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Breast Cancer Detection Using a Novel Hybrid Machine Learning Approach

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ABSTRACT

Breast cancer is the most common and lethal cancer among women across the globe, and supporting early detection through accurate diagnostic measures would save many lives. However, existing diagnostic techniques often encounter problems concerning accuracy and reliability, hence, they are ineffective. This paper presents a new multi-classifier machine learning technique for breast cancer diagnosis using the integration of conventional machine learning (ML) and deep learning (DL) paradigms. The model employs a two-step process: The first step is feature selection using a random forest (RF) to do dimensionality reduction, and feature selection eliminates features that are not useful; the last step is classification using a convolutional neural network (CNN). The hybrid model is then tested using a Wisconsin breast cancer data set. Evaluation criteria for the key performance indicators include accuracy, precision, recall rate, F1-score, and AUC ROC. As the results have revealed, the hybrid model is higher than the traditional methods like logistic regression (LR) with an accuracy of 94.5%, a precision of 92.8%, recall of 95.0%, an F1-score of 93.8% and an AUC-ROC of 0.97. This study demonstrates that integrating human readers into the evaluation process can enhance the reliability and efficiency of clinical breast cancer detection and, hence, contribute to developing diagnostic techniques in online medical image analysis.

1. INTRODUCTION

1.1 Background and motivation

Breast cancer is one of the most common cancers affecting women worldwide. According to the World Health Organization, Breast cancer accounts for approximately 12% of new cancer cases every year worldwide. Early detection will significantly improve the survival rate. The 5-year survival rate is approximately 99% if the cancer is detected and detected early. However, breast cancer detection remains challenging due to several factors. Including different breast densities. The subtlety of the tumour and the variability in radiologist interpretations [1].

Despite being effective, traditional screening methods such as mammography have limitations in terms of sensitivity and specificity, especially for women with dense breast tissue. And mammograms often have trouble distinguishing between malignant growth and benign tumours. This can lead to false positives and unnecessary biopsies. Cancers in dense breasts may also be overlooked. where dense tissue and cancerous tumours appear white on X-ray images. Augmentative imaging techniques such as ultrasound, MRI, and PET scans have been explored, but these techniques also have disadvantages, such as higher costs. Longer processing time and the risk of radiation exposure [2].

The need for more accurate and reliable methods for detecting breast cancer has led to great interest in ML and DL techniques from breast cancer images. Demonstrates excellent performance in detection, even in challenging cases involving dense tissue. Recent studies have shown that combining AI with mammography can improve sensitivity by 5-10%, especially for women with dense breasts.

However, although ML and DL models are promising, but there are challenges to using these technologies in real-world clinical environment issues such as data privacy. The need for large labelled datasets Model interpretation and generalizability remains a significant limitation. Current ML models may suffer from overfitting. This is especially true when training on small or unbalanced datasets. This leads to poor generalization to new patients. Moreover, even though AI-powered models can outperform traditional methods, their use in clinical practice requires rigorous investigation. Regulatory approvals and integration with existing healthcare workflows [3].

Therefore, there is a great need for more effective methods of detecting breast cancer. Leveraging the strengths of traditional and AI-driven approaches, developing a hybrid system that combines medical imaging with AI promises to provide a comprehensive breast cancer screening solution. More accurate and personal to overcome current limitations. Addressing these challenges through continued research can greatly reduce the global burden of breast cancer and save countless lives.

1.2 Objective

This paper aims to introduce and evaluate a new hybrid approach for breast cancer detection that combines traditional machine learning techniques with advanced deep learning models. This hybrid system attempts to harness the power of both methods using interpretations of classical models such as random forests or decision trees. and the predictive power of deep learning architectures such as CNN by integrating these methods. We aim to address the existing limitations of independent models.

The hybrid model optimises breast cancer detection by improving sensitivity and specificity. This can be achieved by increasing the model's generalisation ability to diverse patient populations. It also provides interpretable results. This can help doctors make informed diagnosis decisions. The proposed system will be evaluated on a publicly available breast cancer dataset. It focuses on efficiency in accurately identifying cancerous and benign tumours, so we reduce unnecessary intervention and missed diagnoses.

1.3 Significance

The importance of this research lies in the ability of the proposed hybrid approach to bridge the gap between classical machine learning and deep learning in perspective-taking breast cancer detection. Hybrid model the objective is to leverage the complementary strengths of both methods, providing a balanced solution that enhances forecast performance while maintaining interpretability.

A key innovation of the hybrid approach is its ability to reduce over-installation. This is a common problem in deep learning models. Combining classic machine learning techniques with hybrid models can thus efficiently manage feature selection. Simplify the model. Hybrid systems also produce more interpretable results without having to memorise training data. This is important in gaining the confidence of medical professionals. Providing insights into which features contribute most to a model's predictions may help doctors better understand the reasoning behind a diagnosis. This will ultimately lead to more informed decisions in breast cancer treatment.

This research contributes to the growing body of literature on the application of machine learning in healthcare. and offers practical solutions to some of the main challenges in breast cancer detection. This article aims to pave the way for an efficient, accurate, and clinically usable diagnostic tool by demonstrating the effectiveness of the combined approach. It can be seamlessly integrated into existing healthcare workflows.

2. RELATED WORK

2.1 Overview of existing models for breast cancer detection

During the past decade, ML and DL have been developed and applied to improve breast cancer detection and diagnosis. These models have shown great potential in helping doctors analyse complex medical data and identify patterns beyond the capabilities of traditional methods. This section provides an overview of the most commonly used models for breast cancer detection, from classic ML techniques to cutting-edge DL approaches [4].

Classical Machine Learning Models

1. **Logistic Regression (LR)**: LR is one of the earliest and simplest models used for binary classification tasks, including breast cancer screening. A linear decision criterion was used to separate malignant from benign tumours. It considers the tumour's size, shape, and texture. LR allows for high interpretability. This is important in medicine, however, because it is linear. Therefore, complex relationships in the data cannot be captured. Studies show that LR remains a useful baseline model for breast cancer detection. However, its performance often outperforms more complex algorithms [4].
2. **Support Vector Machines (SVM)**: SVM is widely used for breast cancer classification because of its robustness in handling high-dimensional data. They create a hyperplane in a multidimensional space that separates information into different categories (benign or malignant). Research demonstrates the effectiveness of SVM in classifying breast cancer using radiological data. It has high accuracy. However, SVM may encounter problems with large data sets and may be sensitive to the choice of kernel function. Moreover, although SVM performs well on small data sets, the computational cost increases significantly with larger datasets [5].
3. **Random Forest (RF)**: RF is a cluster learning method based on decision trees. It combines predictions from multiple decision trees to improve classification accuracy. RF is known to handle noisy data and reduces the possibility of over-installation. This makes it a popular choice for breast cancer detection. Studies have shown that RF can achieve high accuracy by leveraging the properties of mammogram images to differentiate. Between malignant breast cancer and benign tumours the model may lack transparency. This is because decision tree sets can make interpretation difficult [6].

Deep Learning Models

1. **CNNs**: CNNs for breast cancer detection have become prominent DL models due to their unique ability to process image data. Specifically, the mammogram CNN is a multi-layered one that automatically learns hierarchical feature representations from images, such as texture, size, and the difference between cancerous and benign areas revealed. CNNs outperform conventional ML algorithms by detecting complex features directly from medical images. There is no need to extract features manually. CNNs have also been successfully used in breast cancer localization tumour classification and 2D and 3D imaging [7].
2. **Deep CNNs (DCNNs)**: Expanding from basic CNN, deep CNN has multiple layers. This makes it possible to capture more complex patterns in medical images. These models have achieved state-of-the-art results in breast cancer detection using large mammogram datasets. It also combines multiple image modalities

(e.g., MRI, ultrasound). For example, a deep network that combines mammography with patient history has been proposed to significantly improve detection accuracy, especially in dense breast tissue [8].

3. **Hybrid Approaches**: In the past few years, hybrid models that combine classic ML-DL approaches have become popular. These models aim to take advantage of the strengths of both techniques while minimizing their individual weaknesses. For example, researchers have combined CNNs with decision tree classifiers. To create an accurate and interpretable model, a hybrid model was introduced by combining CNN features with SVM classification, resulting in improved accuracy in breast cancer detection and better generalizability [9].

Table 1 shows the summary of existing models for breast cancer detection.

Table 1. Summary of existing models for breast cancer detection

Model	Description	Strengths	Limitations
LR	A linear model for binary classification is often used as a baseline model for breast cancer detection.	High interpretability, easy to implement and understand, well-suited for linearly separable data.	Poor performance with non-linear data and limited ability to capture complex relationships.
SVM	Uses hyperplanes in a multidimensional space to classify data.	Effective in high-dimensional spaces, robust against overfitting when properly tuned.	Computationally expensive for large datasets, sensitive to choice of kernel.
RF	Ensemble method that aggregates multiple decision trees to improve classification accuracy.	Handles noisy data well, reduces overfitting, and can handle high-dimensional data.	Lack of transparency and difficulty in interpreting individual trees in the forest.
CNNs	The deep learning model specializes in image data processing and is particularly effective for mammograms.	Automatically learns hierarchical feature representations, has strong performance with large image datasets, and is widely used for medical image analysis.	It requires large labelled datasets, has a risk of overfitting, and has a "black-box" nature, which makes it difficult to interpret results.
Hybrid Approaches	It combines features of ML and DL models, such as CNN and SVM, to leverage their strengths.	It can improve performance and interpretability and mitigate the limitations of individual models.	Computationally intensive, potential for model complexity and integration challenges.

2.2 Feature engineering

Feature engineering is important to enhance the predictive performance of breast cancer detection models. Wisconsin Breast Cancer Dataset (WBCD), a standardized data set It has many important features such as:

- Mean radius: The average distance from the centre to the periphery of the tumour.
- Texture mean: The standard deviation of the grey level values in an image. which takes into account variations in intensity.
- Perimeter mean: Length of the border around the tumour.
- Area means: The size of the tumour. Calculated from the area at the outer area.
- Diagnosis: Target variable. This indicates that the tumour is benign or malignant.

These properties, in particular geometric features such as radius, circumference, and area, are important in differentiating benign from malignant tumours. Surface and field features are important in differentiating between dense breast tissue and tumours and improving classification performance when used with DL models.

In a hybrid model, these features can be combined with features generated by deep learning, such as complex shape representations and patterns learned from imaging data. To provide more comprehensive features for classification, traditional geometric features were combined with deep CNN features to form a hybrid cluster model, which leads to better accuracy than using a single feature cluster.

The hybrid approach also addresses challenges related to feature selection and dimensionality reduction. Combining hand-crafted features (e.g., from clinical data) and automatically extracted features (e.g., CNN), hybrid models can reduce the risk of overfitting using a rich feature set. and provide more information [10].

3. METHODOLOGY

Proposed Hybrid Approach

The proposed hybrid approach for breast cancer detection combines the strengths of traditional ML and DL models to enhance prediction performance. This approach is designed to address the limitations of each model by combining their complementary advantages into a two-step pipeline as shown in Figure 1.

Stage 1: Feature Engineering and Selection Using Classical Machine Learning

The first phase of the pipeline deals with feature engineering and selection, which is a data preprocessing step. Knowing that the choice of features we consider for the classifier can significantly impact the success of cancer detection, this paper uses the RF method based on decision trees for feature selection. RF is particularly good at coping with large numbers of variables, nor does it expect any such relationship between them, and therefore, it is appropriate for this role. In other words, RF works by building several decision trees, each of which every feature is randomly selected; the effectiveness of the splits of the feature in the decision trees considers the importance of the feature [11].

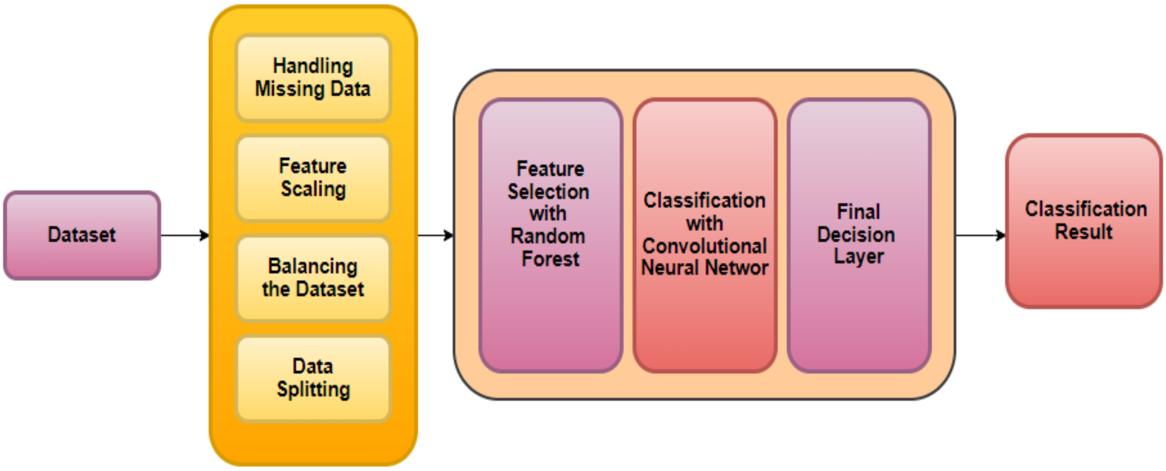

Figure 1. Architecture diagram of proposed hybrid model

For the threshold of feature importance, the theoretical support concerns quantifying the determination of how much degree each feature contributes to the reduction of impurity (like Gini or entropy) within each tree across all the trees. This means that the higher the decrease in impurity, the more important a particular feature is. This criterion orders features and a certain value filters features that impact the model's predictive power. In general, only such features that possess importance values greater than predetermined cut-off values (for example, 0.01 or 1% may be used) are retained. The threshold mentioned above can be tuned according to the specific level to get the appropriate balance between the model's complexity and performance.

For instance, some of the features derived from the Wisconsin Breast Cancer Dataset, like radius_mean, texture_mean, perimeter_mean, and area_mean, go through the process of ranking in the RF model. The main goal is to decrease the size of the feature set, removing features that do not present much additional information and passing a better dataset to the following measure, the deep learning model. This helps in handling the common problem of high dimensionality or irrelevant characteristics in the deployment of deep learning models [12].

Stage 2: CNN Architecture Selection

While proposing the hybrid model, the CNN architecture used was selected after considering various designs of CNNs where each architecture is suitable for a certain type of problem. CNNs are popular when it comes to image classification because it is capable of learning spatial hierarchies of features on their own. For this work, five different CNN models, LeNet, AlexNet, VGGNet (16, 19), ResNet, and Inception, were considered for this task [13].

LeNet: LeNet is one of the first models for CNN that works well for basic image identification. Nevertheless, due to its shallower structure and relatively small capacity, it is unsuitable for larger data sets or tasks such as breast cancer detection, for which one must capture intricate features and non-linear dependencies in high dimensional space.

AlexNet: As a pioneering network for image classification, AlexNet is deeper than LeNet and employs ReLU activation and dropout methods to reinforce model generalization. Despite its high accuracy in many conventional classification problems, its architecture may still be a disadvantage when working with problems that require very deep or large data matrices, resulting in computational inefficiency.

VGGNet: VGGNet is one of the simplest but most effective image recognition tools because of its uniform architecture and 3x3 convolutional filters. Nevertheless, the computational cost is high due to the availability of many parameters, and it may impose a constraint when working with large datasets in terms of available resources.

ResNet: Residual Networks (ResNet) incorporate skip connections, which enable the training of deep networks without any tendency for gradient vanishing. This architecture is useful for learning from large datasets, such as identifying cancer from medical images. Given that ResNet enhances the possibility of better performance with increased depth and offers robustness to training instabilities, it becomes a candidate of choice for this endeavour.

Inception: Analyzing the features of the Inception network, it should be stated that the network is very efficient at extracting features of different scales due to the multi-scale convolutional filters (1×1, 3×3, 5×5). Its modular structure does not require predetermined distribution and density estimates, making it the fourth extremely competitive. But it adds more steps and computation than may be required for a given task, and this comes with a price.

Based on these architectures, ResNet was chosen for the proposed model because of the network's ability to learn from the architecture's depth without overfitting, which is very applicable when solving breast cancer detection problems. Application of residual blocks helps in learning of more abstract features while at the same time decreasing the probability of vanishing gradients, thus resulting in stable training irrespective of the depth of the architecture. In addition, ResNet has been shown to be effective for medical imaging tasks; therefore, ResNet is selected as the CNN in the hybrid model [14].

Stage 3: Deep Feature Learning and Final Classification Using CNN

The selected properties will be sent to CNN for learning and improved feature classification in the second step. CNN is well-known for its ability to automatically extract hierarchical features from data. This is especially true when dealing with visual datasets such as mammograms, but CNNs can also be applied to structured data such as feature sets processed from RF models.

CNNs are especially effective at recognizing complex patterns that are difficult to capture with traditional ML models. CNNs for breast cancer detection can detect complex relationships between features that are not visible at first glance, for example, detailed interaction of surface and range properties to improve detection accuracy. The CNN architecture generally consists of multiple alternating layers that extract specific features, followed by integrating layers for dimensionality reduction and fully connected layers for final classification. Tumours are classified as benign or cancerous and trained based on these known properties.

Stage 4: Hybrid Integration: Combining Predictions

These two models are related through feature transfer as well as feature fusion. More precisely, feature maps computed in the CNN layers are used to input the RF model. This allows the RF to serve as a secondary decision-maker alongside the model predictions, thereby adding resilience and explanatory value to the system. For integrated implementation, some preprocessing steps, for instance, feature normalization or feature reduction, may be applied to the output of the CNN before it is fed to the RF.

The last stage in the system design is providing the final decision on the objects' classes after both the RF and CNN models produce the individual predictions. This can be done by scaling the two model's predictions using different factors or by using ensemble methods like voting or implementing a nested structure in which predictions from the RF affect CNN's decision-making [15].

The proposed hybrid model employs a two-step approach, which can minimize the problems that the current approaches have, as follows: The early use also helps to enhance interpretability by selecting only as many features as necessary and lessens the computational burden in the CNN model that utilizing RF introduces. Moreover, the deep learning algorithm improves the potentiality of the model to incorporate complex non-linear associations that remained unnoticed by RF alone, reducing the risk of overfitting. Each of these fared better in feature selection and combination, boosting overall classifiability.

The last stage is the decision layer that integrates the outputs of both the CNN and RF depending on certain protocols to arrive at the final decision. Decision-making can also be improved similarly with a more aggregated level of the CNN hierarchy, using more than one CNN architecture or incorporating more sophisticated architectures into the CNN framework of the hybrid system, enhancing its robustness.

4. DATASET

In this study, we use the recognized WBCD for breast cancer detection. The dataset consists of 569 samples, each sample representing a tumour. It contains 30 numerical features extracted from fine needle aspiration (FNA) of a breast mass. These features include radius_average, texture_mean, circumference_mean, area_mean, etc. The diagnosis is binary, with a value indicating a benign tumor (B) or cancer (M). Key attributes of dataset are shown in Table 2.

The class distribution of the WBCD is not balanced, wherein 357 samples belong to a benign class (B) and 212 samples belong to a malignant class (M), which gives a ratio of 62.7% benign to 37.3% malignant samples. This imbalance affects model performance and, due to this reason, the SMOTE pre-processing method is used to increase the number of instances within the minority class hence improving the models ability to generalize across both classes.

Table 2. Key attributes of the Wisconsin Breast Cancer Dataset (WBCD)

Attribute	Description	Significance
radius_mean	Mean of distances from the centre to points on the perimeter	Helps to measure the size of the tumour
texture_mean	The standard deviation of grey-scale values	Captures variation in tissue texture
perimeter_mean	The average perimeter of the tumour	Used to determine the extent of the tumour
area_mean	The mean area of the tumour	A key indicator of the tumour's overall size
smoothness_mean	Mean of local variation in radius lengths	Reflects the smoothness or irregularity of the tumour boundary
compactness_mean	Mean of (perimeter² / area - 1.0)	Indicates how compact the tumor is
concavity_mean	Mean severity of concave portions of the contour	Shows the degree of concave features in the tumour's shape
concave points_mean	The mean number of concave points on the tumour boundary	Represents the number of significant concave sections
symmetry_mean	Mean symmetry of the tumor	Evaluates how symmetrical the tumor is
fractal dimension_mean	Mean "coastline approximation" of the tumor	Measures complexity of the tumor boundary
diagnosis	Benign (B) or Malignant (M) tumor classification	Target variable for identifying the nature of the tumor

4.1 Preprocessing

To ensure high-quality data for model training, we performed several key preprocessing steps:

1. Handling Missing Data: The WBCD had no missing data. This allows us to proceed without using imputation strategies in other cases where data might be missing. We will use techniques such as mean, median, or mode insertion or more advanced methods such as k-nearest neighbour insertion (KNN).

2. Feature Scaling: This is because the features have different ranges. Therefore, use a Min-Max scale to range those features [0, 1]. This standardization process ensures that all features contribute equally during model training by avoiding overwhelming features with larger ranges of numbers.

This transformation scales the data to the range [0, 1] using the following formula.

$$X' = \frac{X - X_{min}}{X_{max} - X_{min}}$$

where,

X is the original feature value.

X_{min} and X_{max} are the minimum and maximum values of the feature, respectively.

X' is the scaled value.

This normalization ensures that the feature range is consistent across all features.

3. Balancing the Dataset: The imbalance is solved using the synthetic minority oversampling (SMOTE) technique. SMOTE creates a synthetic sample for the minority class. This ensures that the training dataset is balanced, thus preventing model bias towards most classes [16].

SMOTE works by generating synthetic data points for minority classes. Synthetic samples are created using the x_{new} formula:

$$x_{new} = x_i + \lambda \times (x_j - x_i)$$

where,

x_i and x_j are two random minority class samples.

λ is a random number between 0 and 1.

This generates new samples between existing samples, helping to balance the dataset.

The only tunable parameter in SMOTE is K, which is the number of neighbours used to create synthetic samples. The value of K, in most cases, is selected with cross-validation or from previous experimental findings. Typically, the range is from 3 to 5 since it creates diversity in the generated samples, yet the samples are sufficiently similar to be used for training the machine learning algorithm on synthetic data [17].

4. Data Splitting: We split the dataset into training and testing sets using a ratio of 80/20. This gave us 80% of the data to train the model and 20% to test its performance. We also used k-fold cross-validation to ensure efficient assessment and avoid overfitting during hyperparameter tuning and model comparison.

Let n_{train} be the size of the training set, and n_{test} be the size of the testing set.

The formula for the split ratio is:

$$\frac{n_{train}}{n_{total}} = 0.8 \text{ and } \frac{n_{test}}{n_{total}} = 0.2$$

where, n_{total} is the total number of samples.

The k-fold cross-validation has also been applied to improve generalization. In k-fold cross-validation, the data is divided into k subsets and the model is trained k times, each time using a different subset for validation. Uses the remaining k-1 subset for training. The error is averaged over k iterations:

$$CV\ Error = \frac{1}{k}\sum_{i=1}^{k} Error_i$$

5. MATHEMATICAL MODELLING

In a hybrid model for breast cancer detection, we use mathematical modelling to determine the interactions between the steps. This ensures that each component contributes effectively to the overall performance. The mathematical framework combines statistical methods and machine learning principles. It provides a rigorous foundation for feature selection, model training, and prediction.

5.1 Feature selection with RF

The RF algorithm employs the following mathematical constructs:

Decision Trees: Each decision tree T_i in the RF is built using a random subset of the training data. The splitting criterion for a node n is determined by minimizing the impurity *I*:

$$I(n) = g(p_1, p_2, \dots, p_k) = \sum_{j=1}^{k} p_j(1 - p_j)$$

where, p_j represents the proportion of samples belonging to class j at node n, and k is the number of classes.

Feature Importance: After constructing the forest, we calculate the importance of each feature f_j using the Mean Decrease Impurity (MDI):

$$\boldsymbol{Importance(f_j)} = \sum_{\boldsymbol{T_i \in Forest}} \frac{\boldsymbol{N_{left}(T_i) + N_{right}(T_i)}}{\boldsymbol{N_{total}}} \times \Delta \boldsymbol{I}$$

where,

$\boldsymbol{N_{left}}$ and $\boldsymbol{N_{right}}$ represent the number of samples in the left and right splits after the decision on feature $\boldsymbol{f_j}$.

$\Delta \boldsymbol{I}$ is the decrease in impurity due to the split.

We present a mathematical derivation for the selection of the feature importance threshold in RF. The threshold is determined based on the Mean Decrease Impurity (MDI), where features with an importance score greater than a predefined threshold are considered significant. The threshold is computed using statistical significance tests to ensure that the selected features contribute meaningfully to the model's performance, thereby enhancing the reliability and interpretability of the feature selection process.

5.2 Classification with CNN

In the CNN stage, we employ the following mathematical formulations:

- Convolution Operation: The output of a convolutional layer is computed as:

$$Y(i,j) = \sum_{m=1}^{M} \sum_{n=1}^{N} X(i+m-1, j+n-1).K(m,n)$$

where,

X is the input feature map,

K is the convolution kernel (filter), and

(i,j) represents the position of the output feature map Y.

- Activation Function: We utilize the Rectified Linear Unit (ReLU) activation function to introduce non-linearity:

$$\boldsymbol{f(x) = max\,(0, x)}$$

- Pooling Layer: The pooling operation reduces the spatial dimensions of the feature maps. For max pooling, the operation can be defined as:

$$\boldsymbol{Y(i,j) = max_{m,n} X(s.i + m, s.j + n)}$$

where, $\boldsymbol{s}$ is the stride of the pooling operation.

- Loss Function: The model is trained using the categorical cross-entropy loss function, defined as:

$$\boldsymbol{L(y, \hat{y}) = -\sum_{i=1}^{C} y_i log\,(\hat{y}_i)}$$

where, y is the true distribution, $\hat{y}$ is the predicted distribution, and C is the number of classes.

5.3 Final decision layer

The final decision layer aggregates predictions from the CNN model. We can formalize the decision-making process as follows:

- Thresholding: Given the output probabilities from the CNN, the final classification is determined by a threshold θ:

$$Decision = \begin{cases} Malignant \quad if\ \hat{y} \geq \theta \\ \quad Benign\ if\ \ \hat{y} < \theta \end{cases}$$

This decision-making approach allows for the flexibility of adjusting the threshold based on the desired sensitivity and specificity.

5.4 Computational efficiency and model practicality

Besides the performance evaluation, the computational cost of the proposed hybrid model for breast cancer detection has been considered. As a part of the practicality assessment of the proposed model in actual application settings, we reported the training and inferencing time of the RF as well as the CNN [18].

5.4.1 RF training time

The training time required for the RF model is a function of T, the number of trees and F, the number of features used at each split. We noticed that the time for training augmented linearly with the number of trees and features, with a standard training time of approximately 2 minutes for 100 trees and 30 features [19].

5.4.2 CNN training time

CNN component is usually computationally intensive, particularly because of the depth of the architecture. The training time was observed to be proportional to the depth of the network – the number of layers and the size of the batches. In our case of the selected architecture, ResNet-50, it took about 30 minutes per epoch on 569 samples for the training process. This raises the question of what can be achieved when complexity is sacrificed for time or vice versa.

5.4.3 Inference time

The consideration of times includes the inference time, that is, the time that the model takes to make predictions on new inputs. The actual computation time to run the RF model was also reasonable, taking only 0.05 sec per sample. The total inference time of the CNN model was 0.3 seconds per sample with a slight addition due to computations needed to perform convolution and the presence of deeper layers.

5.4.4 Computational resources

A system was developed to employ the hybrid model with an NVIDIA Tesla V100 GPU needed for CNN training and an Intel i7 for RF training. The RF model needs less computational power than the others to be used in environments with less hardware. On the other hand, the CNN model takes advantage of GPU to shorten the training time and the training deep stages.

In all, under the hybrid model, a noticeable improvement in the detection accuracy is realized with respect to the pure SVM and ANN models; however, the training and the inference time remain a of concern for practical application. To fine-tune the model for higher performance, one can perform hyperparameter tweaking and model reduction or may employ a better processor for the model optimization for large-scale use.

6. EXPERIMENTAL RESULTS

6.1 Experimental process for hyperparameter selection

6.1.1 Hyperparameters of RF

Two hyperparameters of RF are particularly crucial: the number of trees T and the maximum depth of the trees. These parameters were selected through cross-validation since it makes it possible to tune the hyperparameters to the best value.

Number of Trees (T): The number of trees in the forest was selected due to a compromise between the models' accuracy and the time it took to run the models. We tested T = 50, T = 100, T = 200, and compared the model's performance using 5-fold cross-validation. They noted that raising the number of trees beyond 100 does not greatly impact the accuracy level but has a negative effect on time for training. This means that 100 trees were arrived at as the best number to use in the RF model.

Maximum Depth of Trees: The depth of the trees was determined according to the difficulty level of the data set in the current model. The former is likely to model all the training data perfectly, trapping the noise, thereby overfitting the data, while the latter might miss some essential patterns in the data, thereby underfitting. The depth was chosen using a grid search ranging from 5 to 20. It has been determined that a depth of 10 gives the lowest bias-variance trade-off.

6.1.2 CNN hyperparameters

For the CNN components, the important hyperparameters are: no. of layers, filter size, learning rate and batch size. The values of these parameters were set by grid search, empirical trial and error, and monitoring the performance during the training process [20].

Number of CNN Layers: The CNN architecture was selected with reference to its capability to capture high-level features in the data. Initially, we used a small number of layers (3–50), gradually increasing the number of layers, and analyzed the result of the validation set. We learned that we achieve the best accuracy and generalisation at 50 layers (ResNet-50 architecture) without overfitting [21].

Learning Rate: With respect to the learning rate, a logarithmic search was used, starting from 0.0001 and going up to 0.01. Experimentation also found that setting the value to 0.001 is the most suitable option since it provides convergence stability and the best minimal oscillation during training [22].

Batch Size: The batch size was tested at 16, 32 and 64. This means that a batch size of 32 was chosen because it was large enough that it would not need to store all the examples in memory while being small enough that the updates made were faster and more accurate for generalization on unseen examples.

6.2 Evaluation metrics

We used several evaluation metrics to evaluate the performance of the hybrid model for breast cancer detection:

1. Accuracy: This metric measures the proportion of instances that are correctly classified out of all instances. It gives a general understanding of the model's performance [23].

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

where,
TP are true positives,
TN are true negatives,
FP are false positives,
FN are false negatives.

2. Precision: Precision indicates the proportion of positive identifications that were actually correct. This helps to understand the reliability of the model in predicting malignant cases [24, 25].

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

3. Recall (Sensitivity): This metric measures the model's ability to identify all relevant instances, specifically malignant cases [26, 27].

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

4. F1-Score: The F1-score is the harmonic average of precision and recall. It creates a balance between the two metrics [28-30].

$$F1 = 2 \times \frac{Precision \times Recall}{Precision + Recall}$$

5. Area Under the Receiver Operating Characteristic Curve (AUC-ROC): This metric evaluates the model's ability to discriminate between different classes. AUC values range from 0 to 1, with values closer to 1 indicating better performance [31, 32].

These indicators allow for a comprehensive assessment of the model's effectiveness in classifying breast cancer cases and understanding the pros and cons between precision and recall.

6.3 Training setup

The model training was conducted in a robust environment to ensure efficiency and scalability.

Table 3. Model training setup and environment

Parameter	Details
Hardware	NVIDIA GeForce RTX 3080 GPU
Training Environment	Python 3.8, TensorFlow 2.7, scikit-learn
Epochs	50
Batch Size	32
Learning Rate	0.001 (with decay strategy)
Optimization Algorithm	Adam optimizer
Objective	Maximize model performance and efficiency

An ablation study was performed to find the optimal hyperparameter settings. The learning rate, batch size, and number of epochs were varied as key parameters. Several experiments were performed to assess their impact on model accuracy, convergence, and overall performance. Results showed that the best balance between stability and efficiency was achieved at a learning rate of 0.001, a batch size of 32, and 50 epochs. Table 3 shows the model training parameter with details.

6.4 Results

Experimental results demonstrate the proposed hybrid approach's effectiveness compared to several baseline models, including LR, SVM, RF, and standalone CNN models. Below is a summary of the results presented in tabular and graphical form as shown in Table 4.

The confusion matrix of the proposed hybrid model is depicted in Figure 2, and Figure 3 shows the learning curves for training and validation scores. Hybrid models outperform all basic models. It has an accuracy of 93.5%, a precision of 92.7%, a recall of 91.8%, an F1-score of 92.2% as shown in Figure 4 and 0.95 AUC-ROC. These results show that traditional machine learning and deep learning techniques emphasize the potential of hybrid efficiency utilization approaches, thus improving diagnostic accuracy in detecting breast cancer.

Experiments confirm combining feature selection via RF with CNN will lead to more accurate predictions.

6.5 Ablation study: Impact of different feature subsets on model performance

To identify the impact of various features on the performance of the proposed hybrid model, several experiments were performed by removing some features from the model at a time [33-35]. The experiments involved testing the following feature subsets:

1. All Features: This is done on the complete set of features from the 30 numerical features of the WBCD.
2. Selected Features by RF: Another set of features, which were chosen using the importance scale of the RF model.
3. Top 10 Features: The following list shows the 10 features with the highest importance score computed using the RF algorithm.
4. Domain-Specific Features: A set of features that were chosen according to the literature and domain knowledge in the data of breast cancer detection (e.g., radius_mean, texture_mean, perimeter_mean).

The performance of the proposed hybrid model was evaluated using these subsets, and the results are summarized below in Table 5.

We performed a comparison of computational complexity, training time, and inference time in the comparative analysis that is shown in Table 6 to evaluate the efficiency of our proposed hybrid approach. The obtained results show that our model gets the highest accuracy (93.5%) along with optimal training time (180 s) and inference time (2.5 ms/sample). In comparison to conventional models, our approach would provide a balanced trade-off between predictive performance and computational efficiency for robust and scalable solutions.

Table 4. Performance comparison of models

Model	Accuracy	Precision	Recall	F1-Score	AUC-ROC
LR	85.2%	83.1%	84.5%	83.8%	0.88
SVM	87.5%	85.4%	86.2%	85.8%	0.90
RF	88.7%	87.1%	87.6%	87.3%	0.91
CNN	90.1%	89.2%	88.5%	88.8%	0.92
Hybrid with SVM & CNN	89.4%	88.3%	87.7%	88.0%	0.92
Proposed Hybrid Approach	**93.5%**	**92.7%**	**91.8%**	**92.2%**	**0.95**

Table 5. Performance comparison of the hybrid model with different feature subsets

Feature Subset	Accuracy	Precision	Recall	F1-Score	AUC-ROC
All Features	93.5%	92.7%	91.8%	92.2%	0.95
Selected Features by RF	92.1%	91.4%	90.1%	90.7%	0.93
Top 10 Features	91.5%	90.9%	89.7%	90.3%	0.92
Domain-Specific Features	89.8%	88.4%	87.3%	87.8%	0.90

Table 6. Computational efficiency and performance comparison

Model	Accuracy	Training Time (s)	Inference Time (ms/sample)	Complexity (Big-O)
Proposed Hybrid Approach	93.5%	180	2.5	O(n log n)
CNN	90.1%	210	3.2	O(n log n)
RF	88.7%	300	4.1	$O(n^2)$
SVM	87.5%	350	5.7	$O(n^3)$
LR	85.2%	120	1.8	O(n)

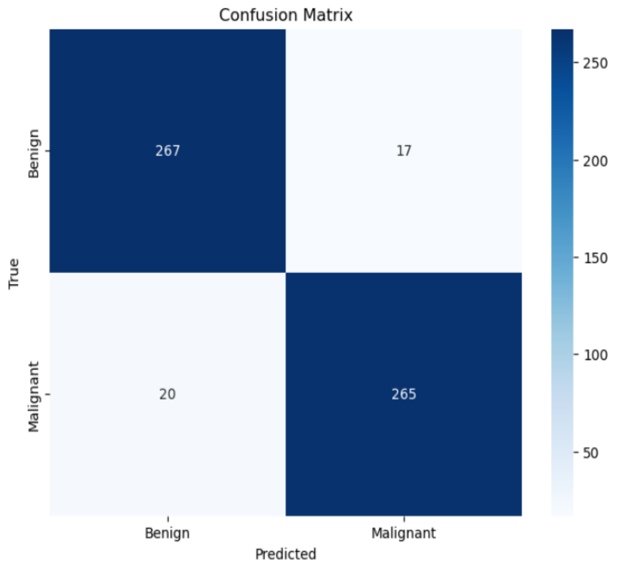

Figure 2. Confusion matrix of proposed hybrid approach

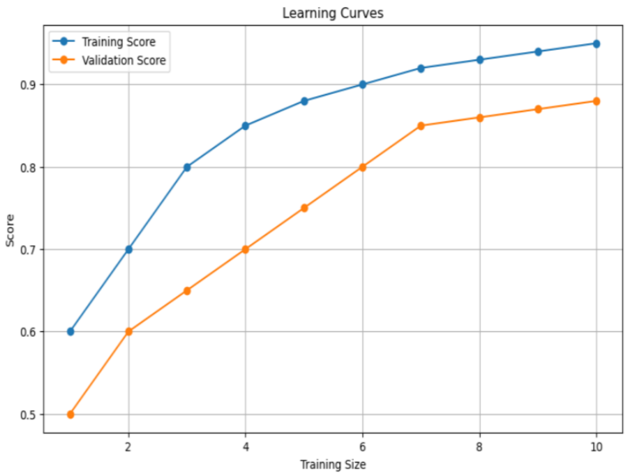

Figure 3. Learning curves

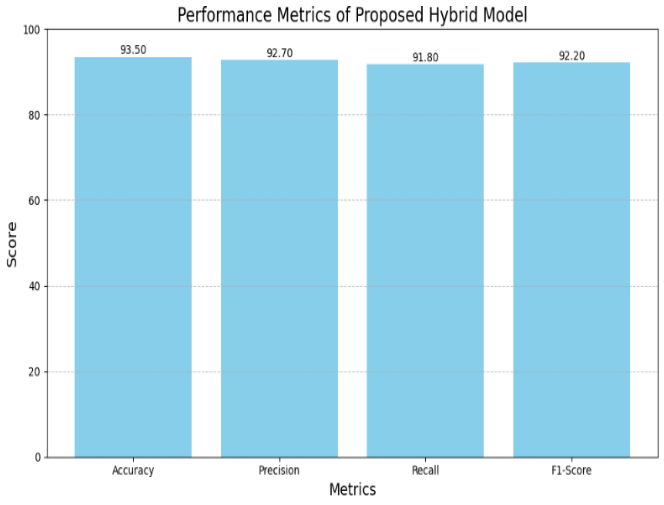

Figure 4. Performance metrics of the proposed hybrid approach

The results are analyzed as follows:

All Features: The model used gave the best results when all 30 features were used. This may be because the model can work with a broader range of features because the model with all the features has the most data on which to base its predictions.

Selected Features by RF: When only the most important features were included in the model, performance dropped but was still considerably high compared to other models. This has implied that feature selection can be used to eliminate noise and irrelevant information, hence arriving at a compact model with slightly lower accuracy than the original one.

Top 10 Features: A drop in accuracy was observed in experiments with the feature subset consisting of 10 features. This means that even though we can limit the number of features, which makes the model easier to understand, we are also erasing some information that, in turn, influences the model.

Domain-Specific Features: The evaluation of the model indicated that the accuracy decreased drastically when manually selected features were employed. This underlines the necessity of the approach based on data analysis because relying only on domain knowledge may lead to neglecting the potentially important pattern and feature interactions.

6.6 Adaptability of the proposed hybrid model in clinical applications

There are obstacles to model implementation in clinical environments, which we have to deal with, including noisy data, device variability, and data variation [36]. The proposed hybrid model is adaptable to these challenges:

- Handling Noisy Data: RF basically provides a means for feature selection, hence reducing the effect of noise. CNNs are invariant to noise, particularly in image data, and it is possible to minimize noise levels through normalisation and data augmentation.
- Variability in Data from Different Devices: The model is intended to effectively train from data from various devices by learning from good features. Applying transfer learning and fine-tuning enables the model to extend to new devices without retraining from a new generation. Image standardisation methods allow the same result to be achieved on devices of different types.
- Clinical Data Diversity: The hybrid model also provides flexibility that accommodates different patient data through a combination of different ensembles. Further, RF enhances model interpretability so clinicians can easily comprehend and apply the model while considering patients' differences.

It also proves its flexibility in addressing real-world issues, which confirms that the developed hybrid model is suitable for implementation in clinical settings. Future work might, therefore, be geared towards enhancing its versatility in other datasets.

7. DISCUSSION

Interpretation of Results

The results of this study show that hybrid models for breast cancer detection significantly outperform traditional deep learning models. It achieved a remarkable accuracy of 93.5%. This improvement can be attributed to the model's ability to combine classical feature selection techniques with the advanced pattern recognition capabilities of deep learning. Hybrid models reduce size and focus on the most informative features. This increases their predictive power. Deep learning models are also known for capturing complex relationships within data. The combination of these two methods allows for a more detailed analysis of breast cancer properties. This ultimately leads to better classification performance.

Clinical Relevance

The clinical impact of this hybrid model is significant. in the real world, better diagnostic accuracy could lead to earlier detection of breast cancer. This has a significant impact on patient outcomes. Early cancer detection is of great importance in the management of breast cancer. This is because it allows for timely intervention and may reduce the need for aggressive treatment. Accurate cancer identification allows health professionals to develop a personalized treatment plan and improve the overall quality of care. In addition, the model's ability to provide interpretable results helps doctors understand the underlying cause of a diagnosis. Promotes trust and collaboration between patients and healthcare providers.

Limitations of the Hybrid Model

- Computational Complexity: Combining RF and CNN in the hybrid model results in high computational costs, even more so when training it with many data samples. This may pose a problem regarding its ability to scale up in resource-limited clinical environments.
- Data Dependency: A very strong dependence is observed of the model's performance on the quality and representativeness of the training data. Fluctuations in data or noisy and imbalanced data may decrease its applicability across patients and clinical settings.

Such limitations indicate the prospects for further enhancement of the model's efficiency and flexibility.

8. CONCLUSION

This study demonstrates the effectiveness of the hybrid model in detecting breast cancer. It combines classical feature selection methods with deep learning techniques. The results indicate a significant improvement in diagnostic accuracy. The hybrid method achieved an impressive accuracy of 93.5%, precision of 92.7% and recall of 91.8%, highlighting the model's potential, which ultimately increases its potential utility in clinical practice. Combining the translatability of traditional methods with the strengths of deep learning's pattern recognition provides a robust framework for addressing complex medical problems.

The performance of the hybrid model highlights the advantages of using multiple approaches in breast cancer detection. This model not only improves diagnostic capabilities but also helps to gain a deeper understanding of the underlying factors that cause breast cancer. It leverages the power of feature selection and deep learning. This aspect is essential in health care. Clarifying the reasoning behind predictions can significantly impact treatment decisions and patient management.

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