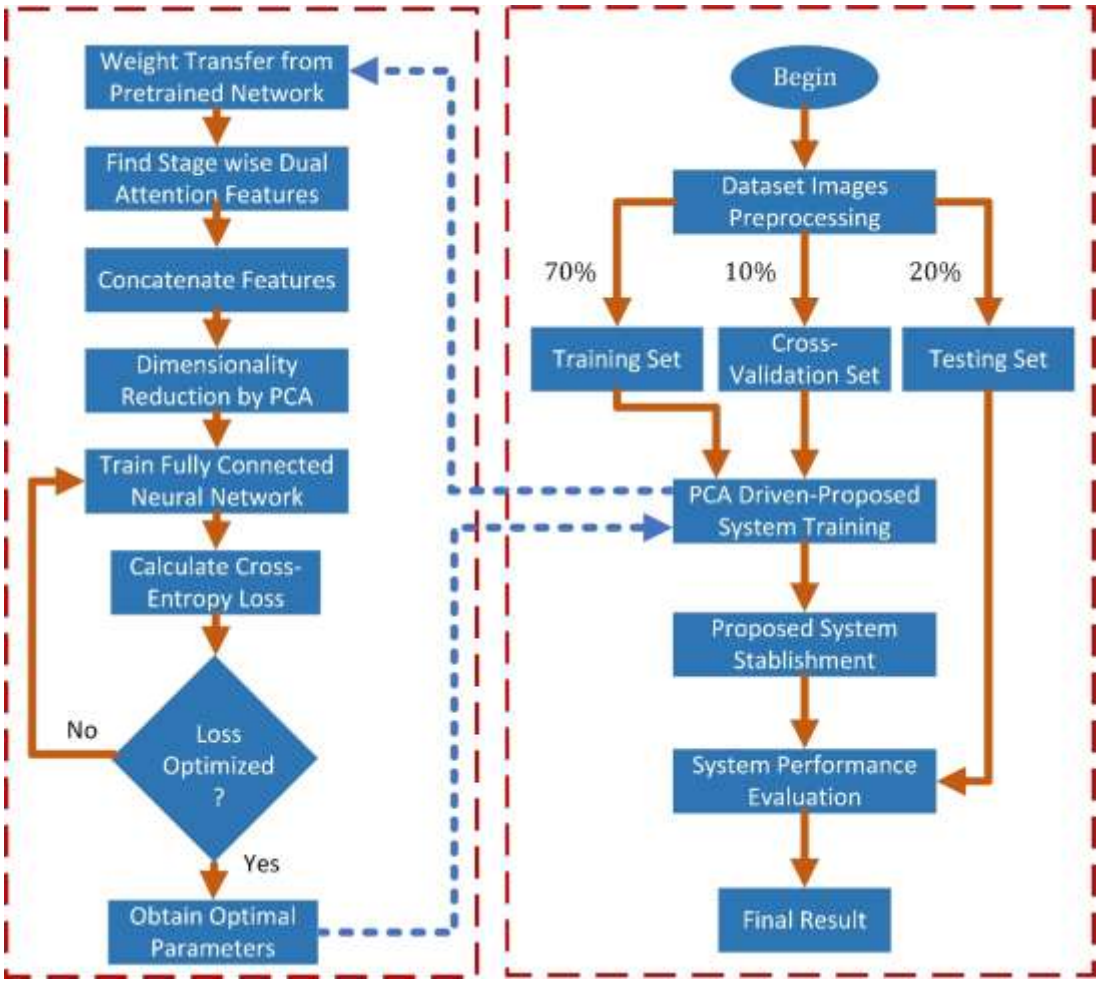


Fig. 1 Proposed model for the classification of Breast Cancer from Histopathology images

2.1 Experimental Setup
The proposed model is developed on the Python 3.9.7 platform, using TensorFlow 2.5.0 and Keras 2.4.0. The processor used for development is Intel Core i7 HP with a 2.7 GHz NVIDIA GeForce GTX 1080 GPU, 16 GB RAM, and Windows 10 (64-bit) operating system.

2.2 Datasets
BreakHis databases are used for analyzing breast cancer. BreakHis contains 7909 image samples of breast cancer (2480 benign and 5429 malignant). The complete dataset is divided into training, testing and validation sets for 70%, 20% and 10% of the total samples, respectively. The ICIAR-2018 dataset includes 200 image samples (100 benign and 100 malignant), and the data split is similar to that of BreaKHis for training, testing, and validation.

2.3 Data augmentation
Data augmentation has several advantages: it provides more training data, enhances generalizability, and reduces overfitting. The vast majority of BreakHis images are re-oriented through flipping, re-sizing and/or rotation of 30°, 90°, 120°, and 180°. This step has returned 4072 additional image samples.

2.4 Proposed model
The proposed model encompasses various submodules such as; (1) feature-extraction module (2) feature-selection module (3) feature-enhancement module and (4) classification module.

2.4.1 Feature extraction module
VGG19 CNN is used as a base model for the feature extraction module due to its simple architecture. To minimize training time, VGG19 is used in transfer learning mode on the ImageNet dataset. The weights of the pretrained network are utilized in feature-extraction layers. The intermediate layer features of the base network are concatenated with the input features. Mathematically, we can write the expressions as,
Let the input feature samples be $F^i \in R^{M \times M}$

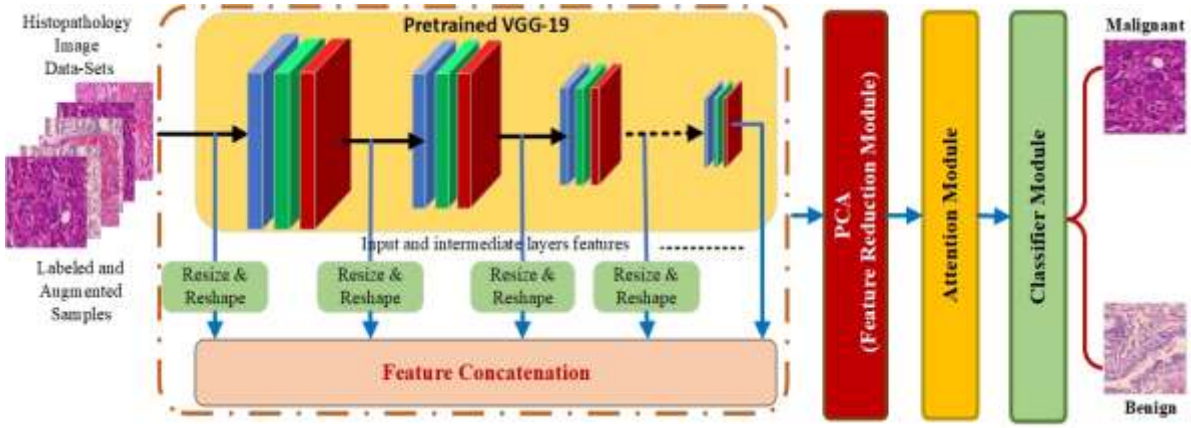


Fig. 1 Proposed model for the classification of Breast Cancer from Histopathology images

Let's the features at every stage are $X^s \in R^{N \times N}$. Where $s = 0, 1 \ldots . n$ and N is the size of the feature map. In proposed model, feature maps from all the 6 stages of VGG19 are concatenated. This concatenation of feature results gradient preservation presented as,

$$X_c = \text{concat}(X^0, \ldots \ldots, X^n) \quad (1)$$

2.4.2 Principal component analysis (PCA)
Big dataset is increasingly common problem to represent and handle for machine learning applications. To handle and overcome this issue by some dedicated methods for dimensionality reduction with loss minimization. Principal Component Analysis (PCA) is one of the famous and effective technique for that [16]. PCA does not need priory distribution and is a descriptive tool [15]. In this work the features collected from the intermediate layers of the pretrained VGG19 network are concatenated to overcome the feature loss. So, there are large number of extracted feature maps available and class related most appropriate feature maps are to be selected to improve the classification. The concatenated features are used to make sample matrix 'X', this matrix is considered as the input to PCA. Mathematical expression for PCA expressed as,
Let's the sample matrix X analyzed by PCA having J observations and described by K variables and matrix represented by $X^{J \times K}$ and $x_{jk} \in X^{J \times K}$ is the element of this matrix. The rank L of the matrix X can be written as $L \leq \min\{J, K\}$.

The principal component matrix is further decomposed as,

$$X = PDQ^T \quad (2)$$

Here D is the diagonal matrix (J × K) of singular values, P is the J × L upper half matrix singular vectors and Q is the K × L lower half matrix of singular vectors. D^2 is the square of the diagonal matrix whose diagonal elements are the eigen values of the XX^T. New data matrix which is actually a principal matrix, a redundant feature less matrix and can be expressed as,

$$X_{PC} = XQ, \text{ with } QQ^T = I \quad (3)$$

Now these features are enhanced and increased discrimination between pixels by attention module and finally the classifier module would be able to learn better.

2.4.3 Attention module

Let the features which are extracted from the base model are $X_{PC} \in R^{H\times W\times C}$, after channel attention the channel features are $X_{CA} \in R^{1\times 1\times C}$ and after spatial attention spatial feature are $X_{SA} \in R^{R\times W\times 1}$.

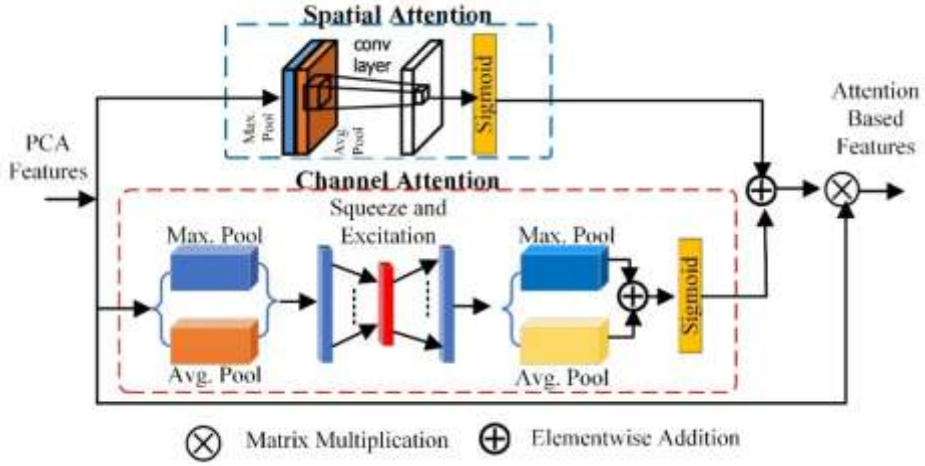


Fig. 2 Attention Module

$$X_{CA} = \sigma\left(MLP\left(Avg.\,Pool(X_{PC})\right) + MLP\left(Max.\,Pool(X_{PC})\right)\right) \quad (4)$$

Here, σ is the Sigmoid function and squeeze and excitation is actually a multi-layer perceptron (MLP) with less amount of perceptron at hidden layer (H. Lei, 2020).
and

$$X_{SA} = \sigma\left(Conv\left(Avg.\,Pool(X_{PC}), Max.\,Pool(X_{PC})\right)\right) \quad (5)$$

Overall, attention is modeled as-

$$X_F = X_{CA} \oplus X_{SA} \quad (6)$$

Features after attention mechanism are $X_A \in R^{R\times W\times C}$ which are the result of elementwise product of the feature extracted from the based model and the features after attention procedure.

$$X_A = X_{PC} \otimes X_F \quad (7)$$

2.4.4 Classification module

Finally, the features $X_A \in R^{R\times W\times C}$ followed with the Global Average Pooling (GAP) after attention procedure. To avoid the overfitting, proposed model's classification part uses Batch Normalization (BN) and dropout layers. It enhances the learning ability to return improved performance in breast cancer classification. Two hidden layers are employed with Rectified Linear Unit (ReLU) activation function along with of BN and 40% Dropout.

As the proposed model is a binary classifier, SoftMax is used to identify the probability of associated classes interprets interpreted into particular class level (0 or 1). The SoftMax function mathematically defined as:

$$(G^i)_{SoftMax} = \hat{y}_j = \frac{\exp(G^i)}{\sum_{j=1}^{k}\exp(G^j)} \quad (8)$$

Here G^i is the input feature vector and k=2 while $\hat{y}_j$ is the predicted value of respective class. Let y_j is the true lable or ground truth then cross-entropy loss:

$$L = \underbrace{H\left(y_j, \hat{y}_j\right)}_{Cross-Entropy} \quad (9)$$

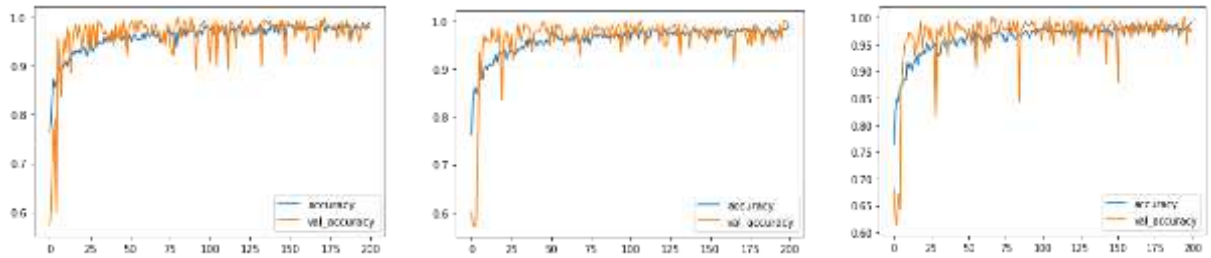
In proposed model, cross entropy loss is used for the training of network's top layers including attention network. In proposed design, Adam optimizer is used for optimizarion.

$$L = -\frac{1}{2}\sum_{j=1}^{2} y_j . \log(\hat{y}_j) + (1 - y_j). \log(1 - \hat{y}_j) \quad (10)$$

3 RESULTS ANALYSIS

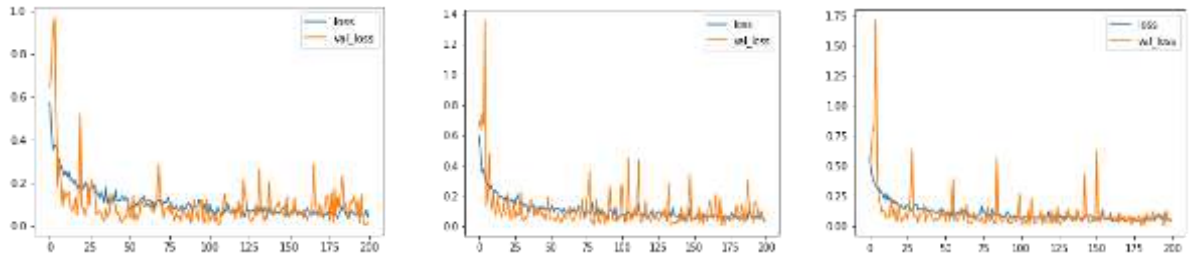
The PCA driven proposed Breast Camcer classification model in trained, validated and tested using BreakHis dataset. It has achieved higher classification accuracy when evaluated with existing methods. The problem of feature discrimination among the retrieved features from the base model is mostly resolved by the attention network. These days, it is not a better option to use current networks.

Therefore, mechanism-based networks are also more widely used and better at enhancing network performance. Figures 3 and 4 depict the training accuracy plot, the training accuracy plot, and the training losses plot, respectively.



(a) (b) (c)

Figure 3 (a) Training and Validation accuracies for the model with residual concatenated features , (b) Training and Validation accuracies for the model with residual-PCA features, (c) Training and Validation accuracies for the model with residual-PCA-Attention features



(a) (b) (c)

Figure 4 (a) Training and Validation losses for the model with residual concatenated features only, (b) Training and Validation losses for the model with residual-PCA features, (c) Training and Validation losses for the model with residual-PCA-Attention features.

As shown in Table 1, the confusion matrix indicates a significant difference in the counts of accurately and misclassified samples.

Table 1: confusion matrix for the Binary classification of Breast cancer from the BreaKHis dataset. The confusion matrices are shown for the respective classification methods used: (a) using residual features, (b) using PCA-driven residual features, and (c) using PCA-driven residual features with an attention mechanism.

(a)

	Confusion Matrix	
	B	M
B	475	21
M	35	1051

(b)

	Confusion Matrix	
	B	M
B	474	22
M	23	1063

(c)

	Confusion Matrix	
	B	M
B	480	16
M	19	1067

In Table 1 (c), it is clearly visible that the proposed model classifies 1582 image samples out of which only 35 samples are misclassified, while 1547 samples are accurately classified into their respective classes i.e. Benign and Malignant. Different models with the proposed model are evaluated and giving overall accuracy of 97.79%, which is better than the other methods reported in Table 1. The classification is binary classification, in which the benign and malignant classes are classified with the proposed model.

Table 2 depicts the parametric performance of the proposed Breast Cancer HI classification method as compared to existing methods in the domain. As BreakHis is the most popular and most frequently used dataset of breast

histopathology images, it is used to evaluate performance against the state of the art. In association with this, the proposed model's performance has also been investigated on the ICIAR-2018 dataset to demonstrate its generalization ability.

Table 2: Performance evaluation of the proposed model with existing state of the art.

	Methods	Accuracy (%)	Precision (%)	Recall (%)	F-1 Score (%)
BreaKHis Dataset	[23] (K. Daset al. 2020)	93.06	88.89	94.44	95.28
	[24] (V. Rachapudi et al., 2020)	>90.00	97.00	92.00	94.00
	[25](M. Gour et al., 2020)	92.52	93.45	93.23	93.69
	[10] (Y. Yari, et al., 2020)	96.97	-	-	-
	[26] (S. Dabeer et al., 2019)	93.45	-	-	-
	[19] (F. Shahidi et al. 2020)	92.52	93.23	93.69	93.45
	[27] VGG19 + Residual Features	95.76	92.82	93.75	93.28
	VGG19 + Residual-PCA Features	97. 16	95.37	95.56	95.47
	Proposed	**97.79**	**96.19**	**96.77**	**96.48**
ICAIR-2018 Dataset	VGG19 + Residual Features	77.50	78.95	75.00	76.92
	VGG19 + Residual-PCA Features	90.00	90.00	90.00	90.00
	Proposed	**95.00**	**95.00**	**95.00**	**95.00**

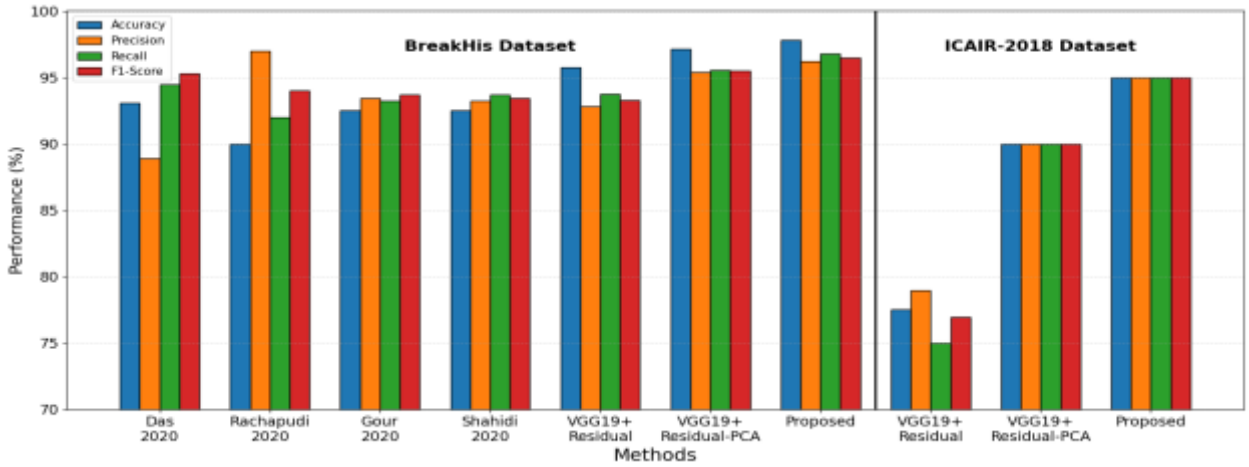


Figure 5. The performance comparison bar plot for the BreakHis and ICIAR2018 datasets

Here, Figure 5 visually emphasizes the comparative performance of the proposed model with the state-of-the-art existing methods. The proposed model is achieving better performance with an accuracy of 97.79% on BreakHis dataset and an accuracy of 95.00% on ICIAR-2018 dataset.

4 CONCLUSION

In this paper, breast cancer classification methods using histopathological images based on the Attention-Based DCNN with transfer learning are extensively explored. The features are extracted by the base model and the mixed-attention mechanism in the proposed network could automatically put more discrimination among the image samples. The MLP based dense network in the top layers classify these discriminated features for classifiing the samples in benign/malignant classes using SoftMax activation. With 97.79% accuracy, 96.19% precision, 96.77% recall, and a 96.48% F-1 score, the suggested approach is more effective than the state-of-the-art techniques. This work may be investigated further to create innovative network architectures that are more effective.

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