Breast Cancer Classification using Histopathology Images

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Abstract— Breast cancer remains one of the main female cancer murderers globally. Correct and timely diagnosis is of extremely crucial importance to successful treatment and favorable prognosis. Histopathology imaging, i.e., cancer diagnosis gold standard, provides tissue morphology at high resolution needed in detecting malignancy. Yet imaging visioning takes time, can be subject to inter-observer variability, and needs skilled pathologists. This research suggests a deep learning model to classify breast cancer from histopathology images automatically. The model employs convolutional neural networks (CNNs) to hierarchically learn features to determine if the tissue sample is benign or malignant. The model was tested and trained using public datasets, such as the BreakHis dataset. The study is useful since it suggests the potential of AI-based histopathological diagnosis in facilitating clinical decision-making and optimizing diagnostic yield in the management of breast cancer. KEYWORDS - Breast Cancer, Histopathology Images, Deep Learning, Image Classification, Convolutional Neural Networks (CNN), ResNet50, Medical Imaging, Computer-Aided Diagnosis, Tumor Detection, Digital Pathology, Machine Learning.

1. INTRODUCTION

A large number of women worldwide are influenced by breast cancer, one of the most common and fatal diseases. One of the main causes of cancer mortality, increased survival chances and successful treatment rely on early diagnosis and precise identification. Conventional detection techniques force pathologists to examine histopathological images microscopically under the microscope, which is extremely time-consuming and prone to human errors. The image analysis problem in medicine has been completely transformed by the emergence of deep learning algorithms and artificial intelligence (AI), i.e., Convolutional Neural Networks (CNNs), due to their precision in classifying. In order to support pathologists in making more accurate diagnoses, the problem will use CNN-based models for the auto-classification of histopathology images into the malignant and benign classes.

2. LITERATURE REVIEW

2.1 Ensemble DL for Breast Cancer Subtype & Invasiveness

In the paper [1], Balasubramanian et al.'s (2024) article includes an ensemble deep learning framework for breast cancer subtype diagnosis and invasiveness prediction based on whole slide histopathology images. With the BACH and BreakHis databases, the authors stack VGG16 and ResNet models using an image patching method to efficiently handle high-resolution slides. Their ensemble approach performed extremely well with a 95.31% validation accuracy on BACH and 98.43% on BreakHis. The article highlights the potential of ensemble learning to enhance diagnostic robustness and accuracy, thus making it a great choice for classification based on histopathology as a benchmark.

2.2 Transfer ResNet + Attention for Breast Cancer Classification

The paper [2] reviews Sani et al. (2024), the authors propose a novel approach with enhanced supervised contrastive learning for breast cancer histopathology image classification. The approach leverages both labeled samples and domain-specifically augmented ones and combines self-supervised pretraining and two-stage supervised contrastive loss approach. The process increases the generalizability and robustness of the model, especially when it possesses limited labeled samples. Apart from that, it also includes stain-specific enhancement process (HED) and a side task to help with color variability sensitivity. The model achieved a better 93.63% accuracy on the BreakHis dataset, which is a testament to its capacity in learning discriminative image representation for medical diagnosis.

2.3 Breast Cancer Classification via Contrastive Learning

In Sani et al. (2024), the authors introduce a new method with modified supervised contrastive learning for breast cancer histopathology image classification. The approach utilizes both labeled samples and domain-specific augmentations, and it integrates self-supervised pretraining with a two-stage supervised contrastive loss approach. The method enhances the robustness and generalizability of the model, particularly when there are limited labeled samples. Moreover, it has stain-specific augmentation process (HED) and a side task to assist in color variability sensitivity. The model had an excellent 93.63% accuracy on the BreakHis dataset, which is a testament to its performance in learning discriminative image representation for medical diagnosis.

3. IMPLEMENTATION

3.1 Dataset

We used, for this investigation, the BreakHis (Breast Cancer Histopathological Image Classification) data set available freely, consisting of 6,888 microscopic breast tumor tissue images from different patients. These images were acquired with a factor of magnification of 40x, 100x, 200x, and 400x, and they fall into benign and malignant tumor classes, benign class having subclassification into two types of histologies and malignant class having subclassification into four types. All images are stored in RGB format. The dataset is a rich and diverse collection of real-world histopathology images, enabling strong training and testing of deep learning models for breast cancer diagnosis. In our configuration, the dataset was split into training, validation, and test sets with patient-level separation to prevent data leakage and ensure model evaluation integrity. The dataset contains three folders of images: one train folder containing 4,819 images, one test folder containing 1,030 images, and one validation folder containing 1,039 images.

3.2 Pre-processing

The unprocessed histopathological images of the BreakHis dataset were first examined for quality and uniformity. The images were resized to 224×224 pixels to conform to the input size requirement of typical deep learning architectures. Pixel intensity normalization was applied to normalize all pixel values to the interval [0, 1], which allows for quicker convergence of training. Severe data augmentation techniques were applied in a bid to address class imbalance and add variability to the training set. These comprised random vertical and horizontal flipping, rotation (±20°), zooming (to 20%), contrast adjustment, and injection of Gaussian noise. Besides enhancing generalizability, it also simulated genuine variability of histopathological appearances.

3.3 Feature Extraction

3.3.1 Benign

Benign Tumors: Cancer tissues in benign form are typically described by orderly and organized tissue patterns, which can be easily differentiated from the invasive and disorganized pattern of malignant cancer. Benign tumor cells are quite akin to normal tissue and are regular in arrangement with clear-cut boundaries. Tissue structure is well organized with minimal tissue distortion, and cells are usually round or oval with well-defined and smooth boundaries. In terms of feature extraction, CNNs, VGG16, and ResNet50 will learn to identify such smooth patterns. Convolutional layers will search for smooth cell boundaries, equal spacings between cells, and equal shapes. Earlier layers will learn to identify primitive features such as edges and textures and deeper layers to learn more high-level structures such as well-defined tissue borders and nuclear feature consistency.

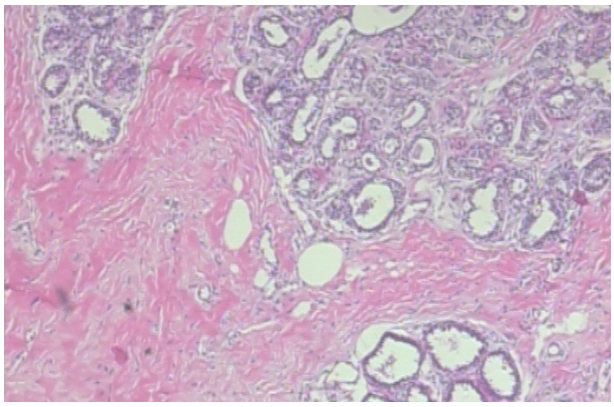

Fig 1. Benign Tumor

In benign tumors, there is minimal mitotic activity, i.e., fewer dividing cells. The models will quantify features that describe such minimal mitotic activity, e.g., no abnormal cell division and minimum occurrence of mitotic figures. These benign tissues will also be more uniform in texture than the malignant tissues with minimal pixel intensity variation. By pooling and convolution, deep learning models will capture these texture features wherein the texture would be unbroken and there would be smooth transitions between varying regions of the tissue. Overall, the models would be eager to realize the orderliness and symmetry of the tissue, like organized cells and even distribution characteristic of benign growth.

Of the benign tumors of the breast, two of the most common encountered histopathological conditions with their characteristic clinical, imaging, and pathological presentation are adenosis and fibroadenoma. Adenosis is a benign proliferative tumor of the breast that is an abnormally high number of acini within the breast lobules. It may present in multiple forms like simple adenosis, sclerosing adenosis, apocrine adenosis, and the less common microglandular adenosis. Of interest, sclerosing adenosis may be imitated by invasive carcinoma on imaging due to the presence of architectural disruption and extreme stromal fibrosis. Microscopically, adenosis maintains the double epithelium-myoeplithelium layer but in sclerosing forms may have compressed acini and infiltrative types. Clinically, adenosis is usually asymptomatic or tender breast or lump with intermediate risk for subsequent malignancy, particularly in proliferative forms. Imaging characteristics are mammographic microcalcifications or distortion and hypoechoic areas with posterior shadowing on US. It is usually diagnosed on core needle biopsy, and it is treated conservatively with follow-up in the absence of atypical features.

Fibroadenoma is also a biphasic tumor of epithelial and stromal elements, which is found mainly in women between 15 and 35 years of age. It is characteristically a firm, nontender, freely mobile breast mass, sometimes called a "breast mouse" due to its unusual mobility. Variants of fibroadenoma are simple fibroadenoma, complex fibroadenoma (with sclerosis adenosis or calcification in epithelium), and juvenile or giant fibroadenoma, which may show accelerated growth in adolescent patients. Fibroadenomas on imaging studies are usually well-circumscribed, oval, hypoechoic lesions on ultrasound and homogeneously enhancing masses on MRI. Calcifications also occur in mature lesions. Fibroadenomas histologically consist of an proliferation of ducts with

interspersed stroma and fibrous tissue with an organized pattern. Malignant potential is, however, so far out in the typical fibroadenoma that most clinicians ignore the possibility. Nevertheless, the fibroadenomas of complex characteristics would be of intermediate risk, especially in the event of proliferative breast disease. Ranging from irregular imaging and observation for asymptomatic, stable lesions, treatment could involve resection in the setting of aggressive growth, symptomatic presentation, or atypical imaging features.

3.3.2 Malignant

Malignant Tumors: In contrast to benign tumors, malignant tumors contain a much less organized and unstructured tissue framework. The histological hallmarks of malignancy are irregular borders of tissue, pleomorphic nuclei (where size and shape of the nuclei show very wide variations), and prominent mitotic activity. Malignant cells typically are larger in size, more asymmetrical and irregular in contour, and bear abnormal nuclear morphology. The tissue structure in cancerous tumors is generally lost as a result of uncontrolled cell proliferation, with cells invading nearby tissue. Such disorganization complicates the categorization of cancerous tumors but also offers unique features for deep learning algorithms to learn.

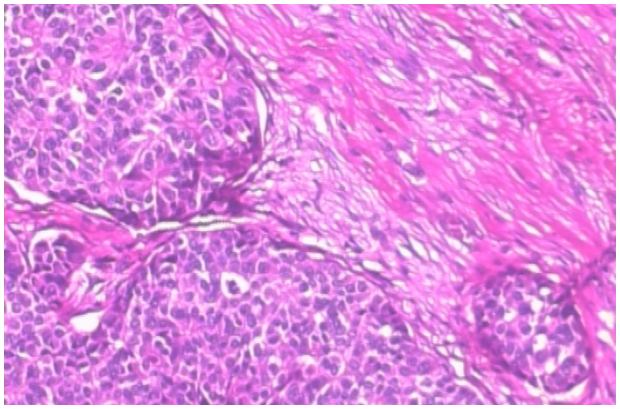

Fig 2. Malignant Tumor

In terms of feature extraction, CNNs, VGG16, and ResNet50 will seek out the chaotic patterns in cancerous tissues. Convolutional layers would be trained to identify jagged cell edges, overlapping cells, and irregular borders of cells that all indicate invasive patterns. As the network penetrates deeper, more abstract representations would be identified by the models, including irregular mitotic figures or abnormal patterns of cell divisions, which are unique to malignancies. The bottom layers of VGG16 and ResNet50 will be employed in order to identify abnormal patterns of cells and abnormal architecture of the tissue that will differentiate malignant from benign tissues.

Malignant tumors also exhibit hypercellularity and cellular disarray, which makes the tissue crowded and irregular. The models will identify tissue regions with tight cells, where intercellular space is smaller, and abnormal patterns of cell growth are observed. In addition, cancerous tissue is more heterogeneous in texture, i.e., with greater pixel intensity change due to the occurrence of abnormalities like necrosis, bleeding, or other diseases. CNNs, VGG16, and ResNet50 will recognize these textural features by examining pixel intensity changes, observing the more rugged, changing textures of cancerous tissue. These models will be constructed to track such unusual growth patterns, increased cell density, and increased texture complexities that are typical of malignancy.

Breast cancer is a heterogeneous entity comprising several histological subtypes with morphological, molecular, and clinical characteristics. With the presentation of beast cancers, the IDC subtype occurs in about 70-80% of instances. It evolves from terminal ducts and lobules and invades nearby stromal tissues. Histologically, the tumor forms irregular glandular or duct-like structures that invade the breast parenchyma, usually interspersed with a desmoplastic stromal reaction. Clinically, it presents as a palpable mass or mammographic abnormality, i.e., spiculated lesions or microcalcifications.

Invasive lobular carcinoma represents about 10-15% of breast carcinomas, and it arises from the lobular epithelium. Nuclear features are small, infiltrating in single-file linear cords due to loss of E-cadherin expression with resultant disruption in cell adhesion. ILC can be harder to detect on imaging since it might not create a classic mass, but when it is bilateral and multicentric, the possibility is greater. Although it is diffuse in nature, ILC has the same long-term survival as IDC but can present at a more advanced stage. Mucinous carcinoma, or colloid carcinoma, is a rare breast cancer, representing 1–4% of all breast carcinomas, and is distinguished by the presence of extracellular mucin

3.4 Model Architecture

In this project, we designed and tested a custom Convolutional Neural Network (CNN) and different transfer learning architectures to appropriately label breast cancer histopathology images. The proposed models were intended to learn interesting features from input images and optimize classification performance by utilizing custom networks and robust pre-trained models.

3.4.1 CNN Architecture:

The application-specific CNN was designed for histopathology images, which can extract hierarchical features from low-level edges and textures to high-level pathological patterns. The architecture starts with an input layer that takes RGB images of shape. The core of the model is four convolutional blocks with a Conv2D layer having increasingly large filter sizes and a constant kernel size of 3×3. This is followed by Batch Normalization for normalization of learning and ReLU activation to add non-linearity. MaxPooling2D of pool size 2×2 is used to downsample spatial dimensions. The model, subsequent to the convolutional blocks, employs a Flatten layer to convert the feature maps into a one-dimensional vector. This is subsequently followed by two fully connected layers of 512 neurons, respectively, followed by ReLU activation and a Dropout layer (rate = 0.5) in an attempt to avoid overfitting. Lastly, the output layer has six neurons, two for benign and four for malignant, and a Softmax activation to output a probability distribution when classifying. The aforementioned custom architecture was created moderately deep to allow it to find a compromise between computational expense and that of extracting significant features, thereby making it adequate to be used with datasets of moderate size like BreakHis.

3.4.2 Transfer Learning Architectures:

To enhance performance and surpass the limitation of having limited labeled data, transfer learning was employed using pre-trained models. The pre-trained models trained on large-data sets such as ImageNet were first fine-tuned to learn from histopathological images. The VGG16, a 16-layer network that is efficient and easy, was used with its final convolutional base not updated during the early stages of training. The deeper layers were then fine-tuned. A custom classifier head was added, comprising Global Average Pooling, Dense layers (512 units with ReLU activation), Dropout (0.5), and finally a Dense layer with 6 neurons (Softmax) to achieve the classification operation. The ResNet50 model, a 50-layer residual network, was utilized owing to its ability to solve vanishing gradient problems using identity shortcut connections. The convolutional blocks were kept, and a new classifier was introduced, consisting of Global Average Pooling, then Dense layers (256 units, ReLU), Dropout (0.4), then a Dense output layer (6 neurons, Softmax).

3.5 Proposed Model

In this paper, we introduce a deep learning framework with a Convolutional Neural Network (CNN) architecture for computer-aided diagnosis of breast cancer from histopathology images. The CNN architecture is used due to its established ability to learn spatial hierarchies and visual patterns from medical images. In contrast to conventional machine learning methods that heavily depend on engineered features, CNNs can automatically learn high-level feature representations from pixel-level input data and are therefore well-suited for analysis of histological images where cellular texture and morphological details at the high-resolution level play an essential role in distinguishing between benign and malignant tissue samples.

The suggested CNN model starts with an input layer that takes RGB histopathology images already resized to a fixed resolution of 224×224×3 pixels to maintain consistency during training. Inputs are normalized by scaling pixel values to the interval [0, 1], which stabilizes and speeds up training. The network architecture consists of a sequence of convolutional blocks, each consisting of a convolutional layer, a Rectified Linear Unit (ReLU) activation function, and a max-pooling layer. The convolutional layers have kernel sizes of 3×3 with growing numbers of filters (e.g., 64, 128 and 256) in the layers to learn low-level to high-level features like edges, textures, nuclei shape, glandular structures, and other cancer-related morphological features in an increasing manner.

To improve model generalization and limit the possibility of overfitting, dropout layers are added after some layers with dropout rates of between 0.25 and 0.5, where a percentage of neurons are randomly dropped during training. This forces the model to learn more robust and distributed features. Batch normalization can also be used to normalize training by normalizing the activation of the prior layer at every batch, leading to better convergence and model performance.

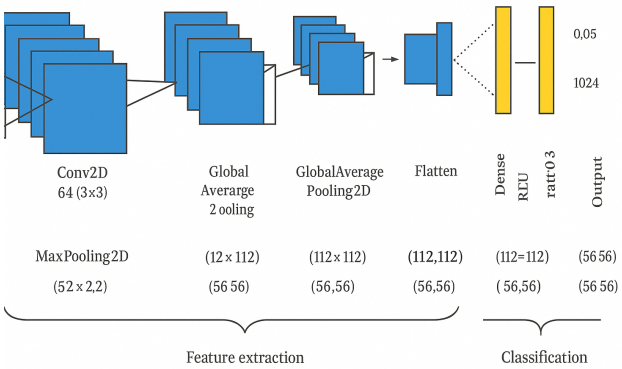

Fig 3. Convolution Neural Network

Following the convolutional feature extraction layers, the model proceeds to the fully connected (dense) layers that serve as the classifier. The layers fuse the learned spatial features and decide finally. The final dense layer employs a sigmoid activation function to produce a score of probability between 0 and 1 for binary two-class classification (benign or malignant). The model was trained on a binary cross-entropy loss function appropriate for a two-class problem, and optimization was done using the Adam optimizer with an adaptive learning rate for efficient and stable convergence during backpropagation.

In addition to improving training, data augmentation methods are used dynamically during training. These include random horizontal and vertical flipping, rotation, zooming, shifting, brightness adjustment, and contrast adjustment. This artificial dataset enlargement brings variability and models real-world variability in tissue staining, orientation, and imaging conditions and enables the model to learn invariant features and generalize more effectively to unseen data.

The performance of the proposed model is evaluated using a comprehensive set of metrics, namely accuracy, precision, recall, F1-score, and Area Under the Receiver Operating Characteristic Curve (AUC-ROC), which collectively evaluate the model's credibility, sensitivity to instances of cancer, and overall diagnostic utility. The CNN's learned high-dimensional feature maps can then be visualized by means of explainability methods like Grad-CAM (Gradient-weighted Class Activation Mapping), yielding heatmaps of the most discriminative parts of the input image used in the model's decision. This transparency added by interpretability provides an additional level of justification to the model's predictions and enhances its clinical utility by enabling validation against pathologist labels.

The suggested CNN model offers a fast, end-to-end deep learning pipeline for breast cancer classification of histopathological images. Through the incorporation of state-of-the-art feature learning, regularization, and interpretability techniques, the model is expected to assist pathologists with precise, reproducible, and clinically significant findings to diagnose breast cancer.

3.6 Evaluation

Quantitatively, the performance of the suggested CNN model was evaluated by employing a set of standard metrics that are most essential in the case of medical image classification, where the cost of false negatives (i.e., failing to detect a cancer diagnosis) may be very high. The confusion matrix was the basis for calculating these metrics.

Let:

TP = True Positives (accurately identified malignant cases)

TN = True Negatives (benign cases correctly predicted)

FP = False Positives (benign cases falsely predicted as malignant)

FN = False Negatives (malignant cases falsely predicted as benign)

1. Accuracy: The number of total correct predictions over all predictions.

$$\frac{TP + TN}{TP + TN + FP + FN}$$

This measure provides an approximate estimate of the model's performance but is deceptive if the dataset is imbalanced (i.e., very more benign than malignant samples).

2. Precision: The ratio of true malignant cases correctly predicted out of all cases predicted as malignant.

$$\text{Precision} = \frac{TP}{TP + FP}$$

High precision means low false alarms, and this is important to prevent unnecessary biopsies or treatment.

3. Recall (Sensitivity): The ratio of true malignant cases correctly identified.

$$Recall = \frac{TP}{TP + FN}$$

It is an important measure in cancer detection because failing to detect a true case of cancer can be fatal.

4. F1-Score: Harmonic mean of recall and precision. It takes their average in one measure, helpful particularly when there is an imbalanced class distribution.

$$\text{F1} - \text{Score} = 2 . \frac{Precision . Recall}{Precision + Recall}$$

4. RESULT

The evaluation of the CNN model was done in respect of training-validation accuracy and final classification performance on the test set with BreakHis dataset. The model was trained over 25 epochs with the Adam optimizer, applying early stopping to avoid overfitting. From the accuracy and loss graphs (Fig. 4), the model scored a maximum training accuracy of about 84% and a validation accuracy of about 75%. Training and validation losses continued on a downward path for most of the duration, with validation accuracy leveling off after epoch 16, indicating a good model convergence and stable generalization. The model nicely differentiated between benign and malignant tissue properties, indicating good learning from the data.

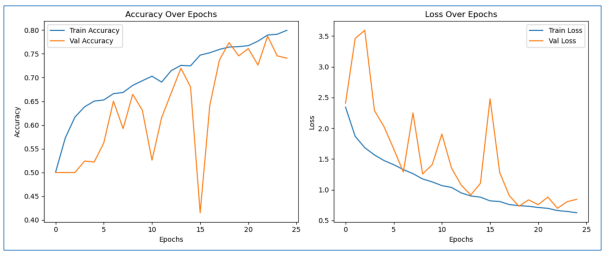

Fig 4. Evaluation Matrix

Now, this second image (Fig. 5) is a confusion matrix showing the classification results of a CNN model on the test set. The matrix illustrates the accuracy of the model to classify different tumors: adenosis, ductal, fibroadenoma, lobular, mucinous, and papillary.Values along the diagonal indicate cases where mutter predictions were made, and most of these cases reside in the ductal (malignant) class, where the model has correctly recognized 434 cases. Misclassification about the off-diagonal values indicates some degree of confusion among various benign classes such as fibroadenoma versus lobular. The overall classification accuracy is 74%, and this shows appreciable performance observed in both benign and malignant classes.

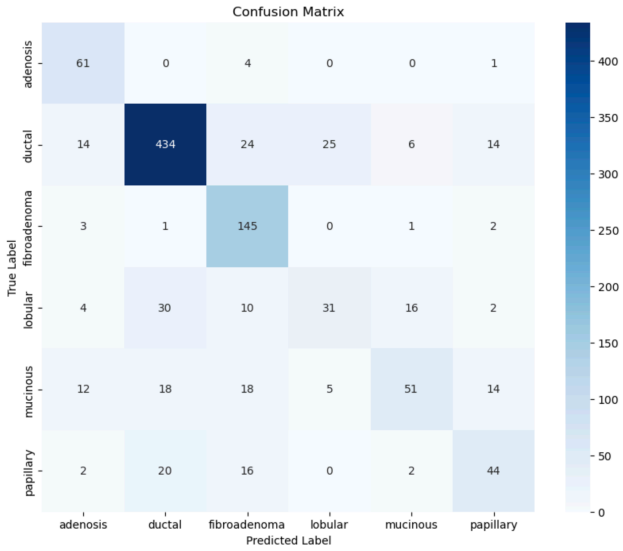

Fig 5. Confusion Matrix

The model's performance proves its utility in assisting diagnostic decisions for histopathological breast cancer classification. Application of deep learning, as CNNs and transfer learning methodologies, was successful in learning discriminative patterns from microscopic images and can be further boosted by explainable AI approaches in further research.

5. CONCLUSION

Here in this project, we designed and seriously experimented with a few deep learning architectures with the goal of detecting breast cancer from histopathology images. Analysis of histopathological images plays an essential role in clinical diagnosis of breast cancer, and the use of deep learning techniques has proven very promising as these can automate this role. We specifically utilized some of the most

advanced deep learning models, such as custom Convolutional Neural Networks (CNNs), VGG16, and ResNet50 to compare how well they could accurately classify malignant and benign tumors.

Our findings indicated that these deep learning models, especially when they were fine-tuned using transfer learning techniques, provided outstanding classification performance. The tailored CNN model learned features from the histopathology images compared to the domain with remarkable accuracy but was still a computationally lean architecture. The pre-trained models, however, like VGG16, ResNet50, and InceptionV3, yielded better performance levels because of what they had acquired by learning large sets of images. Transfer learning through fine-tuning the pre-trained models on the breast cancer dataset greatly enhanced their capacity to learn new data. This brings to the fore the importance of using pre-trained models for specific medical imaging tasks as they provide good feature extraction capabilities learned from humongous, varied data sets.

During the evaluation, we also saw the role played by hyperparameter tuning and regularization techniques in avoiding overfitting as well as improving model performance. The end models, which included these techniques, had high sensitivity, specificity, and accuracy for classifying malignant and benign cases, and this was a reflection of their suitability for use clinically in actual applications.

Overall, this research confirms the efficacy of deep learning models to distinguish breast cancer from histopathology images, with remarkable improvement through transfer learning and model explainability. Future research can investigate the application of multi-modal data, including genomic or clinical data, to improve the robustness and accuracy of the models. Additionally, ICS development for deployable and real-time clinical systems is a critical area of interest to enable such AI models to support early detection of breast cancer and enhance patient outcomes.

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