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Classifying Breast Cancer Using a Hybrid Approach

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Breast cancer remains one of the leading causes of cancer-related mortality among women worldwide, and early diagnosis significantly improves survival rates. Histopathological image analysis plays a crucial role in breast cancer diagnosis; however, manual interpretation is time-consuming and susceptible to inter-observer variability. This study proposes a hybrid magnification-invariant deep learning framework named the Magnification Invariant Classifier (MIC) based on an enhanced UNET encoder-decoder architecture for automated breast cancer histopathology image classification. The proposed framework was evaluated using the publicly available BreaKHis dataset containing 9,109 histopathological images acquired at 40×, 100×, 200×, and 400× magnification levels. The dataset was divided into 70% training, 15% validation, and 15% testing subsets. Data augmentation techniques including rotation, flipping, cropping, and shearing were applied to improve model generalization and reduce overfitting. Experimental results demonstrate that the proposed model achieved an accuracy of 91.23%, precision of 94.51%, recall of 90.99%, F1-score of 92.71%, and an AUC score of 0.94, outperforming UNET, UNET++, VNET, and RESNET models by approximately 5–9% in classification accuracy. The proposed architecture effectively extracts both local and global tissue features while remaining robust across varying magnification levels. The reduced loss value of 0.0876 further confirms the efficiency and stability of the proposed framework. The findings indicate that the proposed model can serve as an effective computer-aided diagnostic tool for assisting pathologists in accurate and early breast cancer detection.

Keywords: Tumor, Breast Cancer, MRI, CT scan, CNN, Mammogram, Deep learning, Histopathology.

Introduction:

Cancer is a disease that is quite common and has a high mortality rate. It is one of the most prevalent diseases in the world There are many different types of cancer, but the three most prevalent are skin, breast, and lung cancer. Cancer is characterized by rapid cell division and abnormal growth. The three most typical signs of cancer are rapid weight loss, persistent coughing, and irregular bowel movements. The second most frequent type of cancer in women is breast cancer. The abnormal proliferation of breast tissues is what leads to this type of cancer. Breast lumps, breast form changes, and red spots on the breast are all indications of breast cancer. [1] The top cause of death worldwide is breast cancer. Doctors and other medical professionals use digital biomedical photography analysis to identify cancer. Mammograms can detect breast cancer. [2] This technique is effective and practical for detecting breast cancer. Breast cancer is detected through mammograms, and the diagnosis is confirmed by a biopsy. The majority of individuals are unable to afford it since it is a costly program. According to population forecasts, an additional 2.4 million instances of female breast cancer would be identified worldwide in 2018. Although Asian nations have lower breast cancer rates than Western countries, Asian countries already suffer a far bigger proportion of the global burden of this illness. Because of the disease's increasing prevalence, one in every nine Pakistani women will acquire breast cancer over their lifetime. [3]. In the past, women between the ages of 60 and 64 had the largest incidence rates of breast cancer; therefore, it is estimated that between 2016 and 2025, these rates will rise drastically among women in this age group. The overall incidence of breast cancer is predicted to increase from 23.1% in 2020 to 60.7% in 2025. In 2020 and 2025, the percentage of cases of breast cancer discovered in younger women (30-34 years) would increase from 70.7 to 130.6% when compared to 2015. The rate of breast cancer appears to be increasing more rapidly in postmenopausal women than in women in their twenties and thirties (15–29 years old) (aged 55 to 59). In addition, these results indicate that middle-aged women in Karachi, Pakistan can expect to see an increase in the rate during which they develop breast cancer in the future. Understanding the healthcare requirements of a growing population and the associated pressures on the healthcare system as a result of an increase in cancer incidence. [4]. Age-adjusted rates show that Pakistan has one of Asia's highest rates of breast cancer. [5]. Due to delayed treatment and inappropriate facility referrals, the country's percentage of breast cancer-related mortality is, sadly, greater [6]. Machine learning algorithms have the potential to significantly improve all aspects of medicine, from clinical decision-making to drug development, and would therefore drastically change the current state of medical practice. The current success of machine learning algorithms in computer vision tasks is extremely opportune as medical records are increasingly being kept digitally. Between 2007 and 2012, office-based physicians in the US increased their usage of electronic health records (EHR) by a factor of two, from 11.8% to 39.6%. Currently, radiologists examine medical images as part of a patient's EHR but are restricted by speed, stress, and experience. A licensed radiologist must finish years of training at a significant financial cost, which is why some medical institutions utilize teleradiology to outsource radiological reporting to countries with cheap labor, such as India. An incorrect or delayed diagnosis has negative effects on the patient. This makes medical image analysis a perfect application for an automated, precise, and powerful machine- learning method. Because the data is well structured and annotated, medical picture analysis is a prominent topic for machine learning research. In this case, it is anticipated that patients will first engage with useful artificial intelligence systems. This is significant for a few reasons. First, using medical image analysis as a litmus test as a testbed for human-AI interaction demonstrates how receptive patients will be to seeing a non-human actor make decisions that could affect their health, demonstrating how artificial intelligence systems can be put to the test to determine whether they increase real-world patient measures, such as patient survival and outcomes. [7][8].

Therefore, the survival percentage for breast cancer may be improved with early diagnosis and treatment. It has a particularly negative effect on Pakistani women because there are more of them than men and no systematic, scientific method has been taken to address the issue. Unfortunately, there are no regularly collected data on cancer incidence, mortality, or death rate in Pakistan.

Medical imaging is a technology and a method that includes capturing images of the interior of a person for clinical evaluation, and medical intervention, and to explain how certain organs or tissues are performing. Because of its rapid advancement, medical imaging now assists in illness identification and treatment, and it plays an important part in modern medicine. Ultrasound, x-rays, mammography, computed tomography (CT scans), and nuclear medicine are all examples of medical imaging tools.

Medical image analysis helps professionals make an accurate diagnosis and choose the most effective course of treatment for their patients. As it has a substantial impact on clinical diagnosis and therapy (CAD), medical image analysis is a crucial part of computer-aided detection (CADx) and computer-aided diagnosis (CAD). Due to the significance of the performance of crucial parameters including accuracy, F-measure, precision, recall, sensitivity, and specificity, it is generally advocated that these metrics produce high values in medical image analysis. Since there are more digital images that contain clinical information available, it is vital to use an approach that is most effective for large-scale data analysis. [9][10][11].

Artificial Intelligence (AI) is now the most debated topic in medical imaging research, both for diagnostic and therapeutic purposes. Artificial intelligence has been used by researchers to objectively measure radiographic features and automatically find complicated patterns in imaging data. Doctors can identify issues considerably more rapidly as a result of AI's application in medical imaging, urging early intervention. AI can assist radiologists in working more efficiently and with less workload. AI has improved the healthcare industry. By automating time-consuming and repetitive tasks, radiologists may free up time in their hectic schedules and give more attention to other critical issues. AI has improved the healthcare industry. By automating time- consuming and repetitive tasks, radiologists may free up time in their hectic schedules and give more attention to other critical issues.

An automated method to identify breast cancer in B-mode ultrasound images is being developed using artificial intelligence techniques like computer vision and deep learning. The performance gap between urban and rural physicians can be closed more quickly with this strategy by improving the front-line medical professionals' ability to accurately diagnose patients. It has significant social ramifications and is undoubtedly medically required. A particular type of machine learning known as "deep learning" enables its users to conceptualize the world as a layered hierarchy of concepts, where each concept is defined in reference to a simpler concept, and more abstract representations generate by using less abstract ones. We don't have to explicitly design everything in deep learning. a tried-and-true idea: deep learning. It has lasted for a while. It is more common now since we have access to more data and computing capacity than in the past. Processing power has increased dramatically over the past 20 years, which has sparked the creation of deep learning and machine learning. This learning process results in the creation of deep learning systems with extraordinarily high levels of power and adaptability.[12]. The use of cutting-edge technologies and the provision of the proper care for the appropriate patient at the appropriate time have ushered in a new age in healthcare. The most potent tool for machine decision-making is deep learning, which enables the computer to learn from vast amounts of data. In numerous clinical applications, researchers discovered that integrating pharmacological data with multi-layer neural networks yields precise predicted decisions. A deep learning structure, which would be based on a hierarchical learning framework, may integrate data to offer a higher level of generalizations.

Deep learning is preparing the way for the next-generation health service, which will be capable of handling billions of patient records, detecting diseases, and offering prescriptions, clinical testing, and treatment recommendations. [13].

Research Objectives:

The primary objectives of this study are:

To develop an automated deep learning framework for classifying breast cancer histopathology images into benign and malignant categories.

To design a magnification-invariant encoder-decoder architecture capable of processing multi-resolution histopathological images.

To improve classification accuracy and reduce model loss compared to existing CNN-based models.

To evaluate the proposed framework using standard performance metrics including accuracy, precision, recall, F1-score, and AUC.

To analyze the robustness of the proposed model across different image magnification levels.

To contribute toward reliable computer-aided diagnosis systems for early breast cancer detection.

Research Novelty and Contribution:

The proposed Magnification Invariant Classifier (MIC) introduces a hybrid deep learning framework capable of classifying breast cancer histopathology images across multiple magnification levels without requiring separate models for each resolution. Unlike conventional UNET-based approaches that primarily focus on segmentation tasks, the proposed framework integrates magnification-invariant feature extraction with enhanced encoder-decoder learning for simultaneous segmentation and classification.

The major contributions of this study are summarized as follows:

Development of a magnification-invariant hybrid CNN architecture capable of handling 40×, 100×, 200×, and 400× histopathological images.

Integration of enhanced feature extraction and skip-connection optimization within the UNET framework.

Application of extensive data augmentation to improve robustness and generalization.

Comparative evaluation against UNET, UNET++, VNET, and RESNET models.

Achievement of superior classification accuracy with reduced computational loss.

Improved detection performance for malignant tumors, reducing false negative predictions.

Literature Review:

Three freely open mitotic datasets that are utilized to test the adequacy of the proposed method in which, the ICPR 2012, and ICPR 2014 highlights are produced automatically by mitotic recognition algorithms. The AMIDA13 datasets served as the basis for the study of the strategy review, and the evaluated explanations are bounding boxes of mitotic districts created by the A-FCN model trained on fully labeled data surrounding centroid pixels. Additionally, we employ a stochastic slope plunge (SGD) with underlying learning rates of 0.001 for the first 50,000 iterations and 0.0001 for the subsequent 50,000 iterations. We use the proposed A-FCN partition model and the anticipated MS-RCNN identifier to show that the suggested A-FCN partition model performs poorly on the ICPR 2014 and AMIDA13 datasets. For the purpose of identifying mitosis in hematoxylin and eosin- stained histology images, we suggest Tiny Mitosis, a unique design combining the MS-RCNN and A-FCN models. We achieved an F1 score of 0.902 on the challenging ICPR 2012 dataset, far exceeding all prior detection techniques. We achieved F scores of 0.495 and 0.644 on the ICPR 2014 and AMIDA 13 datasets, respectively. The findings revealed that our strategy outperforms state-of-the-art methods significantly. [14].

During the investigation, pathologists take a lot of time and cost to examine breast cancer disease tissues at different levels of magnification it is necessary to study various amplifications because human translation might be challenging. With the use of computer-assisted demonstration frameworks and the analysis of histological breast cancer malignant development images, the goal of this review is to investigate the significance of AI tactics. The dataset that the researcher selected is known as BreaKHis, and it includes pictures that are arranged in various ways and have a width of 700 by 460 pixels, an 8-bit color depth in each channel, and a three-channel RGB color depth. Several techniques were employed to enhance the images, including Histogram Leveling (HE), Combined Histogram Balance (CHE), Quadrant Dynamic Histogram Evening out (QDHE), and Differentiation Restricted Versatile Histogram Evening out (CLAHE). In the process of "Histogram Leveling," Right-sided histograms are associated with eye-catching images, while left-sided histograms are associated with unattractive images. Widely spread histograms are associated with the most prevalent (and ideal) images. The results of our suggested model are clearly superior to models of profound learning that have been established in advance with the amplification level (40X and mix). When compared to machine learning methodologies, the recently introduced non-parametric methodology produces fascinating results. Our suggested 'Deep-Hist' model is magnification independent and achieves > 92.46% accuracy with Stochastic Gradient Descent (SGD), outperforming pre-trained models for image categorization. The Profound Hist model gives conceivable outcomes during preparation contrasted and other pre-prepared models (AlexNet, Crush Net, Res-Net, Thick Net, and VGG-Net). [2].

Until now, disease researchers and specialists have directed many analyses to find and assess new and inventive programmed malignant growth evaluating frameworks to speed up their helpful determinations and eventually empower more effective visualizations. These components include solidity lattice (SM), a numerical model that integrates mathematical, morphometric, and shape-based highlights, completed neighborhood twofold example (CLBP), which provides textural highlights, measurable second entropy (SME), and. Accordingly, the suggested planned mitotic discovery framework has predetermined processes that can be summed up as the following stages, such as pre-handling, division, highlight extraction, and arrangement. Factual Entropy highlights and CLBP highlights are divided article-wise in the component extraction block. The layouts of blocks restrained in the running lines serve as a means of distinguishing and highlighting SMs in addition to the extraction of CLBP and Entropy highlights. The full elements are divided from all the mitosis and non-mitosis up-and-comers by the following block, which causes the deleted highlights to become entangled with one another. These components include measured second entropy (SME), solidity lattice (SM), and completed neighborhood twofold example (CLBP) as textural features. Importantly for the future, rather than focusing on its Eigenvalues, the suggested programmed discovery technique might be enhanced and modified to take into account the unique benefits of the firmness lattice. [15].

A strategy utilizing a crossover profound brain organization, to group breast cancer disease histopathology images. Our dataset does not claim to be the largest publicly available dataset for the distribution of histopathological images of breast cancer, but it does cover the maximum number of subclasses and age groups that are permitted, providing enough information variety to lessen the problem of relatively low characterization precision of benign images. "Bioimaging2015: fourth Worldwide Conference in Applied Bioimaging" included 249 photos that were all related to the meticulous characterization of breast cancer illness. However, compared to public databases that also contain photos of benign breast cancer, these two public datasets respectively limited size (249 and 400 images, respectively) has a significant impact on how well breast cancer images are classified. The ImageNet Large Scale Visual Acknowledgement Challenge (ILSVRC) findings using the ImageNet dataset have produced substantial improvements in computer vision. To separate the element representation vectors of the 12 patches, the fix-wise model, which has previously been developed, is applied to each picture. In order to aggregate the top qualities of the 12 adjustments into a single thorough evaluation of the picture, the last step entails feeding the 12 element vectors (1215376) via a bidirectional LSTM. In this article, we proposed another strategy for breast cancer disease neurotic picture characterization utilizing a mixture of convolutional and repetitive profound brain organization. In light of the more extravagant component portrayal of the neurotic picture fixes, our strategy considered the present moment and the drawn-out spatial connections between patches through an RNN, which is right behind a more extravagant staggered CNN highlight extractor. The experimental findings reveal that our technique beats the state-of-the-art method for the 4- class classification task, with an average accuracy of 91.3%. [16].

A strategy, in this work; for the analysis of mitotic cores in breast cancer histopathology images, we have suggested the "DHE-Mit-Classifier," a further Profound Convolutional Brain Organization (CNN) based Heterogeneous Gathering technique. These patches are first separated from the histopathological biopsy districts by the proposed method and then classified into mitotic and non- mitotic cores using the proposed DHE-Mit-Classifier. In order to prevent the overfitting of complex CNN models during the preparation by expanding a short dataset, two support datasets (MITOS12 and MITOS14), which were used by the scientist at TUPAC'16, were generated as part of the base and meta-classifiers. The proposed technique "DHE- Mit-Classifier" has four key phases: information preprocessing, up-and-coming mitoses determination, heterogeneous troop-based mitoses characterization, and execution of cutting-edge CNNs. To effectively distinguish between mitotic and non-mitotic cores, we have developed the "DHE-Mit-Classifier," a powerful heterogeneous group based on CNN. On the test set, the ensemble outperformed, with an F-score of 0.77, recall of 0.71, accuracy of 0.83, and area under the precision-recall curve of 0.80. Its strong generalization, high F-score, and accuracy show its promise as a pathologist aid. With a detection rate of 99%, the mitotic nuclei selection module displayed remarkable identification abilities, correctly detecting all but one mitosis in a test set. [17].

A programmed Different Elements based Breast Cancer Malignant Growth Recognition (DFeBCD) framework to characterize a mammogram as typical or unusual. Using the common IRMA mammography dataset, two classifiers, an Ensemble Classifier inspired by Extreme Learning and a Support Vector Machine (SVM), are trained on these identifying characteristics (ELiEC). Our tests' outcomes demonstrate that the three individually ordered variations of the highlights perform better than the progressively formed highlights when presented using the DFeBCD framework employing CNN based on interstate organizations. A classifier with the ability to comprehend individuals on a deeper level is used to make use of this mixture highlight space after the four different arrangements of parts are hybridized to create a final data- rich component space. This uses the DDSM dataset, which contains 2796 128x128 image patches extracted from mammography scans, from the IRMA dataset. For both the Train Approval and Test datasets, the approach extracts four sets of highlights: Measurable, LBP, Taxonomical, and Dynamic components. Results from this preliminary work indicate that the proposed Interstate Organization-based CNN outperforms the SVM and ELiEC classifiers in displaying the most salient features of an image, as well as three different configurations of random highlights. [18].

A strategy utilizing Breast Cancer Disease Recognition Utilizing Computerized Mammography Utilizing Profound Convolutional Brain Organizations and Close to Home Realizing. This review identified the double, four, and eighth orders of breast cancer malignant growth histopathology imaging datasets and the best trustworthy models for each. BreakHis, a database of histopathological imaging data related to breast cancer, was examined for the double and eight groups of these models. On the BreaKHis knowledge base, experiments that looked at profound learning models for the double and eight groups were studied and displayed. Furthermore, we reevaluated Beginning ResNet-V2 in our assessment and discovered that, although using around 3.5 times less data to build this model, the exact findings were quite similar. This evaluation ensured Beginning ResNet- accuracy V2's because this model had the highest precision for both paired and eight characterizations on the BreakHis dataset. In spite of the fact that this model was unable to perform effectively for the four classes on the BACH data set from multiple scientists, starting ResNet-V2 produced the maximum exactness results for the four orders on the BACH information base throughout our testing. Although the possibility that SENet-154 may outperform the Inception ResNet-V2 model by up to two groups even with fewer data, our analysis revealed that Starting ResNet-V2 had the highest increased exactness findings for the four orders on the BACH data. SENet-154 was still able to beat the InceptionResNet-V2 model in terms of two groups even with fewer data. Several models were assessed, and varying accuracy ratings were obtained. ResNet-152 has a 98.70% success rate, ResNet-101 has a 98.40% success rate, ResNet-50: 97.8 percent 77.70% for Inception-V4, Inception-V3 (BreakHis database): 96.2% and 98%, respectively, Inception-V3 (TMA and BreaKHis databases): no defined accuracy score 93.60% for Inception-V1 (BreaKHis and TMA databases). VGG-19 and DenseNet-201 (BreakHis database) have the greatest accuracy ratings when compared to other databases, although particular percentages are not given. [19].

In this study, the authors propose two high-performance computational techniques including a designed 20-layer Convolutional Neural Network (CNN) and a conceived Local binary pattern variant Quad-Star LBP (QS-LBP) for automatic preliminary diagnosis of breast cancer from histopathology images. The 20-layer CNN model employs a kernel and Batch Normalization to overcome gradient loss; the QS-LBP method uses unique star-like pixel analysis for statistical texture feature extraction, followed by classification using Random Forest and Optimized Forest techniques. On the extensive BreaKHis dataset and the Pennsylvania/New Jersey dataset, CNN maximum Accuracy has been 98.27% with an F1 Score of 98%, QS-LBP method has been achieved 94.58% Accuracy and 97.9% AUC/ROC. The QS-LBP approach achieved the highest accuracy of 95.99% at 40X magnification. With the superior performance over many existing methodologies, the research is expected to provide robust and objective tools. This would minimize the pathologists' diagnostic workload and misdiagnosis rates. Above all, it would help improve patient outcomes through early diagnosis. [20].

This study reviews the breast cancer detection using mammography from 1970 to 2025. It explains the progression of mammography technology image processing to deep learning. Research divided the methods into three broad categories namely image processing (IP) approach for contrast enhancement, machine learning (ML) using handcrafted features and deep learning (DL) for automated feature extraction. BreaKHis and DDSM dataset analysis shows that legacy ML models like XGBoost and Random Forest reached accuracies of 97% and 98.14%, respectively. As seen, most deep learning architects especially Convolution Neural Networks (CNNs) achieved even better performances. Some hybrid frameworks achieved 100% in binary classification. The meta-analysis involved in the study showed that machine learning algorithms had AUC at 0.89, while human readers were at 0.85. Although these tools demonstrate significant promise for early diagnosis, further clinical validation is required for reliability and interpretability, the researchers emphasize. In the end, this automation can help with the diagnostic workload and improve the 10-year survival rate of the patient. [21].

The aim of present paper is to present a Computer Aided Diagnosis (CAD) of breast cancer based on mammogram. In this study, a multi-stage methodology is proposed, where the first stage involves the detection Stage of suspected lesions using YOLO-V7. The second stage consists of segmentation Stage of breast masses using Associated-ResUNets. The final stage is pathology classification Stage by modified AlexNet (BreastNet-SVM). The validation of the framework was done with Curated Breast Imaging Subset of Digital Database for Screening Mammography (CBIS-DDSM), a large publicly available dataset. The system performance was excellent with the detection and classification of breast masses achieving 99%. As stated by the researcher, the detection accuracy was 98.5 percent while the overall classification accuracy was 99.16. However, it decreased to 95.39 in the mass segmentation step. Using high-end deep learning and image processing techniques, the innovation can act as a strong tool for doctors to decrease manual error and cost of diagnosis and enhance diagnosis of patients with early detection of tumors. Although the incorporated framework has a very high number of trainable parameters, it is a crucial clinical assist for personalized treatments in breast cancer [22].

This work presents a review of the recent development of deep learning applications in breast cancer histopathology imaging with respect to diagnosis, treatment and prognosis. The study traces the growth of DL architectures like Convolutional Neural Networks (CNNs) for image analysis, Transformers which capture global dependencies, and Generative Adversarial Networks (GANs) for generating high-quality image data. In the diagnostic stage, the models are YOLO and RetinaNet. 97.7% accuracy has been developed for identification and classification of mass locations. Moreover, the paper examines how DL can contribute to personalized treatment based on molecular subtyping and exact staging. Prognostic applications, like DeepGrade for recurrence risk stratification and smuLymphNet for metastasis-free survival prediction via germinal center levels in lymph nodes, are showcased. Although performance sometimes exceeds that of seasoned pathologists, paper raises serious issues like the model's 'black box' problem, high hardware costs, and lack of standardized data-controlled sharing across centers. In the end, the review highlights the importance of ongoing interdisciplinary optimization to achieve successful incorporation of these powerful AI technologies in clinical practice to improve long-term patient survivals [23].

Breast cancer is a major health concern in the world and the incidence has reported to increase across the world. The issue of early and proper diagnosis is vital in improving the survival rates, but conventional means, like mammography, is usually constrained especially when the breast tissue is dense. The latest developments in the sphere of artificial intelligence (AI) and machine learning (ML) have transformed the procedures of breast cancer detection. Literature indicates that deep learning (DL) architectures, specifically Convolutional Neural Networks (CNNs), can deliver very high accuracy on the classification of mammography and ultrasound images. The CNN-based methods have shown a maximum accuracy of 99.96 in mammography and a hundred percent in ultrasound scanning. Besides, XGBoost models based on clinical data also demonstrated high performances with accuracy of reaching 99.12. Combination of imaging data and clinical factors in the hybrid model has further increased the early detection. A new promising technique with a cost of low non-invasivity that has a diagnostic ability between 97% to 100% is also the thermal imaging. Although these have been achieved, data variability and model interpretability are still problematic, with recent studies undergoing the importance of integrated and interpretable AI models to be used in clinical practice. Future studies will focus on multi-modal data combination and further enhancing of model transparency and applicability in practice. [24].

Machine learning and deep learning approaches to breast cancer, especially the use of Convolutional neural networks (CNNs), have improved breast cancer detection. Although more classical models such as SVMs and Random Forests have been utilized, they tend to be less effective with more complicated data patterns and high dimensional traits. The application of CNNs in mammogram analysis has demonstrated a high potential, as these algorithms, on their own, are capable of learning based on features and therefore detect mammograms with great accuracy. The use of CNNs however does not work well in extracting the temporal variation, which plays an important part in tumor growth examination. Recent studies have also incorporated Bi-LSTM networks into CNNs and this means that a model would be able to handle sequential information and improve the future predictions. Further, a pre-trained model, EfficientNet-B0, has also been applied to extract features by transfer learning to enhance the efficiency and accuracy of models. Temporal x spatial models have performed better over these hybrid models which using them to provide a classification of breast cancer have detected up to 99.2 percent accuracy of breast cancer types [25].

Image Processing:

Specifically for deep learning models, data augmentation is a crucial stage in the learning process before image classification. For the purpose of preventing overfitting and enhancing model performance, data augmentation aims to expand the amount and diversity of the training dataset. Overfitting is when a model memorizes the training data because it is an incredibly complex, poor generalization of new data. There are three widely used data augmentation techniques: shearing, flipping & flopping, and cropping. After performing image transformations such as cropping, flipping, and shearing, data augmentation was performed on the original set of images, resulting in an increased dataset size. By giving the machine-learning model a larger, more varied set of training examples, this larger dataset is anticipated to improve its performance. A sheared image is one that has been altered by tilting the original image along the x or y-axis. By cropping, you can create a new training example by choosing a section of the original image. These augmentation procedures improve the amount and variety of the training set, which can help the model generalize to new data and avoid overfitting. Additionally, by generating a more varied set of training examples, data augmentation helps to reduce the impacts of biases and lower the risk of overfitting.

Proposed Model:

The proposed Magnification Invariant Classifier (MIC) is developed using a modified UNET-based encoder-decoder architecture. The encoder path contains repeated convolutional blocks consisting of 3×3 convolution layers followed by batch normalization and ReLU activation functions. Max-pooling layers are employed after each block to reduce spatial dimensions and capture hierarchical features.

Mathematically, convolution operation is represented as:

$$F(i, j) = \Sigma\, I(m, n) \times K(i - m, j - n)$$

Where I represent the input image, K denotes the convolution kernel, and F represents the extracted feature map.

The decoder path utilizes transpose convolution layers for up sampling and concatenates high-resolution features through skip connections. This helps preserve fine-grained spatial information essential for accurate tumor classification.

The magnification invariance is achieved by incorporating multi-scale feature extraction layers capable of learning scale-independent representations from histopathological images.

SoftMax activation is applied in the final classification layer:

$$P(y = i) = \exp(zi)/\Sigma\exp(zj)$$

The model is optimized using the Adam optimizer and sparse categorical cross-entropy loss function.

Magnificent Invariant Classifier is a completely new model of image segmentation which we recommend in this study to diagnose benign and malignant breast cancer. The model is developed based on the UNET architecture and using data augmentation methods to increase data diversity. We conduct data exploration, and split the set into a training set and testing set, whose classes were distributed equally. The model employs convolutional layer and batch normalization, and ReLU activation, and then takes care of feature extraction by max pooling. It uses the convolutional transpose layers to up sample and concatenate feature maps. Features the encoder path gathers high-level features, whereas the decoder path restores the segmentation map. The Adam optimizer is used to optimize the model with a learning rate of 0.001 and uses the loss function emu sparsecategoricalcrossentropy and softmax activation, which is used in classification. Measures such as loss and accuracy are used in monitoring training and early stopping is used in curbing overfitting. We assess the model, which is trained on a validation dataset concerning the accuracy, precision, recall, and F1-score. We also compare the performance of models on benign and malignant images and visualize the predicted segmentation masks against the ground truth masks. Lastly, we then optimize the model by estimating hyperparameters of learning rate, batch size, and dropout with grid search or random search to find the best hyperparameters on particular datasets. Our experimental findings indicate the usefulness and promise of our presented Magnificent Invariant Classifier in segmentation problems regarding image pieces in breast cancer. Explained in figure 1.

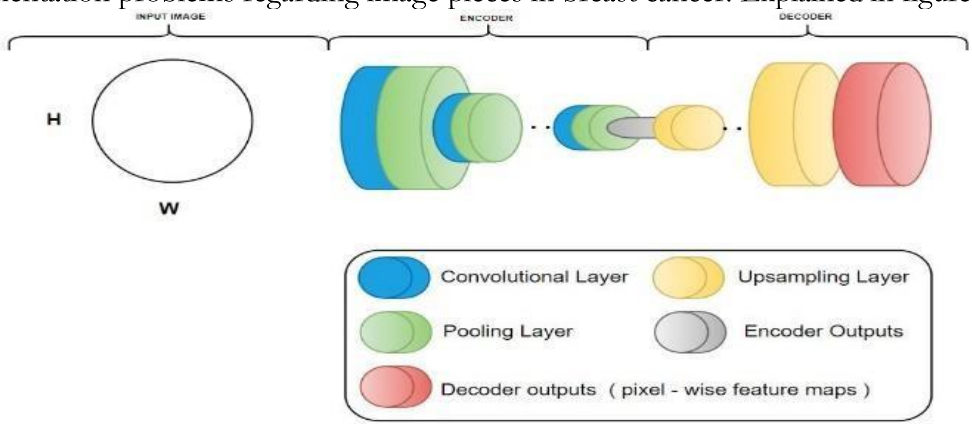

Figure 1. Proposed Model

Methodology:

Research Design:

Objective: The objective of this research is to develop an automated system that classifies breast cancer histopathology images into benign or malignant categories. This classification helps to improve the accuracy and efficiency of breast cancer diagnosis, particularly in resource-constrained settings.

Approach: The research adopts a hybrid deep learning approach, leveraging Convolutional Neural Networks (CNN) for image segmentation and classification tasks. A magnification-invariant encoder-decoder model based on the UNET architecture is proposed to handle histopathological images at different magnification levels (40x and 400x).

Dataset:

BreaKHis Dataset: The dataset used in this study is the BreaKHis dataset, which contains histopathological images of breast cancer, categorized into benign and malignant classes. This dataset includes approximately 9,109 images at multiple magnification levels (40x, 100x, 200x, and 400x).

Data Preprocessing:

Image Augmentation: To prevent overfitting and improve the robustness of the model, data augmentation techniques like rotation, flipping, cropping, and shearing were applied to the dataset. This expanded the diversity of training data and enhanced the model's ability to generalize.

Normalization: All images were resized to a consistent resolution (e.g., 256×256), and pixel values were normalized to the range [0,1].

Model Architecture:

UNET-Based Encoder-Decoder Model: The UNET architecture is chosen because of its ability to capture both local and global features using its symmetric encoder-decoder structure.

The encoder extracts hierarchical features using convolutional layers followed by max-pooling, while the decoder reconstructs the segmentation map using transpose convolutions.

Magnification-Invariant Features: The encoder-decoder is designed to be magnification-invariant, meaning it can handle images from both 40x and 400x magnification levels without losing accuracy or precision.

Loss Function: The sparse categorical cross-entropy loss function is used, and the model is optimized using the Adam optimizer with a learning rate of 0.001.

Training Setup:

Hyperparameters: The model was trained with a batch size of 32, using early stopping to prevent overfitting. Learning rate schedules and dropout were employed to further regularize the model.

Metrics: The model performance was evaluated using standard metrics such as accuracy, precision, recall, F1-score, and area under the curve (AUC).

Evaluation:

Cross-Validation: 5-fold cross-validation was used to ensure that the model's performance is not biased by a specific train-test split.

Confusion Matrix: The confusion matrix was used to evaluate the performance of the model in terms of true positives (TP), false positives (FP), true negatives (TN), and false negatives (FN), which helped calculate additional metrics like precision, recall, and F1-score.

Visualization: Visualizations of the predicted segmentation masks compared to the ground truth were generated to qualitatively assess the model's performance.

Results and Analysis:

Few CNN models, including UNET, UNET++, and VNET, are used in the proposed research. We compare the performance of various models on a BreakHis dataset Accuracy and loss measures are used in the evaluation process. The accuracy of the proposed model, known as the "Magnificent Invariant Classifier," however, outperformed all the models. On the dataset, it attained a remarkable level of accuracy. Additionally, the proposed model's improved performance over the competing models comes from the fact that its loss value is substantially lower than the others. In conclusion, based on the results, the proposed model outperforms the UNET, UNET++, VNET, and RESNET models in terms of accuracy and precision, making it an exceptional contender. We initially use the BreaKHis dataset for testing these built-in models, after which we evaluate each one's accuracy and loss. Then, the proposed model was evaluated on the same dataset, and the accuracy and loss values were compared.

The results of all models on the dataset are presented in Table 1. in the table 1 below:

Table 1. Results of all the models on both of the datasets including the proposed model

Model	Accuracy	Loss
UNET	0.8380	0.4011
UNET++	0.8452	0.3655
VNET	0.8215	0.4441
RESNET	0.8612	0.3331
Magnificent Invariant Classifier	0.9123	0.0876

As shown in the table above, when UNET is applied it gives 83.80% of the data samples tested and the loss value of the model is 0.4011. On UNET++ model achieved an accuracy of 84.52% and a loss value of 0.3655. Then the VNET model achieved 0.8215% accuracy and a loss of 0.4441 afterward the RESNET model achieved an accuracy of 0.8612% and a loss of 0.3331%. Furthermore, as clearly seen in the table the proposed model achieved better accuracy than other CNN models. In summary, The Magnificent Invariant Classifier model, in particular, stands out for its outstanding performance, with 91% accuracy and a significantly lower loss value.

Confusion Matrix:

The confusion matrix, also known as the error matrix, is a matrix that is used to evaluate the effectiveness of the proposed work. While the number of samples (images) that were not correctly predicted and even to the degree of detail as how many of those images were wrongly predicted for which another class is clearly visible from Figure-10 for classes 0 and 1, the Figure shows in detail the number of test images that were present for each class and how many of them were correctly predicted for each class.

The total number of images used during the process of testing belonging to class 0 was 308 and the proposed method accurately recognized 281 images while 27 of them were not recognized. The class 1 representation in the test process was about 511 images while 465 images were correctly recognized. Confusion matrix is explained in figure 2, and Table 2 explains the normalized confusion matrix.

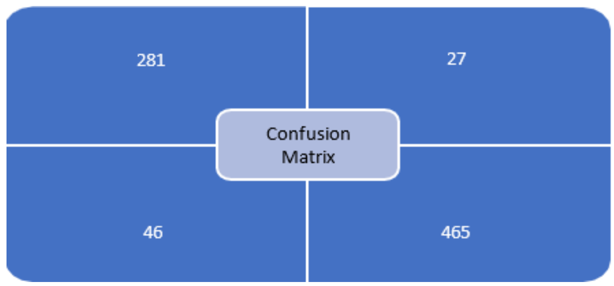

Figure 2. Confusion Matrix

Table 2. Normalized Confusion Matrix 91.09% is the accuracy rate of model.

Actual	Benign	0	0.912338	0.087662
	Malignant	1	0.090020	0.909980
			0	1
	Prediction			

Accuracy of the model:

This section discusses the evaluation metrics used to assess the performance of the proposed model. To evaluate the efficiency of the proposed model. Accuracy, precision, F1_score.

Precision is useful when the cost of a false positive is high. Recall measures the proportion of correct positive predictions that are actually realized. Recall is beneficial when the cost of a false negative is high. The harmonic mean of the two metrics, recall and accuracy, is the F1_score. It is useful for determining how well a binary classification model performs when the distribution of the classes is skewed.

The extent to which a model precisely predicts the outcome is known as precision. The proportion of overall true positives to overall positive forecasts is known as precision. The table 3 below shows the precision, recall, and f1_score for the proposed model:

Table 3. Results of evaluation metrics on the Proposed Model

Dataset	Precision	Recall	F1_score
BreakHis (Benign)	0.8593	0.9123	0.8850
BreakHis (Malignant)	0.9451	0.9099	0.9271

Experiments:

Objective of the Experiment:

The principal objective of the experiments is to assess the accuracy of the Magnificent Invariant Classifier in classifying the image of histopathology of breast cancer as benign or malignant. This experiment not only compares the proposed model with the rest of the state-of-the-art models including UNET, UNET++, VNET and RESNET but also uses BreaKHis dataset. The objective will be to evaluate the performance of all the models in terms of accuracy, precision, recall, F1-score, and loss.

Experimental Setup:

This study was carried out on the BreaKHis dataset that is made up of histopathological images of breast cancer in benign and malignant-categories. The dataset consists of images of different magnifications (40x, 100x, 200x and 400x). To achieve the same homogeneity, the images were also reshaped to 256x256 size and the data augmentation strategies (flipping, cropping, shearing) were used to enhance the number of varied images in the training pool.

Models Evaluated:

UNET: UNET is a popular model of medical image segmentation, based on encoder-decoder design, which finds its uses in medical image segmentation.

UNET++: UNET with additional skip pathways that are introduced to achieve feature reuse and better segmentation.

VNET: 3D variant of UNET, which is used to segment a volumetric image.

RESNET: RESNET is a deep biased network which adds skip connections to solve the vanishing gradient problem and also enable training of deeper networks.

Magnificent Invariant Classifier (Proposed Model): The new improved model that will be based on the UNET architecture as the model that is invariant of magnification with good performance in multiple magnifications.

Performance Metrics:

Accuracy: Both the fractions of correct (benign and malignant) predictions of the model, i.e. the overall effectiveness of the model.

Loss: This gives the performance of the model on the real values. Reduced loss is an indicator of improved performance of the model.

Precision: This is the measure of predicted malignancy to all projected malignancy. Precision is of vitality when false positives are expensive.

Recall: Is a ratio of accurate predictions to actual positive predictions. The latter is especially relevant when the false negatives (missed malignant cases) are at stake.

F1-Score: The harmonic mean of both the precision and the recall, which provides a balanced measure of the model performance particularly where the distribution of different classes is skewed.

Results Comparison:

Magnificent Invariant Classifier were located as the best with the highest accuracy of 91.23 percent, which was the best compared to RESNET (the second-best accuracy of 86.12 percent) and all models. The proposed model also had very low loss (0.0876) thus proving to be more successful.

Comparison through Confusion Matrix:

Further evaluation of the model was done using the confusion matrix which monitors the true positives (TP), false positives (FP), true negatives (TN) and false negatives (FN).

In the case of the benign class (class 0), the model mistakenly correctly classified 281 of the 308 benign images but mistakenly classified as malignant 27.

On 465 of the 511 malignant images of the malignant class (class 1) the model correctly identified and 46 identified as benign.

The total accuracy of the results obtained was 91.09%.

Precision, Recall, and F1-Score:

In the benign group, the model achieved an accuracy of 85.93, recall of 91.23, and F 1-score of 88.50.

In the case of the malignant class, the model was precise: 94.51, recall 90.99 and F1-score was 92.71.

The high precision and recall and F1-scores obtained with both the benign and the malignant classes highlight that the model is highly classified, especially in determining the malignant tumors, which is essential in early detection of cancer.

Analysis of Results:

Magnificent Invariant Classifier is always ranked highest in accuracy and losses in comparison to all other models demonstrating robustness and reliability in classifying histopathology images. It is also especially useful in the clinical practice because of its capability to process images in various magnifications (40x and 400x) without being affected by these magnifications.

The high recall of the malignant cases makes the model to detect the majority of the real malignant tumors thereby minimizing the risks of false negative, a very important scenario in the sphere of medical diagnostics.

The confusion matrix also confirms the performance of model since it demonstrates that most benign and malignant images are correctly categorized and the model experiences fewer misclassifications than other models.

The scores of the F1 show a normal performance, both value and recall play an equal role in the success of the model. This is particularly significant when handling unequal datats such as the one adopted in this research.

Conclusion:

To successfully cure breast cancer within a limited period of time, it should be accurately diagnosed. Thus, accurate identification of benign and malignant tumors could lead to saving of life. The present activity was aimed at augmenting the accuracy of the Break His dataset classification. It consisted of histological photos that were categorized as benign and malignant. This paper will survey the recent findings of machine learning and deep learning-based methods of breast cancer identification and classification. Moreover, the proposed CNN hybrid models simplify the detection and classification of the cancer cells in the histopathological images that may lead to the early diagnoses of breast cancer and an increase in the chances of survival of women. This research has been able to triumph a serious dilemma in breast cancer by designing a new and untainted model that does not put into consideration the degree of magnification. What our research accomplished is the fact that with the help of both 40x and 400x magnifications, we can easily classify breast cancer as benign or malignant and obtain the same and consistent results irrespective of the resolution of input. Imagining a model that is successful in extracting and matching of local features of a specific area at 40x magnification and at the same time a validation of this accuracy against 400x magnification images, this would be a break through to the history of medical imaging and breast cancer research. the work would be ground breaking in the history of breast cancer diagnosis since it has contributed an innovation of an efficient and versatile model that has the capacity of detecting and matching features of a certain area as either benign or malignant on both 40x and 400x magnified images Our study would take us a step closer to transforming the breast cancer diagnostics and eventually transforming the lives of millions of patients around the world by eliminating the difference between the various levels of magnification. The loss value can be minimized more effectively in the future through updating of the loss function better or by means of the change of techniques. Further research may be accomplished later to minimize contextual loss because Contextual loss is currently gaining as a necessary field to conduct research. As far as the problem of the contextual loss is concerned, there is much to be done. Modifying the loss may also aid in alleviating contextual loss. Contextual loss addresses the limitations of traditional pixel- wise loss functions because traditional loss functions do not considered either local or global context information within the image. Alteration of the loss function could be done in several ways, like adding adversarial loss, multi-scale loss, and distance-based loss. Knowledge of the complex tissue architecture and the interactions of abnormalities with the regularly occurring healthy tissues is of great essence when diagnosing breast cancer. The application of the contextual loss can be successfully used to enhance the ability of the model to identify unseen trends and choose significant parts.

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