Journal of Chemical Health Risks

www.jchr.org

JCHR (2024) 14(5), 822-830 | ISSN:2251-6727

Vari Blend Net: An Integrated Multi-Phase Deep Learning Model for Optimizing Breast Cancer Detection from Pre-processing to Explainability

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(Received: 11 June 2024 Revised: 16 July 2024 Accepted: 10 August 2024)

KEYWORDS

Breast Cancer Classification, Histopathology images, Reinhard Colour Normalization, Data Augmentation, Patch Extraction, Median Filtering, Modified U-Net Architecture, Hybrid Golden Mongoose Swarm Algorithm, and VariBlendNet

ABSTRACT:

Introduction: This study introduces an innovative and comprehensive methodology for detecting breast cancer in histopathology images, utilizing a multi-step approach through Deep Learning (DL) methods to enhance both accuracy and interpretability. The implementation consists of four distinct phases: pre-processing, segmentation, feature extraction, and feature selection which is followed by the detection model, VariBlendNet, which integrates multiple neural network architectures like MobileNet, SqueezeNet, LeNet-5, and GRU with Variation Dropout to capture diverse features and temporal dependencies.

Objectives: To develop a deep learning-based model that can accurately detect and classify breast cancer from histopathological images, addressing the aforementioned challenges to improve diagnostic accuracy and efficiency. To experiment various preprocessing, segmentation, feature extraction and feature selection methods and algorithms gradually to see the effect on accuracy and performance of the model. To generate the fusion of CNN along with the transfer learning concept. To compare the results of proposed work with the results of the research papers based on the same Kaggle dataset.

Methods: The development of the model consists of four distinct phases: pre-processing, segmentation, feature extraction, and feature selection. Amongst which, the data preparation phase consists of Reinhard Colour Normalization ensures consistent colour representation, super pixel-based patch extraction focuses on specific regions for detailed analysis, elastic transformations augment the dataset, and median filtering reduces noise. In the segmentation phase, a U-Net architecture is employed, enhanced with Multi-Head Attention Gates, Focal Loss, and improved skip-connections to accurately identify cancerous regions. The feature extraction process integrates a variety of techniques: deep learning-based features are derived from Inception v3, while texture features are obtained using Local Ternary Patterns (LTP), Gray-Level Difference Statistics (GLDS), and Local Gradient Patterns (LGP). For feature selection, a Hybrid Golden Mongoose Swarm (HGMS) Algorithm, which combines Dwarf Mongoose Optimization and Golden Search, is employed to enhance predictive power. The detection model, VariBlendNet, integrates multiple neural network architectures like MobileNet, SqueezeNet, LeNet-5, and GRU with Variation Dropout to capture diverse features and temporal dependencies.

Results: The model was meticulously designed and trained along with many Preliminary enhancement, image analysis, feature derivation, and feature selection methods as well systematically compared grounded on their performance metrics, including Accuracy, Precision, Recall, and F1 score. The model achieved Accuracy, Precision, Recall and F1 Score values as 99.12%, 98.95%, 98.94% and 98.88% respectively and outperforms all the existing ones.

Conclusions: This holistic methodology aims to advance breast cancer detection by leveraging high-tech techniques in data preparation, image partitioning, attribute extraction, and deep learning-based detection, ultimately contributing to improved diagnostic accuracy 99.12% and thereby interpretability of the model.

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JCHR (2024) 14(5), 822-830 | ISSN:2251-6727

1. Introduction

Cancer is marked by abnormal cell division where cells continue to divide uncontrollably, forming new abnormal cells known as benign or malignant tumors. Unlike normal cells that eventually die, these abnormal (cancerous) cells proliferate, displacing healthy cells. Breast Cancer (BC) is the most prevalent cancer among women and ranks as the second leading cause of cancer-related deaths, following lung cancer. According to research by the American Cancer Society, "one in eight women is expected to be diagnosed with breast cancer at some point in their lives." This disease is highly complex, exhibiting a wide range of biochemical, histological, and clinical characteristics. It typically starts in the inner lining of the mammary ducts, milk lobes, and nearby lymph nodes in the armpits, often spreading quickly to lymph nodes or blood vessels (Fig 1). Symptoms of breast cancer include breast pain, changes in skin color, alterations in breast size and shape, and the formation of lumps. Detecting and combating cancer remains a significant challenge for physicians and researchers. Early detection can lead to effective treatment for up to 80% of women with breast cancer. However, late detection increases treatment costs, particularly in advanced stages of the disease. Within the first year of an invasive breast cancer diagnosis, women may experience significant levels of depression or anxiety, negatively impacting their quality of life, adherence to treatment, and overall survival. A variety of imaging techniques are employed to detect BC, including ultrasound, magnetic resonance imaging (MRI), digital mammography, histopathology, and convolutional neural networks [1] [2] [3]. Mammograms, which are the most frequently utilized method for early detection of breast cancer, can reveal suspicious anomalies such as masses, micro calcifications, architectural distortions, and other irregularities (Fig 2). Due to their cost-effectiveness and high sensitivity to small abnormalities, mammograms are widely used for screening. But now a days histopathology images are considered as a gold standard due to its capacity of providing fine details of the tissues. In addition, a biopsy, involving the removal and microscopic examination of a breast tissue sample through surgery or needle aspiration, is a crucial diagnostic tool. The haematoxylin and eosin staining procedures are commonly employed in histopathology. Deep convolutional neural networks (CNNs) are capable of extracting both global and local features, and can also aggregate multi-scale characteristics. Additionally, they function as a data augmentation technique to enhance the training image datasets.

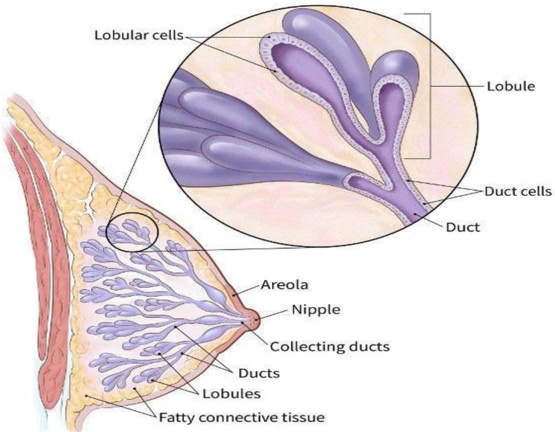


Figure 1: Illustration of Breast Anatomy [1]

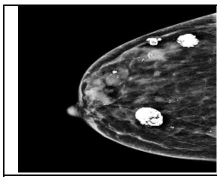
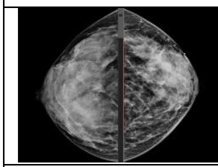
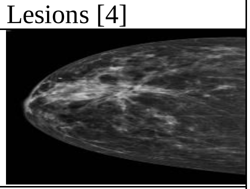
	
Calcification [4]	Stellate/ Spiculated Lesions [4]
	
Asymmetric Density [5]	Architectural Distortion [6]

Figure 2: Some common abnormities found in breast [4] [5] [6]

Computer-assisted image evaluation is essential for improving the analytical and predictive capabilities of histopathology images, facilitating rapid assessment. Preparing histopathological slides allows for the examination and analysis of breast tissue under a microscope to determine if a tumour is invasive carcinoma, benign, in-situ carcinoma, or normal tissue. Laboratory technicians create these slides by staining cell nuclei blue with haematoxylin and counterstaining cytoplasm and other components with eosin to highlight various tissue structures and cellular features. These stained biopsy tissues are then examined under a

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microscope to generate digital histopathology images [7] [8].

This study introduces VariBlendNet, a detection model which is a combination of MobileNet, SqueezeNet, LeNet-5, and GRU with Variational Dropout. The model has been offered with very sophisticated pre-processed data which pass through an efficient modified U-Net based segmentation, various feature extraction methods and hybrid golden mongoose swarm based feature selection algorithm. This approach captures a diverse array of features and temporal dependencies, improving the robustness and precision of breast cancer detection. The dataset used, sourced from Kaggle, includes 277,524 histopathology patches extracted from 162 whole mount slide images of breast cancer specimens, all scanned at a magnification of 40x. Each patch, sized at 50 x 50 pixels, is labelled based on whether Invasive Ductal Carcinoma (IDC) is present or not. Out of the total, 198,738 patches are categorized as IDC negative (Class 0), while 78,786 patches are classified as IDC positive (Class 1). They are named as u_xX_yY_classC.png, where 'u' stands for the patient ID, 'X' and 'Y' represent the x and y coordinates of the patch's cropping location, and 'C' denotes the class (0 for non-IDC, 1 for IDC) [9]. The model has been evaluated based on the two different splits, Allocating 70% of the dataset for training purposes and 30% for testing, or alternatively, using an 80-20 split for training and testing.

This research article expands with literature review, proposed strategy, results and analysis through the comparison with other articles based on the same Breast Histopathology Images Kaggle dataset.

2. Objectives

The key objective is to build a robust CNN-based classification model for Breast Histopathology Images and to experiment with different pre-processing, segmentation, feature extraction, and feature selection methods to evaluate their impact on the model's accuracy and performance. This can be elaborated as follow.

1. To review the existing literature based on varieties of MLTs and imaging modalities.
2. To develop a deep learning-based model that can accurately detect and classify breast cancer from histopathological images, addressing the aforementioned challenges to improve diagnostic accuracy and efficiency.
3. To experiment various preprocessing, segmentation, feature extraction and feature selection methods and algorithms gradually to see the effect on accuracy and performance of the model.
4. To generate the fusion of CNN along with the transfer learning concept.
5. To compare the results of proposed work with the results of the research papers based on the same Kaggle dataset.

3. Methods

3.1 Literature Review

This literature review seeks to examine the diverse methodologies employed in breast cancer detection. It focuses on discussing the different techniques, the sources of data utilized, and the metrics used for evaluation. The key objectives of this literature review are, 1) To summarize the ongoing status of research in the same domain using DL and ML practices, 2) To assess the performance of diverse implementation methods, 3) To reveal the gaps and hurdles in current research plus 4) To provide a foundation for further experimental work in this area. The detailed insights of the reviewed relevant articles are specified as follow.

Nisreen I.R et al. (2018) have conducted systematic review of about 154 research articles published during 2012 to 2017 based on breast cancer diagnosis through CAD to explore the state of the art MLTs along with the different image modalities, features and datasets. The study found that comparing different methods is challenging due to various factors, including the diversity of databases used for evaluation, the selection of image samples, the number of samples involved, and the evaluation approach, such as validation methodology and the division of training and testing sets. Up until 2015, the SVM classifier was widely utilized for classifying breast tissue. But performance is still compromised due to false positive and true negative outcomes caused by poor feature detection and other parameters so that deep learning classifier are more promising trend [10].

Mohapatra et al. (2019) proposed Deep CNN to advance accuracy and effectiveness if classifying Breast Histopathology Images of same Kaggle dataset considered for this investigation. The researchers focus on leveraging advanced neural network architectures to enhance the identification and categorization of cancerous tissues from histopathological slides. The

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challenges they faced were computational resources, model interpretability and data diversity. The model achieved 82% accuracy [11].

Hilaliyah et al. (2022) projected Deep CNN for the same Breast Histopathology Image Kaggle dataset and reported 80% accuracy. By leveraging progressive image processing procedures and DL algorithms, the study seeks to provide a reliable as well as efficient tool for early breast cancer diagnosis, potentially aiding pathologists and improving clinical decision-making [12].

N Ranjan, et al. (2022) projected the CNN-based Hierarchical classifier on The BreaKHis database to investigate the effectiveness of hierarchical framework. Where the model's interpretability was the challenge at the same time dataset's limitations was also associated [13].

V. Snigdha et al. (2022) discussed a blended feature-centric approach with MobileNet for classifying IDC in Breast Histopathology Kaggle dataset of 2,77,524 patches. The study demonstrates how integrating handcrafted features and features extracted using deep learning methods can lead to better performance in identifying IDC, ultimately aiding in more accurate breast cancer diagnosis. They achieved 91% accuracy and associated challenges like model complexity, high computational demand, data dependency and feature selection [14].

Ouf, Mahmoud et al. (2023) presented an improved method for classifying breast tumours utilizing a CNN model, designated as CancerNet for a benchmark Kaggle dataset containing 277,524 patches. The model achieved 86% accuracy [15].

Sharmin et al. (2023) presented Pre-trained ResNet50V2 based ensemble DL methods architectures to boost accuracy and performance of classification and achieved 95% accuracy. By leveraging the metiers of both DL plus ensemble methods, the study provides a robust framework that can possibly advance early finding and action planning for BC patients. The stated challenges are Complexity of the Hybrid Model, Computational Requirements, Data Dependency, interpretability and risk of overfitting [16].

Abdullah, W. (2024) proposed Nuetrosophic conversion based DenseNetB121 model to classify images of Kaggle Histopathology Images dataset consists of 2,77,524 patches. The study likely investigates how neutrosophic sets, which deal with indeterminacy and uncertainty, can augment the effectiveness of DL models in accurately classifying BC cases. The model achieves 79.07% accuracy and faces challenges like Computational complexity and interpretability [17].

Reflecting on the thorough review of literature related to breast cancer detection using deep learning technologies, several key insights and areas for further research can be identified which guides for the further investigation.

3.2 Proposed Methodology

Overview

The proposed research has been commenced by reviewing a wide range of research papers collected from different sources. After conducting an intensive review of articles specified in literature review, it can be articulated that Deep learning, as ML technique in conjunction with efficient data preparation methods, holds potential to expand the knowledge base of breast cancer diagnosis and contribute to saving lives through technological advancements. Following is the detailed description of the Dataset used and the proposed model implemented during this research work [7].

Proposed VariBlendNet Model architecture

The Core components of the proposed methodology for detecting breast cancer are Initial processing, image segmentation, characteristic extraction, and feature selection. The carefully selected feature are then offered to the detection model, VariBlendNet which merges elements from MobileNet, SqueezeNet, LeNet-5, and GRU with variable dropout. This approach is designed to optimize precision and operational efficiency of BC classification in histopathology images. A workflow model for this proposed detection methodology is depicted in Figure 3 [18] [19] [20].

Pre-processing

The initial stage of the breast cancer detection methodology involves several key pre-processing techniques. Firstly, Reinhard Colour Normalization is used to standardize colour representation across histopathology images by replacing reference image's background colour with that of the colour-normalized image. This is followed by super pixel-based patch extraction, which clusters pixels into significant patches to highlight important regions for further analysis.

Patches are generated using the centroid of each super pixel. The ground truth at the pixel level is calculated using the following equation:

$$L = L_{base} \times R_{texture} \tag{1}$$

Here, $R_{texture}$ represents the texture ratio, primarily used to indicate the texture's complexity, and L_{base} is the base count of super pixels while L represents total super pixels.

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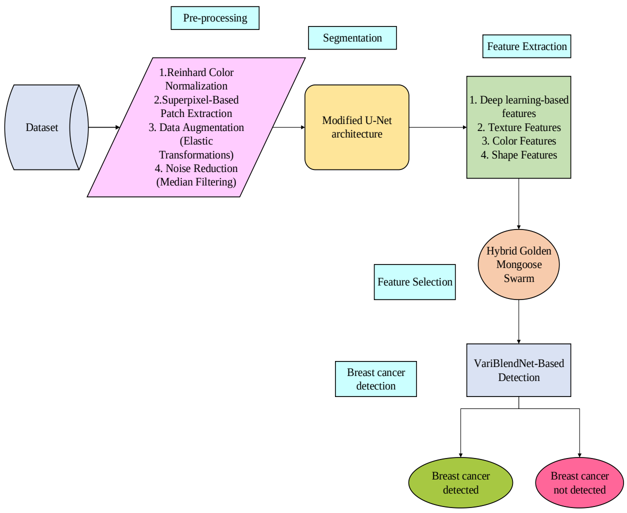

Figure 3: Proposed Model's Block diagram

This is computed as follows:

$$R_{texture} = \frac{t}{T} \tag{2}$$

In this equation, T is the quantity of pixels in first three principal components, and t is the number of nonzero elements in the filtered image, which is generated after applying the Sobel filter. Elastic transformations are then applied to simulate various deformations, augmenting the dataset and making the model more robust to differences in tissue structures. This approach generates a deformation effect on an image by creating a random displacement field, with the intensity controlled by the elasticity coefficient σ and a scaling factor α. The following is a mathematical description of this distortion:

$$I'\big(x + \Delta x(x,y), y + \Delta y(x,y)\big) = I(x,y) \tag{3}$$

$$\Delta x = G(\sigma) * \big(a \times Unif([-1,1,n,m])\big) \tag{4}$$

$$\Delta y = G(\sigma) * \big(a \times Unif([-1,1,n,m])\big) \tag{5}$$

Where $\Delta x \; and \; \Delta y$ represent grids for horizontal and vertical shifts of $n \times m$, I' and I are the deformed and original pictures. The x and y values are generated using a Gaussian filter with a standard deviation σ. This filter is applied to the product of a uniformly random value drawn from the range [-1, 1] and a scaling factor α. Lastly, median filtering is utilized to reduce noise while maintaining structural details, thereby enhancing the overall quality of the histopathology images. In median filtering, neighbouring pixels' median values are used in place of the original pixel values [21] [22].

$$y_{(m,n)} = median(x_{i,j}: (i,j) \in \tau) \tag{6}$$

Where τ represents the nearby neighbours in (m, n).

Segmentation through Modified U-Net architecture

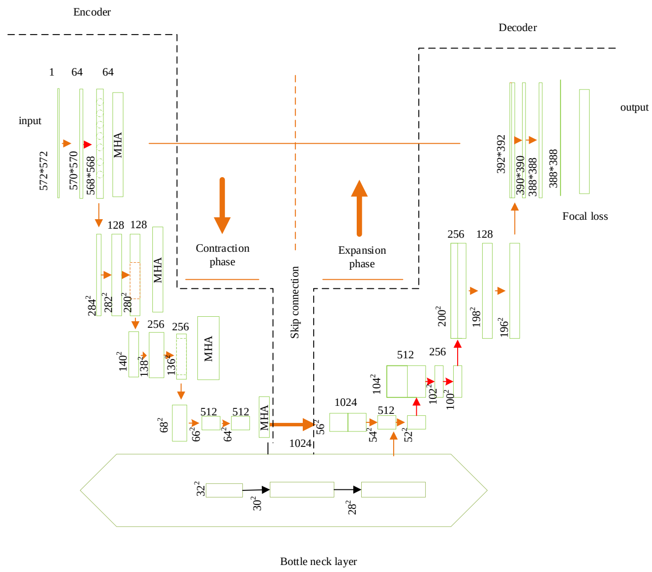

Figure: 4 Architecture of Modified U-Net

The modified U-Net design integrates Multi-Head Attention (MHA), Focal Loss, and improved skip connections to enhance segmentation accuracy for identifying cancerous regions in histopathology images (Fig. 4). The encoder captures high-level context using pooling techniques like max pooling and stride convolutions, while MHA focuses on relevant features through scaled-dot product attention, addressing dependencies in the data. The decoder up samples feature maps to match the input image size, utilizing skip connections for local context and fine-grained features. Focal Loss addresses class imbalance by emphasizing difficult samples, improving model precision. Replacing pooling layers with stride convolutions retains crucial information, enhancing the segmentation's overall effectiveness [23] [24].

Feature Extraction

In this, the pre-processed image is inputted into various techniques to capture intricate details. Using the Inception v3 architecture, deep learning-based features identify complex patterns. Texture features like LTP, GLDS, and LGP detail nuanced textures, while colour histograms represent pixel intensity distribution for colour composition. Zernike Moments extract robust shape features, detailing object shapes. This comprehensive feature set significantly enhances the accuracy of breast cancer detection [14] [25] [26].

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Feature Selection using HGMS

The HGMS algorithm combines the Golden Search Optimization Algorithm with the Dwarf Mongoose Optimization Algorithm to enhance the selection of distinguishing features, refining the prognostic capacity and accuracy of the BC classification model. It executes the sequence like, **Population Initialization:** Randomly generate initial solutions within defined limits. **Population Evaluation:** Evaluate the initial population to select the best solution based on fitness value. **Golden Change:** Sort solutions by fitness and apply a random solution to the lowest fitness item. **Size Evaluation:** Calculate step size to move solutions towards optimal outcomes, balancing global and local searches using a transfer operator. **Size Limitation:** Restrict the movement of solutions to control oscillations and avoid divergence. **Update Position:** Move solutions towards the global optimum using the calculated step size, considering the collective movement of the mongoose group. The features obtained are then given to the VariBlendNet model for breast cancer detection [27].

VariBlendNet Architecture

The VariBlendNet model for breast cancer detection integrates MobileNet, SqueezeNet, LeNet-5, and GRU with Variational Dropout to capture diverse features and temporal dependencies (Fig. 5). The convolutional layer of MobileNet and the fire module from SqueezeNet are incorporated into the LeNet-5 model, whose output is fed into the GRU with Variational Dropout for final detection. This architecture optimizes feature extraction and predictive accuracy, leveraging MobileNet for efficient spatial feature extraction, Maxout activation for non-linearity, SqueezeNet's Fire Module for further processing, and GRU to handle temporal dependencies. The model's CNN structure is adapted with a 3×3 convolution core and a 140×100 image input size, using a batch size of 100 to balance memory use and algorithm convergence. Convolution layers capture local perception features Eq.7, while the Fire Module from SqueezeNet compresses and expands feature maps [28] [29].

$$Conv_s = \sum_i Ftr_{i,j} * Ip_{img} \quad (7)$$

Where, the letters i and j signify the number of input and output frequencies, and $Ftr_{i,j}$ denotes the filter. In conventional convolution, input images (including featured pictures) that utilize a fill style without padding are called Ip_{img}

$$a_{ij}^{l} = \max(a_{nm}^{l-1})\ ,\ \ i \leq m, n \leq i+2 \quad (8)$$

Where, the area that corresponds to the pooling nucleus of a_{ij}^{l} is denoted by m, n.

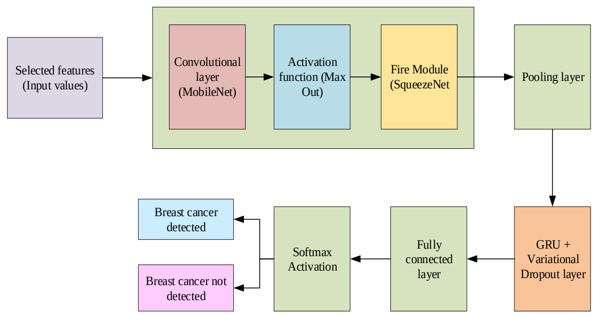

Figure: 5 VariBlendNet Model Architecture

Pooling layers reduce feature dimensions Eq.8, and GRU layers manage data flow through reset and update gates. Variation Dropout generalizes Gaussian dropout for better generalization and mitigating overfitting. The output layer uses weighted summation and softmax activation to produce probabilities for each class, signifying the existence or non-existence of breast cancer. This streamlined architecture balances efficiency and accuracy, making it well-suited for real-world applications in breast cancer detection [30] [31].

4. Results and Discussion

Here, we discuss and compare the results obtained from the proposed VariBlendNet (DL) model, developed for breast cancer histopathology image (The Kaggle Dataset) classification, with the results of research papers based on the same dataset. The model was meticulously designed and trained along with many Preliminary enhancement, image analysis, feature derivation, and feature selection methods as well systematically compared grounded on their performance metrics, including Accuracy, Precision, Recall, and F1 score [7] [18] [32]. The assessment was conducted with two different dataset splits: 70% for training and 30% for testing, and 80% for training and 20% for testing. Table 1 presents a comparative analysis of the proposed model's performance for both dataset splits. **Accuracy,** is a common performance metric, refers to the percentage of correctly classified images among all images evaluated. The proposed model outperforms all the models presented in reviewed research articles by achieving 98.90% accuracy with a dataset division of 70% training and 30% testing and maintains its dominance by increasing its accuracy to 99.125% with a dataset split of 80% training and 20% testing.

Article	Methodology	Accuracy	Precision	Recall	F1 Score
Mohapatra, P. et al. (2019)	Deep CNN	0.82	0.805	0.775	0.775
Kumar, D. et al. (2021)	SGE(stacked Generalized Ensemble) based CNN	0.8780	0.88	0.88	0.88
Hilaliyah, P. K et al. (2022)	Deep CNN	0.80	0.82	0.80	0.799
Snigdha, V. et al. (2022)	MobileNet	0.91	0.88	0.85	0.87
Sharmin, S. et al. (2023)	Pre-trained ResNet50V2 based ensemble DL method	0.95	0.9486	0.9432	0.9457
Ouf, M., Abdul-Hamid et al. (2023, March)	CancerNet (Customized)	0.86	0.81	0.84	0.83
Abdullah, W. (2024)	Nuetrosophic conversion based DenseNetB121	0.7907	0.79	0.79	0.79
Proposed VariBlendNet model (70% training, 30% testing)	VariBlendNet	0.9890	0.9812	0.9865	0.9795
Proposed VariBlendNet model (80% training, 20% testing)	VariBlendNet	0.99125	0.98958	0.9894	0.98881

Table 1: Evaluation of the proposed model's performance relative to results from similar research utilizing the Breast Histopathology Image dataset (Kaggle)

In the context of classification models used for breast cancer histopathology image analysis, **Precision** represents the ratio of true positive predictions (correctly identified cancerous images) to the total number of positive predictions made by the model, including both true positives and false positives. The proposed model attains precision scores of 98.84% and 98.96% when using 70% and 80% of the data for training, respectively. **Recall**, also known as sensitivity or the true positive rate, indicates the ratio of true positive predictions to all actual positive cases. The proposed model obtains a recall of 98.85% and 98.94% for 70% and 80% training data respectively. **F1 score** is a metric that merges both precision and recall into a single value. The proposed model attained F1 scores 98.74% and 98.88% for 70% and 80% of training datasets correspondingly.

5. Conclusion

Throughout this research, a varieties of ML and DL algorithms have been extensively reviewed and a significant demand for deep learning in medical image analysis has been identified, particularly within the medical and software industries. Early in our investigation, the challenges associated with various ML and DL techniques, especially compared to Convolutional Neural Networks (CNNs) and modalities used for medical imaging have been observed. This led to focus the further investigation specifically on CNNs for medical image analysis and histopathology images, with a particular emphasis on

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Breast Cancer prediction. And the proposed research is the result of the same.

This study introduces a comprehensive methodology for Breast Cancer uncovering through histopathology inputs, employing multi-faceted approach that spans pre-processing, segmentation, feature extraction, and deep learning-based detection. Pre-processing techniques, including Reinhard Colour Normalization, super pixel-based patch extraction, elastic transformations, and median filtering, ensure consistent colour representation, focused region analysis, dataset augmentation, and noise reduction. The segmentation phase utilizes a U-Net architecture enhanced with Multi-head Attention Gates, Focal Loss, and improved skip-connections for precise identification of cancerous regions. Feature extraction incorporates deep learning-based features along with texture, colour, and shape features, while the Hybrid Golden Mongoose Swarm Algorithm aids in feature selection. The VariBlendNet detection model integrates multiple architectures with Variation Dropout to capture a comprehensive range of features.

Overall, this methodology aims to enhance the classification of breast cancer by combining contemporary techniques, thereby improving diagnostic accuracy and interpretability in histopathology analysis.

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