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DEEP LEARNING-DRIVEN BREAST CANCER HISTOPATHOLOGICAL IMAGE CLASSIFICATION USING OPTIMIZED CNN

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ABSTRACT

Aim: To use the BreaKHis dataset to develop an ideal Convolutional Neural Networks (CNN) based system for autonomously classifying breast histopathology pictures. A number of current breast cancer classification studies have some limitations in terms of the ability to detect malignant tissues consistently, the variability of images and the over fitting that occurs. The suggested CNN approach uses convolutional layers to extract hierarchical characteristics that characterise disease from histopathology pictures in addition to image preprocessing and scaling to solve this problem. Max pooling layers were employed to minimise the dimensionality of pictures so that they could be processed effectively. Flattening or thickening can make it easier for a system to extract effectiv4 features from and classify benign versus malignant tissue. In additio4 the system makes use of early stopping and dropout regularization in order to prevent over fitting; allowing the model to generalize as well. Image enhancement through augmenting images increases the variability in the image during training so that the system is more reliable and stable during the test phase.

Result: In terms of classification capacity, our suggested CNN architecture greatly outperformed the baseline model for the job of classifying histopathological images. Compared to the baseline model, the accuracy of the suggested model was 1.1 percent greater. Additionally, it led to reduced loss function values, indicating improved model convergence. Additionally, the model generated an AUC-ROC value of 0.93, a higher F1-score, fewer false negatives (from 85 to 51), and a higher malignant recall (from 0.92 to 0.95).

Conclusion: The proposed CNN-based system improved the accuracy of classifying breast histopathology images by enhancing the features learned in an image; by decreasing overfitting; by increasing the sensitivity to malignant cells; and by enhancing generalizability. Additionally, further64 study may also help provide clinicians with a better understanding of their decisions through use of XAI (Explainable AI), such as Grad-CAM.

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LIST OF ABBREVIATIONS

H & E	Hematoxylin and Eosin
CNN	Convolutional Neural Network
BreaKHis	Breast Cancer Histopathological Image Classification
GLCM	Gray Level Co-occurrence Matrix
LBP	Local Binary Patterns
HOG	Histogram Oriented Gradient
SVMs	Support Vector Machines
AI	Artificial Intelligence
ResNet	Residual Network
DenseNet	Densely Connected Convolutional Network
WSI	Densely Connected Convolutional Network
HER2	Human Epidermal growth factor Receptor 2
ER	Estrogen Receptor
PR	Progesterone Receptor
Ki-67	Marker of Proliferation Kiel 67
ROC	Receiver Operating Characteristics
AUC	Area Under the Curve
BACH	Breast Cancer Histology
TCGA	The Cancer Genome Atlas
BRCA	BReast CAncer gene
ACROBAT	Automatic Registration of Breast Cancer Tissue
BCNB	Breast Cancer Core-Needle Biopsy
Camleyon	Cancer Metastases in Lymph nodes challenge
GTEx	Genotype-Tissue Expression - Breast
HER2-Warwick	Human Epidermal Growth Factor Receptor 2-Warwick
CPTAC-BRCA	Clinical Proteomic Tumor Analysis Consortium - Breast Invasive Carcinoma
FCH	Fuzzy Color Histogram
ANN	Artificial Neural Network
PNN	Probabilistic Neural Network
DECaf	Deep Convolutional activation features

MIL	Mutiple Instance Learning
SE-ResNet	Squeeze-and-Excitation Residual Network
BHCNet	Breast Cancer Histopathology image classification Network
ERF	Gaussian Error Scheduler
MTCNN	Multi-task Cascaded Convolutional Neural Network
SDCNN	Supertwisting Deep Convolutional Neural Network
IRRCNN	Inception Recurrent, Residual Convolutional Neural Network
FE-BkCapsNet	Feature Enhanced - Breast knowledge Capsule Network
VGG	Visual Geometry Group
GoogleNet	Google Network
InceptionV3	Inception Version 3
InceptionResNetV2	Inception Residual Network Version 2
MobileNet	Mobile Network
EfficientNet	Efficient Network
ACD	Adaptive Color Deconvolution
ICIAR	International Conference on Image Analysis and Recognition
CBAM	Convolutional Blocks with Attention Modules
GAN	Generative Adversarial Network
MCUa	Multi-level Context and Uncertainity aware
LR	Logistic Regression
ML	Machine Learning
ViT	Vision Transformer
DeiT	Data-efficient image Transformers
MCC	Matthews Correlation Coefficient
SPSS	Statistical Package for the Social Sciences
MedCalc	Medical Calculator
ROCR	Receiver Operating Characteristic R
CAD	Computer Assisted Diagnostics
GPU	Graphics Processing Unit
TPU	Tensor Processing Unit
Grad-CAM	Gradient-weighted class activation mapping
NumPy	Numerical Python
Matplotlib	Matlab-style Plotting Library
Scikit	Science Kit

I. INTRODUCTION

Breast cancer is a reasonably prevalent and potentially deadly type of cancer worldwide. In many developing countries, the incidence of breast cancer is rising at an alarming rate. [1]. Breast Cancer identification using histopathology has become a key to classify breast cancer. The tissue pathology provides a lot of information about cells by viewing them with a microscope. Histopathology as the gold standard of identifying benign, in-situ and invasive cancerous tissues uses H&E staining on biopsy images in many clinical environments. However, this method is time consuming and unreliable [2]. Advances in digital pathology, machine learning, deep learning and in particular CNN-based approaches using histopathological datasets (e.g. BreaKHis) have significantly improved automated classification of breast cancers and accuracy of diagnostic decisions [1,3]. Several ways to extract relevant information from an image exist and have been shown to be useful for identifying a pattern in that image. The most common include wavelet transforms, Gabor features, local binary patterns (LBP), histogram of oriented gradients (HOG), and grey level co-occurrence matrix (GLCM) transforms. Each is designed to recognize specific image attributes, i.e., texture, edge location, shape, orientation, and pixel spatial relationships, all of which are critical to the ability to accurately analyze an image. Once these attributes are recognized through feature extraction, they can then be classified using sophisticated machine learning models like support vector machines (SVMs) and convolution neural networks (CNNs). SVMs and CNNs use those extracted features to make predictions about the class of the image being analyzed and thereby provide much greater accuracy and confidence when determining how well an image fits into one particular category [4,5].

Through computer-based analysis of digital images of pathology slides, advances in deep learning and artificial intelligence (AI) have transformed histopathologic diagnostic procedures for breast cancer. Numerous applications of deep learning architectures, especially CNNs (Convolutional Neural Networks), in the detection, segmentation, and classification of breast cancer have been developed as a result of recent advancements in digital pathology, the availability of very large scale data sets, and the computational resources on high performance computers. This is because CNNs have the advantage of automatically extracting all types of information from microscopic tissue images (spatial, structural, and semantic). For example, some common architectures that have shown good results in identifying benign vs. malignant tissue or in multi-classification are ResNet, DenseNet, Inception, transformers and capsule networks. Additionally, transfer learning has reduced the amount of time spent on manual feature extraction and increased diagnostic accuracy by combining attention mechanisms and feature fusion techniques with deep learning [6,7]. Developments in digital pathology, whole-slide imaging (WSI), and high-performance computing systems make it possible to integrate AI-driven approaches with clinical workflow efficiency. Computational pathology utilizing AI is a tool that allows for better reproducible quantification of extracted features from histopathologic images and allows for combination of histopathologic data with genomic, radiographic, and clinical data for applications in precision oncology [7,8]. AI-enhanced approaches have shown high levels of both clinical and technical performance for HER2, ER, PR, and Ki-67 assessments; improved work flow efficiency; and decreased inter-pathologist variation [8,9,10,11]. The number of accurate predictions is often represented by an "accuracy" figure. When determining whether or not a case is cancerous versus non-cancerous, sensitivity and specificity provide vital distinction. Using the area under the curve (AUC), and receiver operating characteristic (ROC) curve, you can assess the performance of your model across different decision thresholds as the model continues to move through the range of possible decision [12]. This research project suggests a CNN-based optimized framework for histopathological image classification to classify images from the BreaKHis dataset in response to the increased need for accuracy and dependability in automated breast cancer diagnosis. This approach seeks to improve the ability to detect malignant tissues as well as the generalized capabilities and classification stability through the use of preprocessing techniques, data augmentation, and deep feature extraction.

2. LITERATURE REVIEW

2.1 Breast Histopathology Datasets

The BreaKHis Collection is amongst the most commonly utilized public datasets in the area of histopathological image analysis in breast cancer. Many studies on computer-assisted diagnostic tools utilize the BreaKHis dataset. The BreaKHis Dataset includes histopathologically imaged malignant and benign breast tumor biopsy samples. Included within the BreaKHis dataset were 5429 malignant biopsy images representing histopathologic classifications, and 2480 benign biopsy images. Fibroadenomas (benign), tubular adenomas (benign), adenoses (benign), and phyllodes tumors (benign) were some examples of benign tumors found in this data set. Examples of malignant tumors include lobular carcinomas, papillary carcinomas, ductal carcinomas, and mucinous carcinomas. Each biopsy sample was photographed at four magnification levels: 40x; 100x; 200x; and 400x. Therefore, researchers can use these images of varying resolutions when testing their classification algorithms. Because they are photographs of biopsies taken by several individuals at multiple magnifications, the BreaKHis dataset represents a challenging yet realistic model upon which to develop an automatic classification tool for identifying breast cancer tumors [13].

Building on a number of publically available breast histopathology datasets that include but are not limited to BreaKHis, there is an increasing number of computational pathology and deep learning based cancer analysis datasets. The majority of the datasets consist of whole slide images (WSIs) stained with H&E. These images can be taken at various magnifications and resolutions, enabling the examination of a variety of tissue morphologies linked to breast cancer. Tumor classification, subtyping, metastasis identification, and biomarker analysis are just a few of the many uses for these datasets. A few examples of datasets include BACH, TCGA-BRCA, ACBROBAT, BCNB, Camelyon, GTEx-Breast, HER2-Warwick, and CPTAC-BRCA. Many datasets include annotations (in addition to the annotation of the tumor area) and clinical information that make them useful for both predictive and diagnostic analysis. The accuracy and ability of a model to generalize may be impacted by several factors including differences in staining techniques; different types of imaging devices; variations in image quality; and artifact issues such as folding of tissue and variability in staining. Despite this, there has been substantial advancements in using Artificial Intelligence (AI) to identify breast cancer due to the large number of breast histopathology datasets now available [14].

2.2 Approaches for Breast Histopathological Classification

2.2.1 Handcrafted Feature-Based Methods

Hand-crafted feature-based methods for breast histopathology image classification rely on discriminatory features from images that are based on texture, color and shape to distinguish between benign and cancerous tissue. Local Binary Patterns (LBPS), Gray-Level Co-occurrence Matrices (glcms) and Fuzzy color histograms (fchs) are just a few of the feature extraction techniques used to find morphological and textural changes in histopathology pictures. After machine learning classifiers such as Support Vector Machines (svms), Artificial Neural Networks (anns) and Probabilistic Neural Networks (pnns) were used to classify the data by using feature selection and optimization techniques many studies applied these technique to enhance efficiency of classification and reduce redundancy of extracted data. Because of combination of various hand generated descriptors in BreaKHis dataset it resulted in more representative feature vectors which improved diagnostic accuracy for classification of breast cancer at different magnification level [15].

In addition to this research, there has been many additional researchers who have advanced the application of manual feature use in the classification of breast histopathology images through new pre-processing and feature extraction strategies, as well as through optimized classification methodologies. Many researchers have also employed an array of image processing strategies to improve picture quality and generate additional tissue attributes that are more discriminatory than those provided by traditional morphological and color-based features; i.e. stain normalization, contrast enhancement, histogram equalization, segmentation of individual cell nuclei, etc. These resulting feature value sets have then been used to both train and classify tumors using machine learning methodologies (e.g., SVMs, Gradient Boosters). Feature reduction and optimization techniques were also employed in some cases to reduce redundancy in feature data and increase the speed at which classifications can be performed. Handcrafted features drastically cut down on computing time and training data needs as compared to machine-derived features. Additionally, they distinguished between benign and malignant tumor tissues with exceptional precision [16].

2.2.2 CNN-Based Approaches

Convolutional Neural Networks (CNN)-based methods are quite successful in classifying images of breast histopathology. They can learn and extract large amounts of complex visual characteristics, eliminating the need for human extraction. Histopathology slide diagnosis is traditionally done by trained pathologists who take a lot of time and make many mistakes; therefore, computer aided diagnostic systems have grown in importance. Several CNN designs, such as AlexNet, DECaf-based CNN models, Multiple Instance Learning (MIL), Hybrid CNNs, and structured deep learning models have demonstrated potential in differentiating between photos of benign and malignant breast cancer. By employing deep feature extraction, pooling strategies, hierarchical voting, regularization approaches, and data augmentation, these designs increased classification accuracy. Researchers developed lightweight CNN architectures to improve upon limitations including overfitting, high parameter complexity, and reliance on manual hyperparameter adjustment. For instance, two novel CNN architectures named SE-ResNet and BHCNet were suggested by researchers. The BHCNet model was created with fewer model parameters than previous models yet had equal to better performance in comparison to previous models when classifying data as either binary or multi-class on the BreaKhis dataset. The researchers were able to create the BHCNet model by creating smaller SE-Resnet module. In addition, the researchers developed an optimization method called the error scheduler (erf). This is an error function that schedules the learning rate of the network during training. The results showed that CNN-based approaches significantly outperformed hand-crafted feature-based approaches [17].

Building on previous CNN (Convolutional Neural Network) techniques, other CNNs were developed such as:
MTCNN
AlexNet-inspired Fusion Models
SDCNN
IRRCNN
These additional CNNs improved breast Histopathological Image Classification for the BreaKHis dataset. They also provided an ability to classify at both image level and patient level with varying degrees of magnification factor and H&E stained tissue type [18]. Further developments in CNN-based breast histopathological image classification have been focused on better feature extraction, multi-class classification and computational efficiency through use of DenseNet based frameworks (e.g., ResNet), Capsule networks and transformer inspired models. The application of techniques such as residual learning, wavelet based texture analysis, Squeeze-And-Excitation Blocks and Data Augmentation to improve spatial and texture representations of features at a variety of magnifications.

Some of these models (ScoreNet; FE-BkCapsNet; Modified-DenseNet) were able to achieve good results when classifying images from the BreaKHis and BCC2015 databases into either two classes or multiple classes. Despite this, there are several limitations with CNN-based diagnostic systems that include high computational costs associated with training, reliance upon pre-trained models, and limited generalizability to new datasets [19].

2.2.3 Transfer Learning Approaches

While conventional CNN architectures such as ResNet, VGG16, VGG19, and Inception were able to learn features effectively, it is a common issue that there is often irrelevant feature extraction or loss of important spatial information and therefore can be computationally complex [20]. The transfer learning method has addressed two main drawbacks of CNNs in photo classification of breast histopathology images: the limited availability of labeled training data and the lengthy time it takes to train CNN architectures. The use of pre-trained models (AlexNet, VGG16, VGG19, GoogLeNet, ResNet50, InceptionV3, InceptionResNetV2, DenseNet, MobileNet, EfficientNet, Xception, etc.) has allowed for the development of optimized models for both the binary and multi-class classification tasks on BreaKHis dataset. Comparative studies show that transfer learning-based frameworks perform well compared to the CNN's trained from the beginning because they can extract the histopathological features that distinguish them from each other at different magnifications. Furthermore, it was found that incorporating the stain normalization technique called adaptive color deconvolution (ACD) into the feature extraction process resulted in a reduction in inter-image staining variability and therefore an improvement in the consistency of the extracted features in H&E stained images [21].

Pre-trained models were able to increase the accuracy of their classifications at a reduced time (training time) and cost (computational resources) by using pre-existing histopathologic feature knowledge that had been obtained in earlier work thanks to transfer learning techniques. The performance of the EfficientNet based architectures were superior to those previously reported due to their similar distribution of number of layers in each architecture, as well as number of filters/units per layer; and therefore, the spatial resolution of input images. The ability to identify different types of breast cancers with transfer learning from a binary classification model to a multi-classification model also improved [22].

Researchers have also used residual networks, squeeze-and-excitation blocks, adaptive spectral composition, soft attention mechanisms, and two stage CNN architectures to represent both spatial and texture features at various magnifications. Recent developments include self-attention-based frameworks such as DEEP_Pachi, which use multiple self-attention heads in conjunction with pre-trained CNN backbones to capture both global and local histopathologic features and achieve high multi-class classification accuracy rates on the BreaKHis and ICIAR2018 datasets [20].

2.2.4 Hybrid and Ensemble Methods

The development of hybrid and ensemble approaches to improve the robustness and prediction power of breast cancer histopathology image categorization has become more popular in recent years. Several comparative studies that looked at the application of various Convolutional Neural Network (CNN) architectures, including AlexNet, VGG16, ResNet, DenseNet, and EfficientNet, found that building ensembles from two or more high-performance single networks significantly improved classification outcomes [23,24]. A variety of more complex frameworks which use a combination of features extracted by using convolutional blocks with attention modules; CBAM) and/or residual and dense blocks; Siamese auto-encoders; GANs; and attention mechanisms to extract multi-level features and enhance their ability to differentiate between classes leverage the complementarity of strengths among different CNN architectures [24].

The multi-level context and uncertainty-aware (MCUa) model developed hierarchical feature extraction from histopathology image patches across various scales using multiple deep neural network architectures for various convolutional neural network (CNN) variants, namely DenseNet-161 and ResNet-152 [25]. The ability to combine the advantages of differing CNN models allows for enhanced feature extraction and reduces each individual network's limitations. Combining feature extracting capabilities of CNN models with those of traditional ML models like SVM and LR allowed the deep learning models to be used as feature extractors, while the traditional ML models performed the final predictions. Inclusion of systematic testing of various model and hyperparameter permutation scenarios along with serialized preprocessing and static augmentation schemes led to faster comparison times, shortened training time and provided the tools needed to quickly identify the most effective configuration for particular application [23].

One of the ensemble techniques that enhanced BreaKHis's multi-class classification performance was soft voting using ViT and DeiT model combinations, which also reduced false negative rates and increased accuracy, precision, recall, and F1-score. ViT and DeiT models provide attention maps that show a localised improvement in the detection of malignant regions in pictures. Additionally, comparative research has shown that in both magnification-dependent and magnification-independent classification tasks, hybrid and ensemble-based techniques considerably outperform many single architecture-based classifications [26].

2.3 Optimization Techniques in Deep Learning Models

Methods to optimize deep learning models are a significant factor in enhancing convergence time, reducing computation overheads, and enabling improved generalization. The most significant factor that will affect whether your Deep Learning model can reach convergence, stability, and high generality is the Hyperparameter Tuning process. As such, many of these parameters (the learning rate, momentum coefficient, amount of decay, dropout rate, batch size, number of epochs, the type of activation function you use, and the strength of either L1 or L2 regularization) are often optimized [27].

Commonly used methods for optimizing parameters:

- **Regularization Methods (L1 & L2):** Regularization Methods provide ways to discourage algorithm from using overly complex solutions. Large parameter values can lead to high complexity.
- **Data Augmentation:** By using various random changes on photos, data augmentation artificially expands the size of the training set. It offers improved capacity for generalization.
- **Model Selection Techniques:** Based on the complexity of a given problem, model selection techniques assist in identifying the best model.
- **Early Stopping:** Early Stopping is one of the most commonly used optimizations. Training ends when there's no improvement in Validation Loss (indicating the model has learned too much about noise in the training data).
- **Gradient-Based Evidence Criteria:** These are some advanced optimization methods that decide whether the computed gradients are still useful for learning or have been degraded due to the finiteness of the training data [28].

The most promising method of all to avoid overfitting has been early stopping. Early stopping involves terminating the training session at a point where the validation error starts increasing. This can help avoid overfitting. In addition, the use of minibatches with SGD helps scale the training session to larger volumes of data [28].

2.4 Evaluation Metrics in Medical Image Classification

The primary purpose of evaluation metrics in analyzing performance of image classification models is to assess their performance in both diagnostic and predictive contexts. Accuracy assesses the total percentage of the data that was successfully classified, sensitivity assesses the classifier's ability to correctly classify all positive cases, and specificity assesses the classifier's ability to correctly classify all negative examples [29,30]. In addition, precision represents the ratio of correct positive predictions to all positive instances predicted. The F1-score provides an efficient way to combine both the recall and the precision by providing an average of both values. In fact, the MCC (Matthew Correlation Coefficient) has also been proven to be one of the best methods to evaluate imbalances in datasets due to its correlation based nature [30].

Classification performance has been compared across a range of thresholds using Receiver Operating Characteristic (ROC) curves. The area under curve (AUC), provides an overall measure of model accuracy. Higher AUC values provide evidence of superior class-discriminatory power between classes. In general, an AUC > 0.80 is taken to be indicative of good enough discrimination to make decisions. Software packages such as SPSS, MedCalc, Stata, and R packages (pROC and ROCR) have all been used to perform ROC-based evaluations [29].

2.5 Limitations and Challenges

Despite the advances in deep learning and computer-assisted diagnostic (CAD) systems for analyzing breast cancer histopathology images, following challenges limit the efficacy and reliability of the model:

- **Imbalanced and Limited Datasets:** Datasets of medical images are usually under-represented with insufficient and imbalanced samples. Thus, they cause an increase of a model's bias toward the most represented class and lead to the decrease of its ability to generalize the data [19,20].
- **Overfitting and Low Robustness:** Deep learning models are very sensitive to the amount of training data available to them so overfitting is expected when they are trained on limited datasets. This limits the results after preprocessing methods, application of transfer learning, variations in magnifying images [31,32].
- **Limitations of Data Augmentation:** Methods of traditional data augmentation such as rotations, crops, and flips may include losses of data and biases. while GAN-based methods improve the balance of datasets, there are also limitations to GAN-based augmentation including unstable training conditions, difficulty in achieving convergence [31,32].
- **Computational Complexities:** Architectures like VGG and DenseNet require significant amounts of computational resources, large amounts of GPU memory and extended periods of training times which complicates the practical implementation of these models in clinical environments [31,32].
- **Segmenting Cancerous Regions:** The task of segmenting (i.e., identifying) cancerous tissue continues to be difficult since individual cancer cells are frequently small, adjacent to each other, and may appear similar to surrounding non-cancerous cells. Larger size and increased resolution of histopathological images increases the computational resources required to process these images for segmentation purposes [32].
- **Inconsistencies in Histopathological Image Analysis:** Variation exists within the quality of stains, light levels, equipment used to capture images and "noise" associated with capturing images that creates inconsistency and complicates automation [32].
- **Lack of Transparency/Interpretability:** Deep learning models are frequently called "black boxes," since it can be quite difficult to comprehend the reasoning behind some decisions. Lack of openness reduces trust in healthcare applications [32].

2.6 Research Gaps and Study Rationale

There are still several research gaps regarding generalisation, interpretability, computing cost, and application to actual clinical practice, despite the fact that numerous deep-learning approaches for breast-cancer picture classification have demonstrated extremely strong performance:

- Being designed based on limited or singular data sources leads to lack of generalizability to other patient demographics, locations, and institutions [33,34,35].
- Many current deep learning architectures represent "black boxes" that offer little to no interpretability regarding the arrival at a particular diagnosis; this may lead clinicians to be less trusting of the AI system, potentially limiting its use clinically [33,34,35].
- The majority of current designs prioritise the model's accuracy in classifying images, but they fall short in providing sufficient resilience metrics when handling noisy, highly variable, or low-quality medical images. [34,35].
- In addition, many studies fail to adequately address class imbalance issues in their analyses; class imbalance can result in lower reliability of detecting cases of malignancy, and ultimately poorer performance of the model in clinical practice [33,34,35].
- Additionally, ensemble and hybrid architectures also suffer from high computational costs associated with training them, as well as high memory requirements during training; both factors contribute to reduced usability of these architectures in real-time and resource-limited clinical settings [33,34,35].
- Overfitting characteristics observed due to reliance on homogenous datasets and limited cross-validation across datasets [33,34,35].
- Limitation to user's ability to deploy the architecture in a scalable manner due to need for large amounts of computational power (i.e., GPUs/TPUs) and preprocessing time [33,34].
- Lacking in flexibility necessary to accommodate differences in imaging protocols, staining conditions, magnifications, and resolution across multiple datasets [33,34,35].
- Most prior research has provided limited attention to developing light-weight AI frameworks for practical clinical use in terms of computation efficiency, edge-deployment feasibility [33,34,35].

In order to fill in the knowledge gaps identified by earlier research, this work developed a deep learning-based system for classifying images of breast histopathology using the BreaKHis database. The system was improved utilizing a number of methodologies.

These methods included preprocessing the input images before they were fed into the network; augmenting the images to account for variability in the images; using dropout to reduce overfitting during network training; using early stopping as an additional method to reduce overfitting; optimizing the parameters of each network layer; improving feature extraction from inputted images; improving robustness against input image variability; and improving the model's overall capacity to generalize beyond the training set. With improved validation performance stability, fewer false negatives, higher recall and F1-scores, and high ROC-AUC values, the overall findings showed the effectiveness of the suggested approach for automated breast cancer classification. Furthermore, by using Explainable AI approaches like Grad-CAM and validation on larger and more varied external databases, this study will offer guidance for future work on multi-class sub-type categorization and an explanation of how the AI is making its decisions.

3. METHODOLOGY

3.1 Dataset collection and description

This study employed the publicly available BreaKHis histopathology breast cancer dataset. [13]. The Kaggle platform offers microscopic images of breast tissue stained with haematoxylin and eosin (H&E) that were classified as benign or malignant tumors. Several pathology types were included in the dataset at four different magnifications: 40X, 100X, 200X, and 400X.
7,909 RGB pictures of benign and malignant tumors, each with unique types and histological characteristics, were included in the collection. Adenosis, fibroadenoma, phyllodes tumor and tubular adenoma are examples of benign categories. Papillary carcinoma, mucinous carcinoma, ductal carcinoma, and lobular carcinoma are malignant tumor categories. Although there is a large number of tumor subtypes available within this data set, it was classified (benign versus malignant) by one or the other histopathologic image classifications. The images included in the data set have already been categorized; therefore, they may be used to classify images using supervised deep-learning based methods

3.2 Data preprocessing and splitting

Image processing techniques were applied to all histopathological images to ensure that the input data would be standardized in terms of their size and could be efficiently computed [36]. The input images were resized to 128x128 and then standardized prior to model usage. For evaluating the proposed CNN model and its accuracy, the processed images were randomly divided into a training group or test group after this image processing step was completed.

3.3 Convolutional Neural Network (CNN) Framework

To ascertain if a particular histological image is categorized as benign or malignant, a sequential CNN model was developed [37]. The proposed CNN architecture consists of multiple successive convolutional layers. Following each convolutional layer, there is a max-pooling operation. After the final pooling layer, a flatten layer follows which leads into a fully connected layer (with an extremely large number of neurons), then a dropout regularization layer, and finally a single sigmoid activation output layer produces the probability distribution over all possible class labels.

3.4 Training and optimizing model

The Binary Cross Entropy Loss Function and the Adam optimizer were used to train the CNN model. [38].
To increase the model's overall generality and lessen the likelihood of overfitting, augmentation techniques (rotation, flip, zoom, and shift) were applied to each image during training.

In addition to these two overfitting reduction strategies, dropout regularization and early stopping procedures are employed to improve the training process's dependability.

3.5 Performance evaluation

The accuracy, loss, confusion matrix, precision, recall, F1-score, receiver operating characteristic (ROC) curve, and area under the curve (AUC) of the trained CNN model were evaluated [12].

Loss revealed what was being lost as the model attempted to make better predictions, while accuracy assessed how effectively the model could identify the photos. Confusion matrices were used for an image by image assessment of how many samples were correctly classified. Precision and Recall determined whether or not there was enough predictive power when a sample is classified as one type over another. The ROC-AUC measure determined how much better the model performed compared to a random classifier.

3.6 Software and computational environments

The Python programming language was used to carry out the current study in a Google Colaboratory (Google Colab) setting. The CNN model was created and trained using the TensorFlow [39] and Keras [40] frameworks. Libraries such as NumPy and Matplotlib were applied to perform numerical computations, visualizations and to provide graphs. Finally, library such as Scikit-learn [41] was used for evaluating performance of the model through metrics of Confusion Matrix, Classification Report, ROC Curve, and AUC Analysis.

4. RESULTS AND DISCUSSION

4.1 Dataset preparation and CNN development analysis

The pre-processing results showed that the histopathology image database was normalized appropriately before being trained with CNNs. Images were then resized so that all were 128 x 128 pixels. This resulted in a 7909x128x128x3 matrix representing the images, and a 7909x1 vector representing the labels.

Tissue histology pictures of benign and malignant breast tumors made up the processed data set. Each type of disease had several subgroups, including adenosis, fibroadenoma, phyllodes tumor, tubular adenoma, ductal carcinoma, lobular carcinoma, mucinous carcinoma, and papillary carcinoma.

In addition to helping to establish a uniform format for comparing photos in the database, the normalization method employed in the pre-processing significantly decreased the variability among dimensions in the various photographs. Additionally, the differences in cellular shape, tissue texture, and staining intensity were normalized, giving the CNN a more uniform environment to learn from.

4.2 Architecture examination of the CNN model

The CNN that was designed had a clear hierarchical approach in extracting all levels of features in the process of classifying images of breast histopathology. The CNN included several convolutional layers (convolution), max pooling layers, flatten layers, thick layers, dropout layers, and sigmoid output layers to progressively learn tissue properties. When features are retrieved in the first convolutional layer, the image's dimensions change from 128x128x3 (the original RGB colour space) to 126x126x32. To do this, the original image is subjected to a 3x3 convolution operation without padding.

At this stage the 32 feature maps represented important low level characteristic of breast histopathology including boundary lines of tissues, edge lines of nucleus, variation of textures, and microscopic morphologic structures. Each subsequent max pool layer reduces the size of the feature maps. The result is that computations will be reduced but a significant amount of data will remain for the feature extraction process as to represent much of what is most relevant about the image. With increased depth in the architecture, came an increase in the number of convolutional filters used in each successive layer. Specifically, the first layer has 32 filters, the second layer has 64 filters and the third layer has 128 filters in comparison to benign or malignant breast disease, this growth made it possible to depict increasingly complicated tissue.

Ultimately, these two-dimensional feature maps were converted into one-dimensional arrays with 25088 feature extracts using the flatten layer. The final set of fully connected dense layers was then fed these feature extracts to carry out the final classification.

The use of dropout regularization helped improve the stability of the model and prevent over-fitting during training. The final sigmoid activation function produced probability values representing whether a portion of tissue represented either benign or malignant tissue (Table1). Overall, the total number of trainable parameters within the CNN design totaled around 3.3 million, showing a high degree of learning capacity for automatically classifying images of breast histopathology.

4.3 Baseline CNN model performance

The baseline CNN model demonstrated good ability to learn from breast histopathology images. Training accuracy progressed steadily from approximately 77.8 percent at the first epoch to approximately 84.6 percent at the last epoch. Validation accuracy, like training accuracy, also improved — from approximately 83.1 percent to approximately 87.6 percent — suggesting that the CNN model had a reasonable capacity for generalizing the trained models to previously unseen test samples. While some minor variations were noticed in validation accuracy in middle-epochs, overall trends revealed a consistent pattern of learning. Minor variations in validation accuracy in middle-epochs notwithstanding, the general upward trend indicated that the model exhibited consistent learning behavior (Fig.1).
The model had learned the important histopathologic characteristics associated with benign and malignant breast tissue, as evidenced by the steady increases in validation accuracy. Additionally, the slight discrepancy between training and validation accuracy implies that severe overfitting did not occur during the baseline training.
The CNN model continues to minimize prediction error throughout all epochs, as evidenced by the baseline model loss graph's progressive decline in both training and validation loss. While there were certain number of fluctuations in validation loss indicating a slight amount of instability in generalization performance, overall decreases in loss confirmed that the CNN model is able to improve classification performance through continuous reduction of error in prediction with each subsequent epoch (Fig.2).

The baseline model's confusion matrix provided more evidence of its categorization skills.
The model correctly identified 1001 cancer tissue samples and 385 benign tissue samples during evaluation using this confusion matrix.

Nevertheless, the model incorrectly identified 85 malignant tissue samples as benign and 111 benign tissue samples as malignant. (Fig.3).
These misclassifications represent false negatives (i.e., undetected cancers) — a critical concern in clinical practice since delayed or failed diagnoses often result in undue delays and/or inappropriate treatments for patients diagnosed late due to missed cancers.

Additionally, the classification report illustrated that the CNN model possesses very high levels of precision and recall for detecting malignant tissue.
A recall value of 0.92 for malignant tissue illustrated that most cancerous tissue samples were detected by the CNN model. Similarly, a precision level of 0.90 for malignant tissue illustrated a reliable ability to predict cancer with minimal false cancer predictions (Table 2).

Thus, an approximate overall accuracy of 88% demonstrated strong performance for use as an automated classifier for breast histopathology images.

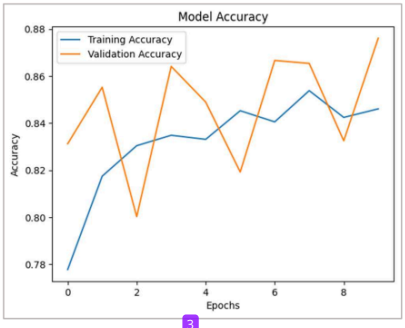

Fig.1. Accuracy curve for training and validating the baseline CNN model

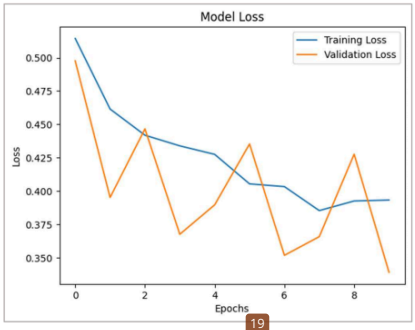

Fig.2. Loss curve for training and validation of the optimized CNN model

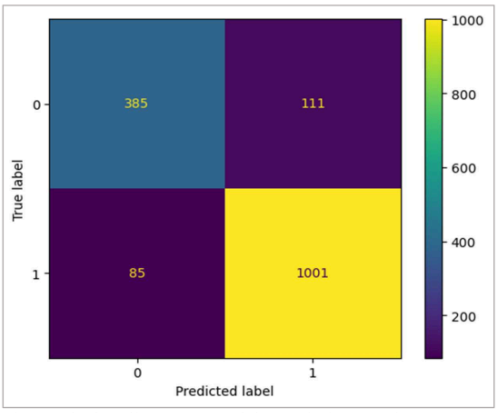

Fig.3.: The baseline CNN model's confusion matrix displaying tissue samples; benign (385), malignant (1001), false negative (85), and false positive (111)

4.4 Performance Improvement using optimization techniques

To increase the models' generalizability, lower the likelihood of overfitting, and produce a model that would function well on test data, a number of optimizations (augmentation, dropout, and early stopping) were combined.

Augmentation created an artificial increase in training variability using transformations of the original histopathological images generated at random during each training iteration. These transformations included rotation, flip, zoom, shift, etc. By doing this, the model learned to represent all images more generally and has a higher level of robustness to different types of image variations.

Early Stopping was implemented to observe whether there was still room for additional improvements in Validation Loss and terminated the training once no improvements were found. All of these optimizations resulted in a model that had greater stability and predictive performance.
The accuracy graph comparing the Baseline Model and Optimized Model shows that the model's classification performance was significantly enhanced following optimization. The modified model demonstrated significantly smoother convergence behavior and higher validation accuracy, as was already mentioned. While validation accuracy increased from about 83.2 percent to about 88.7 percent, training accuracy started at around 84.9 percent and finished at about 86.2 percent. It is reasonable to conclude that the model has significantly improved at capturing the characteristics found in histopathologic images following optimization, as evidenced by the gains in both training and validation accuracy. (Fig.4).

It is also clear based on the loss graph comparing the Baseline Model and Optimized Model that the loss values are lower for the optimized model. The loss for training decreased from approximately 0.38 to approximately 0.33 while the loss for validation decreased from approximately 0.38 to approximately 0.29. The decrease in loss values for validation indicated that the optimization techniques made the model more stable and reduced prediction error for new/unseen testing samples (Fig.5).
Lastly, there was even more increase in the classification skills, as the confusion matrix for the optimized model illustrates. The optimized model correctly identified 368 benign tissue samples and 1,035 malignant tissue samples. Additionally, the number of false negatives decreased significantly from 85 in the Baseline Model to 51 after optimization (Fig.6).

The reduction in false negatives was one of the study's biggest gains. A lower number of false negatives indicates a positive impact on clinical breast cancer diagnosis because patients with untreated cancer will have negative effects on their treatment and survival rates. False negatives happen when a sample containing malignant cells is mistakenly identified as healthy.

While there was an increase in false positives, which were samples identified as malignant but do not contain malignant tissue; the improvement in detection of malignant tissue was considered to be more clinically relevant. The optimized classification report shows that malignant recall was 0.95 or 95%. Recall refers to how many true positives were actually detected out of all true positives. Therefore, malignant recall of 0.95 indicates a high degree of sensitivity of the CNN in detecting cancerous tissues (Table 3).

Finally, looking at the improved model accuracy of approximately 89%, it became evident that augmentation, dropout regularization, and early stopping did contribute positively to the classification performance and model generalization.

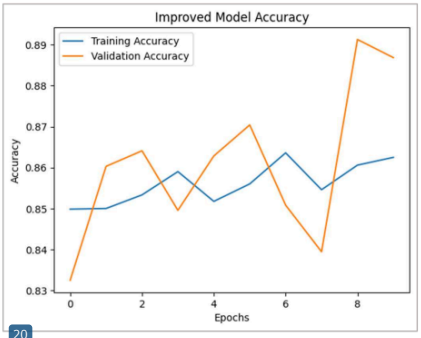

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Fig.4. Accuracy curve for training and validating the optimized CNN model

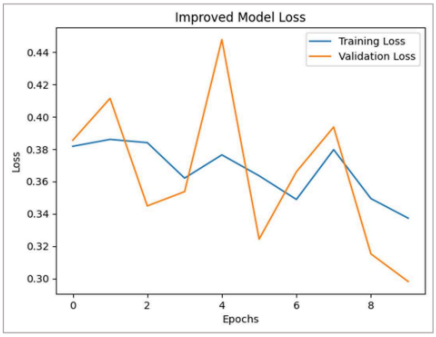

Fig.5. Loss curve for training and validation of the optimized CNN model

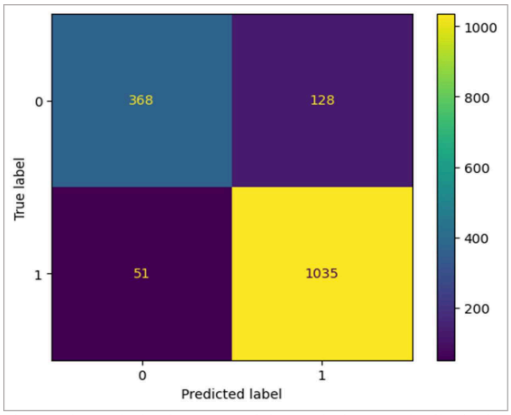

Fig.6.: The optimized CNN model's confusion matrix displaying tissue samples; benign (368), malignant (1035), false negative (51), and false positive (128)

4.5 ROC-AUC analysis

The Receiver Operating Characteristic (ROC) Curve was utilized as an alternative way to measure whether or not the optimized CNN model had effectively differentiated between benign and malign classes. The ROC curve demonstrated that the two classes were clearly defined from each other based upon the fact that the area underneath the curve existed in the top left quadrant of the chart. In addition, it has been determined through this evaluation that the optimized CNN model generated a very high Area Under Curve (AUC) score of approximately 0.93 (Fig.7).

It is widely accepted in medical image classification literature that an AUC score greater than 0.9 signifies that predictions made using this approach are extremely reliable [42]. Furthermore, the high AUC value demonstrated that the created CNN model had good sensitivity and specificity when categorizing histological images of breast cancer.

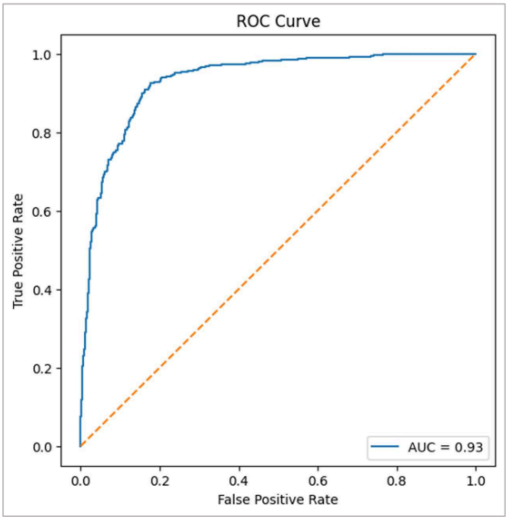

Fig.7. Receiver Operating Characteristic (ROC) curve displaying the optimized CNN model's classification performance with AUC score

Table 1: The Proposed Convolutional Neural Network's Detailed Architectural Overview

Layer (type)	Output Shape	Param #
conv2d (Conv2D)	(None, 126, 126, 32)	896
max_pooling2d (MaxPooling2D)	(None, 63, 63, 32)	0
conv2d_1 (Conv2D)	(None, 61, 61, 64)	18,496
max_pooling2d_1 (MaxPooling2D)	(None, 30, 30, 64)	0
conv2d_2 (Conv2D)	(None, 28, 28, 128)	73,856
max_pooling2d_2 (MaxPooling2D)	(None, 14, 14, 128)	0
flatten (Flatten)	(None, 25088)	0
dense (Dense)	(None, 128)	3,211,392
dropout (Dropout)	(None, 128)	0
dense_1 (Dense)	(None, 1)	129

Table 2. The baseline CNN model's classification performance report

Class	Precision	Recall	f1-score
Benign (0)	0.82	0.78	0.80
Malignant (1)	0.90	0.92	0.91

Table 3. The optimized CNN model's classification performance report

Class	Precision	Recall	f1-score
Benign (0)	0.88	0.74	0.80
Malignant (1)	0.89	0.95	0.92

5. Conclusion

Using the BreaKHis database, this study created a framework for optimizing a CNN-based system to categorise images of breast histopathology as benign or malignant. This approach used dropout regularization to avoid model over-fitting and early stopping to make sure the classifier did not become overly stable during training, in addition to a number of picture augmentations and usual pre-processing techniques.

Results demonstrated that the proposed method was able to demonstrate improvements in validation accuracy from a value of approx. 87.6 percent compared to the baseline to approx. 88.7 percent. Validation loss decreased as well. False negatives were decreased from 85 to 51 and malignant recall was increased from 0.92 to 0.95 which indicated the ability to detect malignant tissue more accurately. The proposed method was capable of achieving higher values for both F1 scores and high values for ROC-AUC scores at 0.93. These two metrics are indicative of high levels of classification and better generalizability. The proposed technique also provides a computationally viable way to handle pathological feature extraction and image fluctuation. Thus, our research demonstrates that deep learning-based automated systems can effectively and efficiently classify images of breast cancer histology.

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