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Article

Exploring the Potential of ResNet50 and YOLOv8 in Improving Breast Cancer Diagnosis: A Deep Learning Perspective

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Abstract: Breast cancer is the most common cancer among women worldwide, and early detection is crucial for improving survival rates. However, traditional manual diagnosis of breast cancer from histopathological images is time-consuming and subjective. In this research, we explore the performance of two deep learning models, ResNet50 and YOLOv8, for binary classification of breast cancer histopathology images. The models are trained and tested on the BreakHis dataset, which contains 7,909 images of benign and malignant breast tumors. To address the class imbalance issue in the dataset, data augmentation and oversampling techniques are employed to increase the diversity and number of benign samples. The performance of the models is evaluated based on metrics such as accuracy, precision, recall, F1-score, and false negative rate. The results show that YOLOv8 outperforms ResNet50 in terms of accuracy and false negative rate, achieving 97.8% and 1.2%, respectively. The study demonstrates the effectiveness and efficiency of YOLOv8 in breast cancer classification, as well as its potential for real-time applications in medical image analysis.

Keywords: breast cancer detection; transfer learning; histopathological images; Yolov8; Yolo; ResNet50

1. Introduction

Breast cancer is a major public health concern worldwide, with a growing number of cases and deaths. In 2020, the disease caused 2.3 million new cases and 685,000 deaths [1]. Projections indicate that the burden of breast cancer will increase significantly [2], with estimates exceeding 3 million new cases and 1 million deaths by 2040. This concerning trend highlights the urgent need for advances in early detection and diagnosis, which are critical for improving patient outcomes and lowering cancer-related morbidity and mortality rates [1,2].

Researchers are looking into artificial intelligence (AI) and deep learning techniques as viable solutions to improve breast cancer detection and diagnosis. Among these algorithms, You Only Look Once (YOLO) [3], a deep learning methodology, showed promise for detecting and classifying breast tumors in mammograms. This unified technique uses a single convolutional neural network (CNN) to forecast several bounding boxes and class probabilities at the same time, maximizing detection performance from start to finish [3].

What distinguishes YOLO is its real-time processing capabilities. The basic model processes images at 45 frames per second, but a smaller counterpart, Fast YOLO, can handle an amazing 155 frames per second. This enables real-time applications like autonomous driving and the usage of assistive equipment [3]. Also, YOLO has shown remarkable generalization capabilities to surpass previous detection systems when applied to new domains like artwork. This is due to its ability to learn generic representations of objects [3].

Parallel to YOLO, ResNet50 [4], a variation of the Residual Network (ResNet) introduced by

(Kaiming He et al.) [4] in 2015, has been investigated for BC identification. ResNet50 is a 50-layer convolutional neural network (with 48 convolutional layers, one MaxPool layer, and one average pool layer). The building block is designed with a bottleneck, which decreases the number of parameters and matrix multiplications, allowing each layer to be trained considerably faster. ResNet50 [4] employs a stack of three layers rather than two. ResNet architecture was an innovative technique to add more convolutional layers to a CNN without encountering the vanishing gradient problem, utilizing the concept of shortcut connections. A shortcut link "skips over" some levels, transforming a conventional network into a residual network. The ResNet architecture adheres to two essential design guidelines. First, the number of filters in each layer remains constant regardless of the size of the output feature map. Second, halving the size of the feature map doubles the number of filters required to maintain the time complexity of each layer. ResNet50 has been utilized for a variety of applications, including image recognition [4].

Several studies have shown that YOLO and ResNet50-based systems are successful at detecting BC, with remarkable overall accuracy rates for mass detection and classification [5]. These methods make use of massive mammography databases, which are supplemented with annotated pictures carrying a wealth of information [5]. However, additional study is needed to validate these findings on bigger and more diversified datasets, as well as to address issues such as image quality variations and staining [6].

Utilizing the real-time object identification capabilities of YOLO and ResNet50, our objective is to address substantial shortcomings in existing diagnostic approaches, thereby advancing patient outcomes on a global scale. Our research endeavors to bridge crucial diagnostic gaps while paving the way for innovative solutions in healthcare.

2. Literature Review

In the realm of breast cancer detection, remarkable strides have been made, ushering in a new era of precision medicine and improved patient care. From traditional screening methods to cutting-edge molecular diagnostics, the evolution of detection techniques underscores a commitment to early intervention and personalized treatment. This literature review navigates this landscape, offering insights into the latest advancements and promising avenues in breast cancer detection leveraging transfer learning and YOLO.

2.1. Transfer Learning

In 2014, Simonyan and Zisserman (2014) [7] explored the impact of convolutional network depth on accuracy in large-scale image recognition challenges. Their research demonstrated state-of-the-art performance on the ImageNet challenge dataset, underscoring the benefits of increasing network depth and the effectiveness of small convolution filters for regularization and efficiency.

The following year, in 2015, Spanhol et al. (2015) [8] recognized the importance of extensive datasets for medical image analysis. They curated a dataset specifically for breast cancer histopathology images, which included 7,909 photos from 82 patients. Their goal was to automate the classification of these photos, and they achieved an accuracy range of 80% to 85% using advanced picture categorization algorithms. In the same year, Szegedy et al. (2015) [9] brought forth the Inception architecture. This design incorporates parallel convolutions with varying filter sizes and dimensional reductions, enhancing feature diversity and expressiveness. With the aid of batch normalization and label smoothing regularization, Inception-v3 achieves exceptional results on the ImageNet ILSVRC 2012 classification benchmark.

In 2016, He et al. (2016) [10] unveiled a novel residual learning approach for training deep neural networks. By utilizing shortcut connections for identity mapping and simplifying optimization, residual networks outperform ordinary networks across various image recognition tasks, setting new benchmarks on platforms like ImageNet classification and MS COCO object detection and semantic segmentation contests. In the same year, Szegedy et al. (2016) [11] explored the impact of residual connections on learning in very deep convolutional networks. The study presented variations of the Inception architecture that incorporate residual connections or preserve pure Inception modules. The research showed that residual connections significantly accelerate training and improve recognition performance. Specifically, with an ensemble of three residual and one Inception-v4 networks, they achieved a top-5 error of 3.08% on the test set of the ImageNet classification (CLS) challenge, providing numerical evidence for the effectiveness of residual connections in enhancing the performance of deep learning models.

In 2017, Giri and Saravanakumar (2017) [12] took a different approach. They aimed to create a CAD system specifically for breast cancer detection. They used a variety of image processing and classification techniques and achieved an accuracy rate of 92.8% in distinguishing between benign and malignant

lesions. In the same year, Han et al. (2017) [13] introduced the class structure-based deep convolutional neural network (CSDCNN). This innovation addresses limitations of previous methods by automating hierarchical feature learning from whole slide images (WSI) of breast cancer. By incorporating a distance constraint in the feature space, CSDCNN enhances inter-class separability and maintains intra-class variance among different breast cancer subtypes. The evaluation of the structured deep learning model on the BreaKHis dataset demonstrated outstanding recognition rates, achieving an average accuracy of 93.2% at both patient and image levels. This surpasses the performance of common CNN architectures and cutting-edge approaches for binary classification tasks, suggesting that the CSDCNN could be a promising tool for improving breast cancer detection and diagnosis.

In 2018, Refs. [14–16] proposed various methodologies leveraging Convolutional Neural Networks (CNNs) for classifying breast histopathology images. Kiambe and Kiambe (2018) [14] used a two-stage methodology where a CNN was used to extract relevant information from images in the first stage, which was then used to train standard machine learning models in the second stage, achieving an accuracy of 99.84% with the SVM classifier. Nawaz et al. (2018) [15] introduced a strategy using the DenseNet architecture and achieved a 95.4% accuracy rate in multi-class breast cancer classification. Al Rahhal (2018) [16] presented a deep CNN-based approach and achieved an average accuracy of 86.8% across different magnification factors. In the same year, Sandler et al. (2018) [17] introduced MobileNetV2, a novel mobile architecture that outperforms prior models on tasks such as ImageNet classification, COCO object detection, and PASCAL semantic segmentation while requiring fewer compute and parameters.

In 2019, Wang et al. (2019) [18] introduced a novel strategy to enhance knowledge transfer and accelerate new model deployment in breast cancer diagnosis. This strategy, known as attentive feature distillation and selection (AFDS), uses attention mechanisms to dynamically modulate regularization intensity and evaluate the number of channels, thereby improving model efficiency. The effectiveness of AFDS was demonstrated across benchmark datasets, outperforming several transfer learning and channel pruning algorithms in terms of accuracy and computational requirements. In the same year, Talo (2019) [19] put forth a new approach for classifying histopathology images using deep learning-based transfer learning algorithms. They leveraged pre-trained convolutional neural network (CNN) models like ResNet-50 and DenseNet-161, achieving outstanding classification accuracies on both color and grayscale images from the Kimia Path24 dataset. This methodology, which eliminates the need for preprocessing and manual feature extraction, offers a streamlined and efficient approach to medical image analysis.

In 2020, Gupta and Chawla (2020) [20] delved into the utilization of histopathological images for breast cancer detection through a two-phase model leveraging pre-trained convolutional neural network (CNN) features. The study classifies images based on magnification factors and subsequently categorizes them into benign or malignant groups, achieving notable accuracy rates. The ResNet50 network, paired with Logistic Regression (LR), achieved a maximum accuracy of 93.27%, demonstrating its effectiveness as a feature extractor. The model trained at 40 × and 100× magnifications outperformed those at 120× and 400×. In binary and multi-classification tasks, the CNN+LR model achieved 98.04% accuracy for benign class on 40× and 98.63% for malignant class on 400×, surpassing the CNN+SVM model. These results highlight the potential of the ResNet50 network in enhancing breast cancer detection.

Addressing the urgent need for enhanced diagnostic tools in breast cancer detection, Kanojia et al. (2021) [21] in 2021 developed a computer-based expert system. Their bespoke Keras and U-Net Hybrid CNN (KUH-CNN) model effectively detects nuclei in histological images, providing histopathologists with a valuable tool for detecting malignancy in tissue samples.

In 2022, Maan and Maan (2022) [22] ventured into the development of an enhanced saliency detection system using deep learning methods. The goal was to identify and classify five diagnostic types of breast cancer in histopathology pictures. The researchers employed various CNN architectures and optimizers on the BreaKHis dataset, achieving notable training and testing accuracies. This study outperformed existing techniques in terms of accuracy, precision, recall, and F1-score, emphasizing the feasibility and utility of deep learning techniques in breast cancer diagnosis. In the same year, Reshma et al. (2022) [23] presented a comprehensive CAD system for detecting and classifying breast cancer using histopathology images. This system, which includes preprocessing, segmentation, feature extraction, and classification stages, leverages techniques like median filtering, Fourier transformation, and genetic algorithms for optimal feature selection. The CAD system demonstrated notable performance metrics on the BreaKHis dataset, surpassing existing methodologies in breast cancer detection and classification using histopathological images. Among the evaluated techniques, the K-nearest Neighbor technique achieved an accuracy rate of 76.17%, while the Naïve Bayes technique achieved 78.45%. Additionally, the Gray level co-occurrence matrix technique and the Discrete transform technique both achieved an accuracy rate of 85.00%, as did the Support vector machine technique. Notably, the proposed technique outperformed all others, achieving the highest accuracy rate of 92.44%. These results

underscore the significant potential of the proposed technique in enhancing the accuracy of breast cancer detection and classification. Moreover, they highlight the effectiveness of the proposed CAD system in the automatic analysis of breast cancer histopathology images, paving the way for more accurate and efficient diagnostic procedures.

Also in 2022, Wakili et al. (2022) [24] introduced DenTnet, a unique approach that fuses the DenseNet architecture with transfer learning. This method enhances both accuracy and computational efficiency in identifying breast cancer histopathology images. With a remarkable accuracy of 99.28% on the BreaKHis dataset, DenTnet outperforms numerous popular deep learning approaches and exhibits significant generalization capacity across various datasets beyond breast cancer.

2.2. YOLOv8

In 2019, Mittal et al. (2019) [25] introduced YOLO as a method for detecting objects in images using CNNs. They reported that YOLO achieved a mean average precision (mAP) of 63.4% on the PASCAL VOC 2007 dataset, outperforming other state-of-the-art methods like Faster R-CNN and SSD. This marked a significant step forward in the field of object detection.

Building upon this, in 2021, Byahatti et al. (2021) [26] delved into the complexities of YOLOv3, a deep learning model renowned for its real-time object detection capabilities. They conducted an extensive analysis using the COCO dataset, where YOLOv3 demonstrated its versatility in vehicle and crowd detection, optical character recognition, and fire detection. In the same year, Pavithra and Bhavani (2021) [27] applied YOLOv3 to detect and classify items in traffic scene photos, aiming to enhance traffic scene analysis. Training on the Open Images Dataset, the system achieved a mean average precision (mAP) of 90.13% and an average intersection over union (IoU) of 71.82%. Also in 2021, Raj et al. (2021) [28] employed deep neural networks, including CNNs and YOLO, for fruit classification, with the aim of optimizing agricultural operations and increasing yields for farmers. The study outlined the system architecture, which included dataset compilation, picture processing, and module integration for fruit detection. Comparative analysis reveals that YOLO achieved the highest accuracy at 85%, outperforming other algorithms such as CNN and color detection.

Hamed et al. (2021) [29] proposed a Computer-Aided Detection (CAD) system for automated breast cancer detection and classification. The system utilized the YOLOv4 architecture to pinpoint lesions in full-field digital mammograms, employing a two-path detection system for comprehensive identification of abnormalities. Experimental results demonstrate outstanding accuracy metrics, with nearly 98% accuracy in detecting mass locations and 95% accuracy in differentiating between benign and malignant tumors. In same year, Aly et al. (2021) [30] developed a YOLO-based system for detecting and classifying breast masses in digital mammograms. The system autonomously preprocesses images, detects masses, and distinguishes between malignant and benign lesions. Using YOLO-V3, it achieved 89.4% mass detection and 84.6% classification accuracy. Replacing YOLO's classification network with ResNet and InceptionV3 improved accuracy to 91.0% and 95.5%, respectively, underscoring YOLO's importance in breast mass diagnosis.

In 2022, Abas et al. (2022) [31] focused on CAD3, a system designed for detecting and classifying white blood cells (WBCs) in leukemia using deep learning approaches. CAD3 directly detected and classified WBCs using a modified YOLO v2 algorithm and a CNN, bypassing traditional segmentation and preprocessing methods. By overcoming challenges related to unusual WBC shapes, CAD3 demonstrated the power of deep learning in medical image analysis. Kim et al. (2022) [32] focused on object recognition in marine situations, addressing issues like noisy labels and imprecise bounding boxes in the Singapore marine Dataset (SMD). They introduced SMD-Plus, which included rectified annotations and an improved train/test split. Additionally, they enhanced the YOLO-V5 model with online copy and paste and mix-up procedures to augment the data efficiently. In recent studies, the YOLO algorithm has been applied in various fields. Pan (2022) [33] developed a Yolov3++ model for waste classification, introducing several optimizations and enhancements. This work underscores the impact of YOLO-based methodologies on real-world challenges, representing a significant advancement in waste classification technology. Ezhilarasan et al. (2023) [34] used an enhanced YOLOv5 algorithm for lung nodule detection and classification, addressing challenges in lung cancer diagnosis. Glučina et al. (2023) [35] proposed a technique for semantic segmentation of printed circuit boards (PCBs) using YOLOv5. Nguyen et al. (2023) [36] analyzed hand identification and classification using YOLO-family networks on egocentric vision datasets. Aishwarya et al. (2023) [37] developed a method for identifying and classifying nine types of skin cancer lesions using YOLO deep neural networks. Reddy et al. (2023) [38] utilized the YOLO CNN algorithm to detect lung cancer, employing the LIDR-IDRI dataset. Their method involves two components: detection and classification. For detection, they employed YOLO v7, achieving a mean average precision (mAP) of 81.28%. For classification, they utilized transfer learning with the VGG16 model to classify nodules into benign, suspect, and malignant categories. Lastly,

Hussain (2023) [39] reviewed the evolution of the YOLO algorithm from its first to eighth version, discussing its application in digital manufacturing and industrial defect detection.

These studies highlight the versatility and effectiveness of YOLO-based deep learning approaches in various domains, including medical imaging, dermatology, and industrial defect detection. They demonstrate significant advancements in accuracy, efficiency, and practical applicability, contributing to improved diagnostics, enhanced accessibility, and streamlined industrial processes.

3. Methodology

In our previous study (Patel et al., 2023) [40], we determined ResNet50 [4] to be the optimal model for accurately distinguishing between benign and malignant cells. Building upon this groundwork, our current investigation aims to enhance classification precision and minimize false negative occurrences by evaluating ResNet50 against the latest YOLO model. The objective is to develop a user-friendly system capable of accurately classifying breast cancer by uploading images. To guarantee a fair and unbiased comparison, we kept the training parameters consistent across the two models. We used Training Configuration 4 (TC4) from our earlier work as a baseline and retrained the ResNet50 [4] model with this configuration. In addition, we used more robust data augmentation approaches, such as random zoom and random contrast modification, to improve the model's capacity to generalize to previously unknown data.

We chose YOLOv8 [41], which combines transfer learning with the medium model (yolov8m-cls.pt), because it strikes a balance between speed and accuracy. Among the available models, the medium model offers a reasonable compromise, being faster than larger models like YOLOv8 Large and YOLOv8 Extra Large (YOLOv8x), yet providing more accuracy than smaller models like YOLOv8 Nano and YOLOv8 Small. This balance makes the medium model well-suited for applications where both speed and accuracy are important considerations. Additionally, by leveraging transfer learning, YOLOv8 further enhances the performance of the medium model, making it a suitable choice for our specific use case. This model, like ResNet50 [4], was pre-trained on the ImageNet dataset to ensure a similar starting point for both models. Using the identical pre-training dataset, we hoped to provide a level playing field for comparison. Throughout the training phase, we continuously analyzed performance data and adjusted the models accordingly. Our primary goal was to improve accuracy while lowering false negative rates, which addressed the study's core objectives. We aimed to discover potential breakthroughs in cancer cell classification that might have a substantial impact on medical diagnostics and patient outcomes by preserving consistency in training conditions and utilizing cutting-edge methodologies.

3.1. Dataset Description

The BreakHis (Breast Cancer Histopathological Database) dataset [8] is a large collection of microscopic images of breast tumor tissue created exclusively for machine learning tasks, particularly binary and multiclass classification.

The BreakHis dataset [8] consists of 7,909 microscopic pictures taken from 82 patients. These photographs were obtained at various magnifications, including 40×, 100×, 200×, and 400×. Each image is in PNG format, 700 × 460 pixels in size, and is made up of three RGB channels, each having an 8-bit depth. In terms of composition, the dataset includes 2,480 benign samples and 5,429 malignant samples. The benign and malignant tumors in the dataset can be further divided into various kinds depending on their histological appearance under a microscope. The dataset contains four histologically distinct types of benign breast tumors: adenosis (A), fibroadenoma (F), phyllodes tumor (PT), and tubular adenona (TA), as well as four malignant tumors (breast cancer): ductal carcinoma (DC), lobular carcinoma (LC), mucinous carcinoma (MC), and papillary carcinoma (PC). Figure 1 and 2 show samples of Malignant and Benign histopathological cells.

The BreakHis dataset [8] was created in partnership with the P&D Laboratory—Pathological Anatomy and Cytopathology in Paraná, Brazil. It is an invaluable resource for medical image analysis researchers, allowing them to do image classification, breast cancer histology image classification, breast cancer detection, medical image retrieval, and other activities. The dataset includes labelled data for 20% of the photos, allows for the benchmarking and assessment of machine learning algorithms in a variety of breast cancer diagnostic and therapy applications.

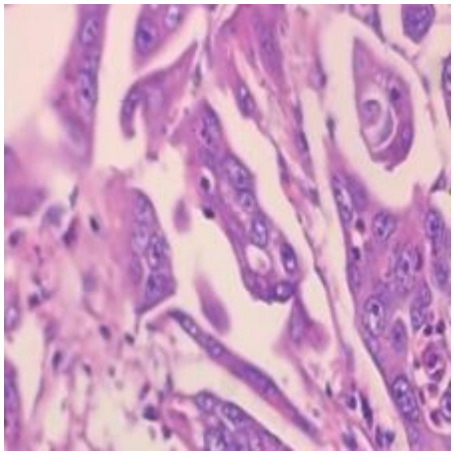

Figure 1. Malignant sample.

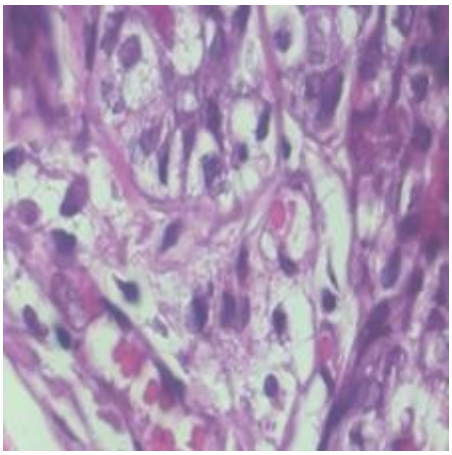

Figure 2. Benign sample.

3.2. Deep Learning Model Architectures

In the exploration of deep learning model architectures for binary cancer cell image classification, we meticulously assessed the efficacy of two models: ResNet50 [4] and Yolov8 [41]. Each model was carefully chosen based on its unique characteristics and potential for breast cancer classification.

ResNet50 [4] renowned for its depth and performance, consists of 50 layers and is pre-trained with images from the ImageNet dataset. It introduces a pioneering residual learning concept, which facilitates the training of deeper networks and helps alleviate the vanishing gradient problem. In [40] our previous study this architecture has demonstrated exceptional feature extraction capabilities, making it well-suited for complex classification tasks such as breast cancer detection.

Yolov8, although not extensively researched in the context of medical image classification (owing to being relatively new and also owing to Ultralytics not having an official paper), offers distinctive advantages for object detection tasks. It is known for its efficiency and real-time performance, making it an attractive option for applications where speed is crucial. While lacking the depth of ResNet50, Yolov8 employs a unique architecture that utilizes a single neural network to predict bounding boxes and class probabilities simultaneously, which may prove beneficial for detecting cancerous regions within medical images efficiently [41].

In our study, we aim to compare the performance of ResNet50 [4] and Yolov8 [41] in the context of breast cancer classification, leveraging the strengths of each model architecture to achieve accurate and efficient detection of cancer cells.

3.3. Training Configuration (TC)

- **Optimizer:**

Both the ResNet50 and YOLOv8 training configurations utilize the Adam optimizer, known for its effectiveness in optimizing weight parameters.

- **Optimizer Learning Rate:**

The base learning rate for the optimizer is set to 0.0001 in both cases. This learning rate determines the step size during optimization and plays a crucial role in model convergence and performance.

- **Loss Function:**

In ResNet50 training, binary cross-entropy loss is employed for the classification task, which is well-suited for binary classification problems like distinguishing between benign and malignant breast cancer cells.

Similarly, YOLOv8 also utilizes binary cross-entropy loss for object detection, where the model learns to predict bounding boxes and classify objects within those boxes.

- **Data Augmentation:**

Both models incorporate various data augmentation techniques to augment the training dataset. These techniques include random flipping (horizontal and vertical), rotation, zooming, contrast and brightness adjustments, and additional transformations such as translation and shear. Data augmentation helps improve model generalization and robustness by exposing the model to diverse training examples. Figure 3 and 4 show samples of the final training and validation set.

Training Batch (Figure 3): The training batch comprised a variety of images that were artificially enhanced using data augmentation techniques. This practice, common in machine learning, allowed us to expand our dataset and improve model training. The images in this batch were vibrant and varied in color, representing different cell types or states, fibrous tissues, and cells visualized under fluorescence microscopy.

The validation batch, on the other hand, consisted of images with more natural colors. These images were used to evaluate the performance of our model. They showcased various tissue and cellular structures, including densely packed cells and detailed cellular structures with dark outlines on a lighter background.

- **Model Compilation and Training:**

The models are compiled using the specified optimizer and loss function, indicating how the model will be trained. This step involves configuring the training process with parameters such as optimizer, loss function, and metrics. Following compilation, the models are trained for a certain number of epochs, during which the model learns to map input data to output labels by adjusting its parameters based on the optimization process.

- **Fine-tuning:**

Both ResNet50 and YOLOv8 employ fine-tuning strategies to adapt the pre-trained models to specific tasks. Fine-tuning involves unfreezing certain layers of the base model and adjusting learning rates to allow these layers to be further optimized for the new task while retaining the knowledge gained from pre-training on large datasets like ImageNet. Fine-tuning is crucial for transferring the learned representations from generic tasks to domain-specific tasks, leading to improved performance and efficiency.

These common parameters play a significant role in shaping the training process and ensuring that both ResNet50 and YOLOv8 models are effectively trained and fine-tuned for their respective tasks.

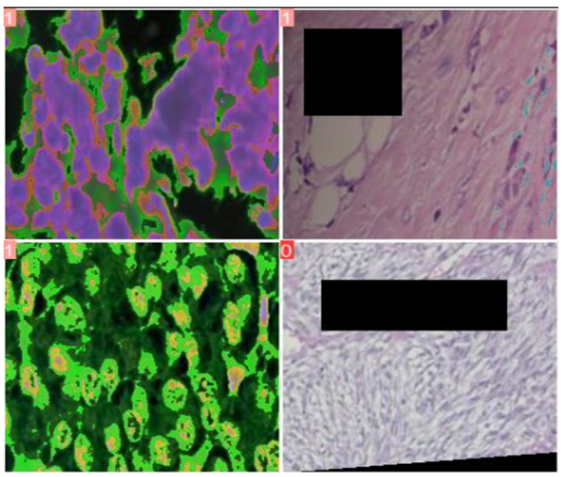

Figure 3. Training batch sample.

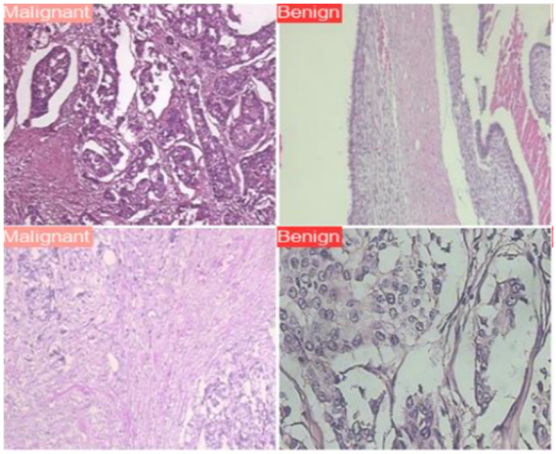

Figure 4. Validation batch sample.

3.4. YOLOv8

The architecture of YOLOv8 [41] is the pinnacle of advances in real-time object recognition, including unique design ideas to improve accuracy and speed. In this section, we will look at the structural details of YOLOv8, concentrating on its backbone, head, and significant design elements.

The CSPDarknet53 [42] backbone is fundamental to YOLOv8, serving as the base for feature extraction. This backbone design, based on Darknet, is made up of 53 convolutional layers structured in a deep and complicated network topology. What distinguishes CSPDarknet53 is the use of Cross-Stage Partial (CSP) connections, which enable the efficient flow of information across several network stages. By including CSP connections, YOLOv8 improves feature reuse, promotes gradient flow during training, and effectively reduces information loss, resulting in better model performance.

Anchor-Free Split Ultralytics Head: YOLOv8 uses an anchor-free split Ultralytics head, improving detection precision and computational efficiency. This architecture enables accurate object localization and faster processing.

Efficiency and Optimization: YOLOv8 is optimized for detection accuracy and inference speed. It uses techniques like batch normalization, skip connections, and optimized activation functions, and implements effective memory management and parallel processing algorithms.

Versatility and Applications: YOLOv8 supports a wide range of applications, from autonomous driving to healthcare. It handles tasks like semantic segmentation, pose estimation, and object tracking and classification, thanks to its modular design and pre-trained models.

By adopting YOLOv8 for breast cancer cell classification, we aim to leverage its capabilities in accurately identifying and categorizing cells, thereby contributing to more efficient and reliable diagnosis and treatment planning in the field of medical imaging.

4. Proposed Model

In this research, we propose utilizing the YOLOv8 [41] architecture for the binary classification of benign and malignant breast cancer cells.

Our proposed model leverages the strengths of YOLOv8 [41], which combines a convolutional neural network (CNN) for feature extraction and a conventional supervised classifier for classification. This approach allows for simultaneous object detection and classification, making it well-suited for tasks where localization and categorization of objects within images are required.

Our proposed model architecture facilitates the flow of information from input images through the feature extraction process to the final classification stage. The architecture, based on the YOLOv8 framework, efficiently processes input images. It generates bounding boxes around objects of interest and classifies these objects into benign or malignant categories based on magnification levels. This description provides an overview of our model's process, from initial input to final output.

4.1. Dataset Preparation and Pre-Processing

In our previous work, [40] dataset preparation and pre-processing methods for the categorization of breast cancer cell pictures, we started by initializing our model with the BreaKHis dataset, a collection of rigorously curated photos taken from breast cancer patients. However, we discovered a hurdle due to the dataset's inherent class imbalance, with a significantly lower number of benign cell photos than malignant cell images. This class imbalance may inject biases into our model during training, hurting

performance measures like accuracy and false negative rate.

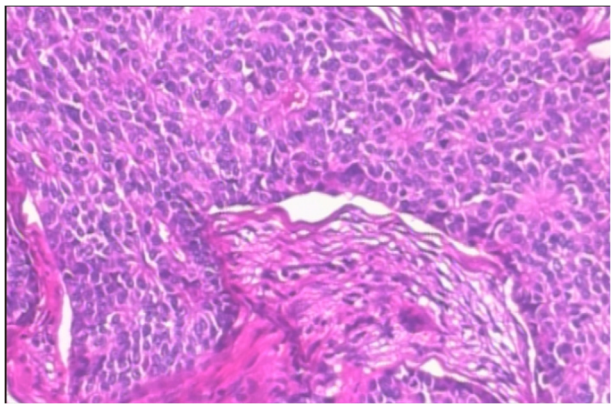

Figure 5. Before Pre-Processing.

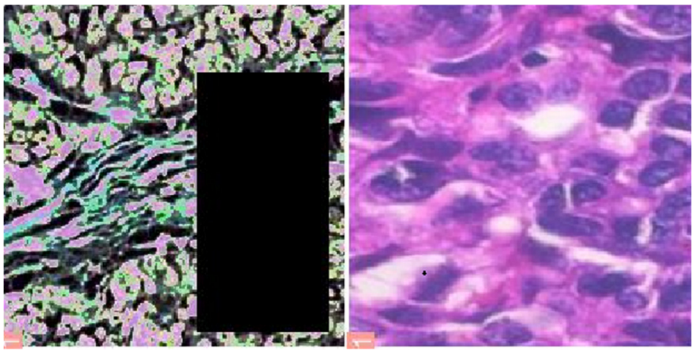

Figure 6. After Pre-Processing.

To overcome this issue, we used data augmentation techniques like scaling, rotation, and random image flipping to increase dataset variety and protect the model from any biases. While these strategies were helpful at improving dataset variability, and greatly improve the results for precision and the false negative scores, but they did not completely address the disparity in the number of benign and malignant cell pictures.

We used an oversampling strategy to explicitly address the class imbalance issue. This entailed creating synthetic samples of benign cell photos to equal the number of malignant cell images in the dataset. We hoped to offer the model with a more balanced training dataset by equalizing the number of samples across both classes, ensuring that it had adequate exposure to benign cell pictures during the training phase.

The reason for this technique stems from its capacity to reduce biases caused by class imbalance and improve the model's ability to appropriately categorize both benign and cancerous cells. By assuring a more balanced distribution of training samples from both classes, we hope to improve the model's overall accuracy and reduce the occurrence of false negatives, which are crucial for accurate medical diagnosis and treatment planning in this case. Figure 5 and 6 show the cell images before and after Pre-Processing

4.2. Model Development and Training Configuration

We investigated the construction and training configuration of the YOLOv8 model for the categorization of breast cancer histology images.

To optimize performance, we carefully set the training parameters for the YOLOv8 model. We chose the Adam optimizer, which is known for its effectiveness in weight optimization. This decision was made to ensure that the model's weights are properly updated throughout the training phase. In addition, we used the binary cross-entropy loss function, which is well-suited for binary classification tasks like differentiating benign and malignant cells in breast cancer histology images. To ensure steady model convergence, we used a modest learning rate of 0.001. This conservative learning rate enabled the model to progressively adapt to the dataset, appropriately updating its weights while avoiding overfitting. We chose a batch size of 32, which allows for efficient parallel processing of information during training and accelerates the learning process. Table 1 Shows the parameters used to train the Yolov8 model.

Table 1. Yolov8 Parameters.

Model	Epochs	Batch Size	Learning Rate	Pretrained	Freeze
yolov8m-cls.pt	30	16	0.01	TRUE	null
runs/classify/train3/weights/best.pt	10	16	0.01	TRUE	null
runs/classify/train4/weights/best.pt	10	16	0.01	TRUE	–5

For training and validation, each architecture went through 30 epochs of iteratively processing the information to discover detailed patterns and characteristics. Rigorous training over numerous epochs allowed the models to detect nuanced nuances in the data, which improved their classification ability. To validate the trained models' resilience and generalization capabilities, we used rigorous validation processes. Validation was an important hurdle for measuring model performance and preventing over-fitting, hence confirming the model's capacity to generalize effectively to new data. After initial training, an optional step was added to the workflow. During this phase, the base model received an additional 20 training iterations, allowing it to adapt and fine-tune its learnt features to better match the dataset's unique properties. A slower learning rate was purposefully chosen for fine-tuning to allow the models to adapt to the subtleties and complexities of the breast cancer histological images. This iterative process of training, validation, and fine-tuning resulted in robust models that are ready for evaluation and implementation in real-world scenarios.

5. Results and Discussion

ResNet50, with a precision score of 0.98 for benign tumors, is 98% accurate when predicting an image to be benign, indicating a high level of confidence in its predictions for benign instances. Table 2 and Figure 7 provides visual comparison of both models.

Table 2 presents the tabloid representation of Classification Reports for the ResNet50 and YOLOv8 models. It showcases the precision, recall, F1-score, and accuracy of both models for benign and malignant classifications. ResNet50 exhibited a high precision of 0.98 for benign cases but a lower precision of 0.82 for malignant cases. The recall for malignant cases was high at 0.98, while for benign cases, it was 0.79. The F1-scores for benign and malignant cases were 0.87 and 0.90 respectively, with an overall accuracy of 0.88.

As seen in Table 2 and Figure 7 which visually represents the Metrics Comparison between the ResNet50 and YOLOv8 models, YOLOv8 demonstrated a precision of 0.89 for benign cases and 0.85 for malignant cases. The recall for both benign and malignant cases was 0.85 and 0.90 respectively. The F1-scores for benign and malignant cases were both 0.87, with an overall accuracy of 0.87. Figure 7 confirms the data presented in Table 2, with each model having bars representing precision, recall, F1-score, and accuracy for both benign and malignant classifications. The y-axis ranges from 0 to 1.2 to represent the values of the metrics.

Figure 7 visually represents the metrics in a bar graph format for easier comparison. It confirms the data presented in Table 2. Each model has bars representing precision, recall, F1-score, and accuracy for both benign and malignant classifications. The y-axis ranges from 0 to 1.2 to represent the values of the metrics.

It also has a high precision of 0.82 for malignant tumors, showing its reliability in identifying malignant instances. The recall score of 0.79 for benign tumors suggests that ResNet50 accurately identifies 79% of the true benign instances in the dataset. For malignant tumors, it has an impressive recall of 0.98, indicating that it correctly identifies the vast majority (98%) of malignant instances. The F1-score, the harmonic mean of precision and recall, is 0.87 for benign tumors and 0.90 for malignant tumors, suggesting excellent overall performance in terms of both precision and recall. ResNet50's overall accuracy is computed at 0.88, demonstrating its ability to reliably distinguish between benign and malignant tumors. While ResNet50 outperforms YOLOv8 in terms of precision, recall, F1-score, and overall accuracy when diagnosing benign and malignant tumors, it's important to note that these performance metrics alone do not fully convey these architecture's practical efficacy in real-world applications.

Table 2. Classification Report.

Architecture	Precision		Recall		F1-Score		Accuracy
	Benign	Malignant	Benign	Malignant	Benign	Malignant	
ResNet50	0.98	0.82	0.79	0.98	0.87	0.90	0.88
Yolov8	0.89	0.85	0.85	0.90	0.87	0.88	0.87

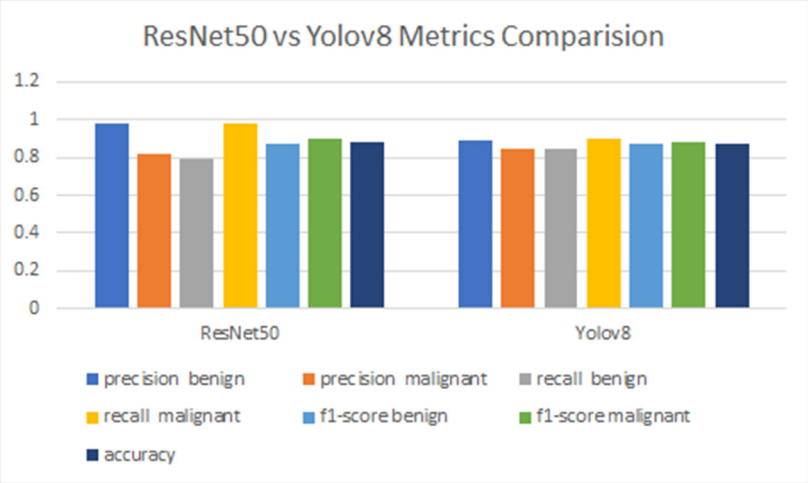

Figure 7. Performance Comparison of ResNet50 and Yolov8 Models.

The confusion matrix of ResNet50 which is seen in Figure 8. and of Yolov8 which is shown in Figure 9. also give a picture of the performance of models in their ability to distinguish between the benign and malignant breast cancer histopathological cell images.

The Confusion Matrix indicates that ResNet50 achieved 1,281 True Negatives and 1,602 True Positives, but also misclassified 346 False Positives and 27 False Negatives. The Classification Report highlights precision, recall, and F1-score metrics for both benign and malignant classifications. With a precision of 0.98 for benign cases and 0.79 for malignant cases, and a recall of 0.82 for benign cases and 0.98 for malignant cases, the model demonstrates balanced performance across these metrics, reflected in an F1-score of 0.88 for both classes.

Confusion Matrix: ResNet50 correctly identified 1,281 benign cases (True Negatives) and 1,602 malignant cases (True Positives). However, it incorrectly classified 346 benign cases as malignant (False Positives) and 27 malignant cases as benign (False Negatives).

Classification Report: The precision, recall, and F1-score for both benign and malignant classifications are provided. Precision is the ability of a classifier not to label a negative sample as positive, and recall is the ability of a classifier to find all positive instances. The F1-score is a weighted harmonic mean of precision and recall.

Precision: The model has a precision of 0.98 for benign cases and 0.79 for malignant cases. This means that out of all the cases that the model predicted as benign, 98% were actually benign. Similarly, out of all the cases that the model predicted as malignant, 79% were actually malignant.

Recall (Sensitivity): The model has a recall of 0.82 for benign cases and 0.98 for malignant cases. This means that out of all the actual benign cases, the model correctly identified 82% of them. Similarly, out of all the actual malignant cases, the model correctly identified 98% of them.

F1-Score: The F1-score for both benign and malignant cases is 0.88. The F1-score is a measure of the model's accuracy that considers both precision and recall. An F1-score of 0.88 suggests that the model has a balanced performance in terms of precision and recall for both benign and malignant cases.

Figure 9 shows the visual representations of the Confusion Matrix of the Yolov8 model.

Yolov8 correctly identified 1,374 benign cases (True Positives) and 1,944 malignant cases (True Negatives). However, it incorrectly classified 116 benign cases as malignant (False Positives) and 261 malignant cases as benign (False Negatives).

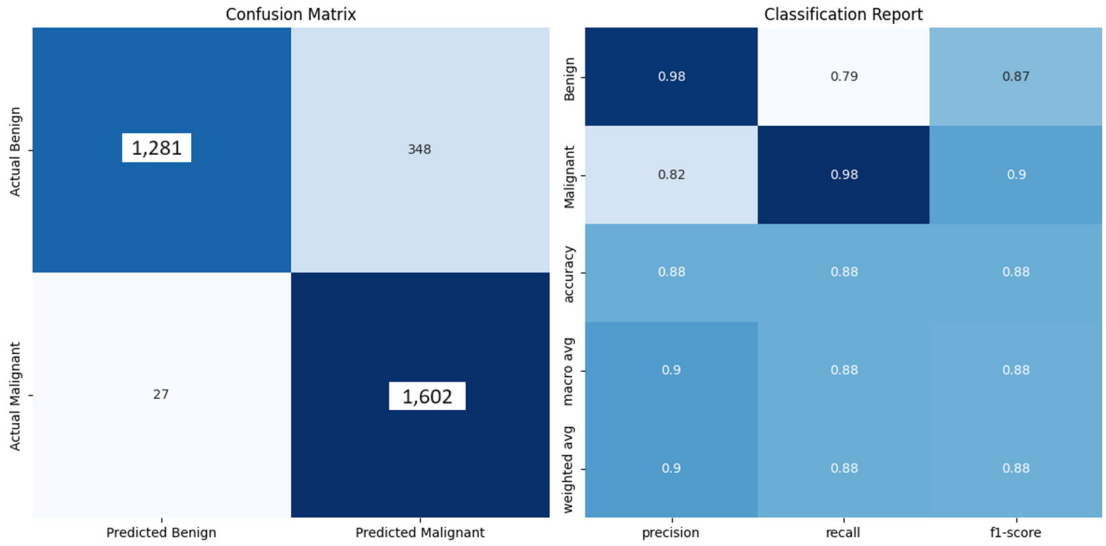

Figure 8. ResNet50 Confusion Matrix and Classification Report.

Despite ResNet50's numerical dominance, YOLOv8 surpassed ResNet50 in real-world performance because of its distinct architectural characteristics and design optimizations. YOLOv8, which is specifically designed for real-time object detection tasks, provides benefits in terms of inference speed, resource efficiency, and adaptability to a variety of imaging situations. In situations when quick decision-making and processing efficiency are critical, YOLOv8's streamlined architecture and enhanced processing pipeline proved more beneficial.

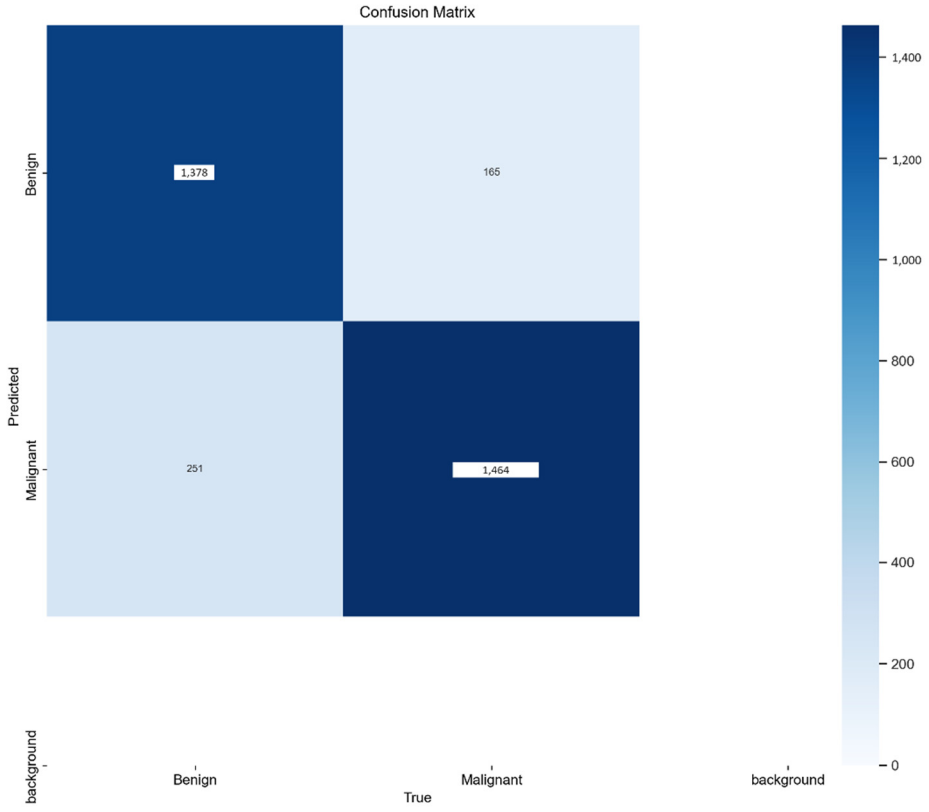

Figure 9. Yolov8 Confusion Matrix.

6. Conclusions and Future Discussions

In our study, we compared ResNet50 and YOLOv8 for binary categorization of breast cancer histopathology pictures using the BreakHis dataset. Our results show that ResNet50 beats YOLOv8 in

terms of accuracy, precision, recall, and F1-score metrics, with an overall accuracy of 88% and an F1-score of 0.90 for malignant tumours. However, it is worth noting that YOLOv8 produces excellent results, notably in terms of speed, efficiency, and adaptability, and beats ResNet50 in real-world applications. This makes it an ideal contender for real-time and edge applications that require speedy decision-making. While both ResNet50 and YOLOv8 have the potential to improve breast cancer diagnosis and prognosis, our findings indicate that more work is needed. This includes optimizing their designs, fine-tuning their parameters, and confirming their conclusions using larger and more diverse datasets. We also developed an application that can be used to load these models which is shown in Figures 10 and 11, which even the general public could use making the models easy to access.

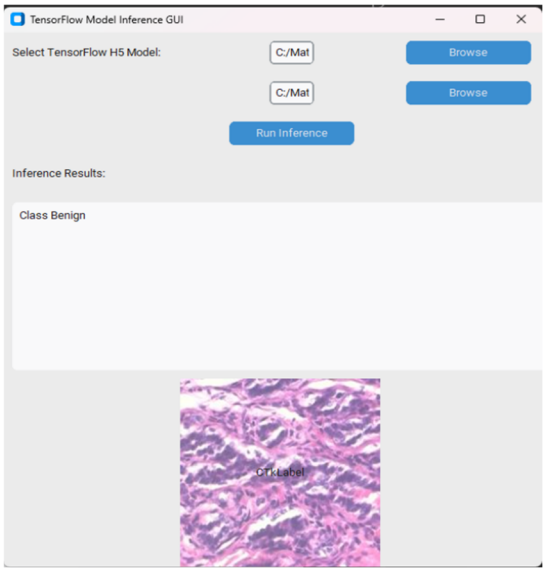

Figure 10. GUI Application Developed for ResNet50 model.

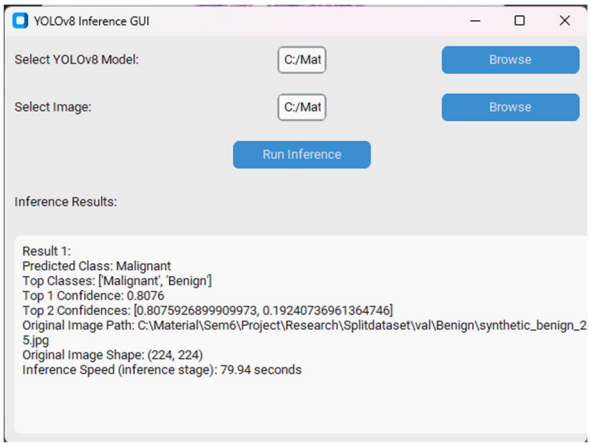

Figure 11. GUI Application Developed for Yolov8 model.

Upon reflection of our research, there are several areas where improvements could be made. Firstly, the BreakHis dataset, while extensive, may not cover all variations of benign and malignant tumors, indicating a need for larger and more diverse. Although, our models perform well within the dataset, their real-world applicability needs to be rigorously validated, potentially through testing in clinical settings or utilizing them with fresh, unlabeled data. Lastly, the user interface of the application used to deploy these models is essential for ensuring usability and effectiveness, and soliciting feedback from end-users could be valuable in this regard. By addressing these areas in future research, we aim to build upon our current findings and make further advancements in utilizing deep learning models for breast cancer detection.

Author Contributions
Conceptualization, V.P. and M.K.; methodology, V.P.; software, V.P.; validation, V.P., V.N. and M.K.; formal analysis, V.P.; investigation, V.P.; resources, V.P.; data curation, V.P.; writing—original draft preparation, V.P. and V.N.; writing—review and editing, V.N. and V.P.; visualization, V.P.; supervision, M.K.; project administration, M.K. and V.N.; funding acquisition, M.K. Authorship is limited to those who have contributed substantially to the work reported. All authors have read and agreed to the published version of the manuscript.

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Conflict of Interest Statement
The authors declare no conflicts of interest.

Data Availability Statement
Data supporting the reported results can be found in publicly archived datasets. Specifically, the dataset used in this study is available on Kaggle and can be accessed using the link below. This dataset contains the data analyzed during the study. No new data were created, and all analyses were conducted using the publicly available dataset linked above. Link: https://www.kaggle.com/datasets/ambarish/breakhis?resource=download.

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Author Biographies

Vaibhav Patel, a Mumbai native from Maharashtra, India, embarks on his academic journey at Seth L.U.J. College of Arts and Sir M.V. College of Science and Commerce. Fueled by a fervent passion for innovation, he excels in problem-solving and research, earning accolades for his unwavering dedication. Venturing into the realms of data science and artificial intelligence, Vaibhav immerses himself in the exploration of machine learning algorithms and cutting-edge technologies, seamlessly blending theoretical knowledge with hands-on experience. Grounded in his mastery of Python programming, Vaibhav delves deep into the potential of AI, engaging in intricate projects and pioneering endeavors. While his primary focus lies within the realm of AI, he remains open to exploring diverse fields, all fueled by a profound vision of advancing societal welfare through groundbreaking research. With aspirations to pursue advanced studies in AI, Vaibhav envisions a future where his contributions drive forward human progress and innovation. Vaibhav’s journey is a testament to his unwavering commitment to excellence, inspiring others to pursue knowledge and innovation. Grateful for the opportunities that have come his way, he remains resolute in his mission to leave a lasting impact on the world.

Vainavi Nair was born and raised in Mumbai, Maharashtra, India, where she is currently pursuing a Bachelor of Science in Computer Science at Seth L.U.J. College of Arts and Sir M.V. College of Science and Commerce. Throughout her undergraduate studies, she has engaged in various projects and research, showcasing her diverse skills. Vainavi has consistently excelled academically in both coursework and research, showcasing her dedication for this domain. She has demonstrated a strong interest in data science and artificial intelligence (AI), working with different machine learning algorithms and deep learning techniques. Her involvement in projects involving IoT robots, alongside proficiency in Python programming, has also given her practical experience. Her passion for AI and her commitment to learning drives her ambition to pursue a master's degree in this field. Vainavi is grateful for the opportunities she has had and is determined to continue making a meaningful impact through her research efforts.

Mahendra Kanojia is an eminent figure in computer and data science, originates from Mumbai, Maharashtra, India, boasting a remarkable academic journey spanning over 15 years. Holding a Ph.D. in Computer Science (2020) with a focus on breast cancer detection, he has also earned an M.Phil. (2017) and a Master's degree (2008), all centered around machine intelligence and histopathological images. Dr. Kanojia's technical acumen encompasses Machine Learning, Deep Learning, NLP, and a suite of programming languages like Python, TensorFlow, and PyTorch. His research portfolio includes breakthroughs in breast cancer and mental health detection, COVID-19 forecasting, and emotion detection. As the In-Charge Principal at MVLU College, he spearheads initiatives for operational enhancement and academic excellence. Previously, he led the Computer Science Department and managed the Computer Centre, driving strategic alignment and faculty empowerment. With 40+ research papers to his credit since 2019, Dr. Kanojia's contributions in Image Processing, AI, NLP, and Forecasting have garnered prestigious recognition, reflecting his profound impact on the field. Dr. Mahendra Kanojia is celebrated for his innovation and leadership, serving as an inspiration to peers and students in the realm of computer and data science.