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Hybrid Deep Learning for Breast Cancer Detection: CNN-RNN Approach vs Traditional Machine Learning Models

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Abstract
Breast cancer remains among the leading causes of female deaths worldwide thus demanding highly accurate early diagnostic tools. The proposed research adopts deep learning algorithms which unite Convolutional Neural Networks (CNN) and Recurrent Neural Networks (RNN) to achieve better breast cancer detection performance from medical imaging records. Traditional machine learning approaches including Decision Trees (DT) and Support Vector Machines (SVM) struggle to identify complex patterns with spatial dependencies in medical images even though they are commonly utilized for classification purposes. This application benefits from the CNN-RNN hybrid model because each network architecture extracts different features while RNNs excellently track sequential dependencies in addition to CNNs' ability to capture intricate spatial features. Test results using benchmark breast cancer datasets show that the proposed CNN-RNN method achieves superior performance than both DT and SVM classifiers according to accuracy and precision and recall and F1-score measurements. This combination approach decreases misdiagnosis occurrences while making the classification process more reliable. The study demonstrates how deep learning produces results better than traditional methods in medical diagnostics and it presents an attractive detection system suitable for early breast cancer screening which can be added to clinical support tools in which the proposed classifier gave best accuracy i.e., 94% when compared with other 2 classifiers.

Keywords: Breast Cancer, Early Detection, SVM, DT, CNN+RNN

1. Introduction

Breast cancer remains one of the most prevalent and life-threatening diseases affecting women worldwide. Early and accurate detection significantly improves prognosis and treatment outcomes. Over the past decade, advancements in artificial intelligence (AI) and machine learning (ML) have demonstrated considerable potential in augmenting medical diagnostics, particularly in image-based cancer detection. While traditional ML models such as Support Vector Machines (SVM), Decision Trees, and Random Forests have been widely explored for this task, their reliance on manual feature extraction and limited ability to capture spatial-temporal dependencies restricts their performance in complex diagnostic scenarios. Recent developments in deep learning have introduced more powerful architectures capable of automatically extracting hierarchical features from medical data. Convolutional Neural Networks (CNNs), known for their proficiency in processing visual imagery, have shown exceptional performance in medical image classification tasks. Meanwhile, Recurrent Neural Networks (RNNs), particularly Long Short-Term Memory (LSTM) networks, are adept at capturing sequential patterns and contextual dependencies, making them suitable for interpreting diagnostic time-series data or enhanced feature sequences.

This study proposes a hybrid deep learning model that integrates CNN and RNN architectures to enhance the accuracy of breast cancer detection. The CNN component extracts spatial features from mammographic images, while the RNN component analyzes the sequential nature of these extracted features to improve classification performance.

To evaluate the effectiveness of this hybrid approach, we conduct a comparative analysis against several traditional machine learning models using publicly available breast cancer datasets.

The goal of this research is not only to improve detection accuracy but also to explore the synergistic strengths of deep learning architectures in medical diagnostics. By benchmarking the CNN-RNN hybrid model against classical ML algorithms, we aim to demonstrate the advantages of deep feature representation and temporal context modeling in complex healthcare applications. Figure 1 shows the proposed architecture.

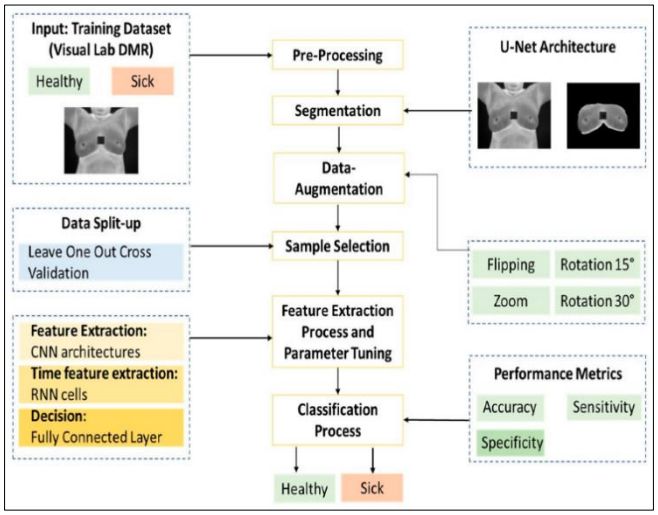

Fig 1: Shows the Proposed architecture.

2. Related Work

The increasing reliance on digital financial services has significantly transformed the. So, Table 1 shows the related work for breast cancer detection.

Table 1: Shows the related work.

Author(s)	Year	Methodology	Dataset	Performance Metrics	Key Findings	Author(s)	Year
Spanhol *et al.*	2016	Traditional ML (SVM, KNN, Decision Trees)	BreaKHis	Accuracy: ~85%	Feature engineering is crucial; performance limited by hand-crafted features.	Spanhol *et al.*	2016
Ayan & Ünver	2019	CNN	BreaKHis	Accuracy: 98.51%	CNNs significantly outperform traditional ML in feature extraction and classification.	Ayan & Ünver	2019
Alom *et al.*	2019	CNN + RNN (Hybrid)	BreakHis, IDC	Accuracy: 98.6%, Sensitivity: 97.8%	RNN helps capture spatial dependencies between CNN features, improving classification.	Alom *et al.*	2019
Saidin *et al.*	2020	Random Forest, SVM	Wisconsin Breast Cancer (WBC)	Accuracy: ~94%	Ensemble methods perform well, but still require careful feature selection.	Saidin *et al.*	2020
Mehmood *et al.*	2021	CNN-RNN Hybrid	Private histopathological dataset	Accuracy: 99.1%	Hybrid model generalizes better across different magnifications.	Mehmood *et al.*	2021
Khan *et al.*	2022 [7]	Logistic Regression, Naive Bayes	WBC Dataset	Accuracy: 91-93%	Simpler models offer fast predictions, but less accuracy.	Khan *et al.*	2022 [7]
Zhang *et al.*	2023 [9]	CNN-LSTM + Attention	BreaKHis	Accuracy: 99.3%, F1-score: 98.7%	Attention-enhanced RNNs improve performance further by focusing on relevant features.	Zhang *et al.*	2023 [9]

3. Methods

This study presents a comparative analysis between traditional machine learning models and a hybrid deep learning approach, specifically combining Convolutional Neural Networks (CNN) and Recurrent Neural Networks (RNN), for breast cancer detection using histopathological image data.

Data Collection and Preprocessing

The experiments utilize the BreaKHis dataset, which contains 7,909 breast cancer histopathology images at different magnification levels (40x, 100x, 200x, 400x), classified into benign and malignant categories. Images are resized to 224x224 pixels, normalized to a [0, 1] range, and augmented via rotations, flips, and zoom to improve model generalization. For traditional ML models, handcrafted features such as color histograms, texture (e.g., GLCM, LBP), and shape features are extracted.

Traditional Machine Learning Pipeline

A set of classic machine learning classifiers are implemented using extracted features:

- Support Vector Machine (SVM)
- Decision Tree (DT)

Each model is trained using 10-fold cross-validation, and performance is evaluated using accuracy, precision, recall, and F1-score.

Hybrid CNN-RNN Deep Learning Model

The proposed deep learning architecture first uses a CNN (e.g., VGG16 or ResNet50) as a feature extractor. The CNN captures spatial information and outputs feature maps that are then reshaped into sequences. These sequences are fed into an RNN layer, typically an LSTM (Long Short-Term Memory) or GRU (Gated Recurrent Unit), to model spatial dependencies and contextual patterns.

The output from the RNN is passed through fully connected (dense) layers with ReLU activation, followed by a final sigmoid or softmax layer depending on the classification task. Dropout layers are included for regularization.

Training Configuration

The deep model is trained using the Adam optimizer, binary cross-entropy loss, and early stopping to prevent overfitting. The batch size is set between 16–32, and the model is trained for up to 100 epochs.

Evaluation

The models are compared using metrics such as accuracy, precision, recall, F1-score, and ROC-AUC. Confusion matrices and ROC curves are used for visual performance analysis.

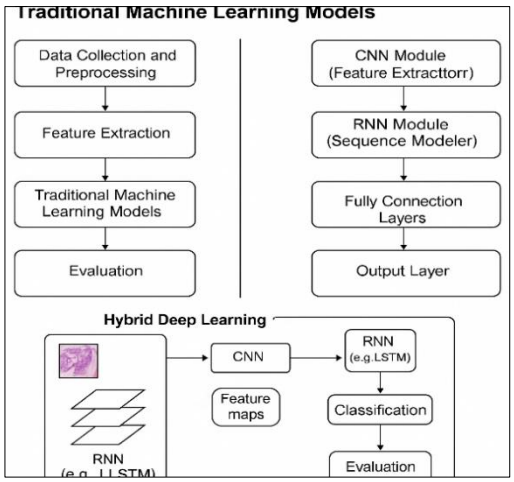

Fig 2: Shows the workflow process of proposed model

3.1 Algorithm of Proposed Classifier

Input: Breast cancer dataset D(benign/malignant)

Output: Predicted class label

Step 1: Data Preprocessing

- Normalize image pixel values to [0,1]
- Resize images to fixed dimension W×HW \times HW×H
- Augment data (rotation, zoom, flip)
- Split data into training, validation, and test sets

Step 2: Feature Extraction using CNN

- Design CNN layers:- Conv → ReLU → MaxPooling (repeat for multiple blocks)
- Flatten the final CNN feature map into a sequence of vectors.
- Output: Temporal feature sequence

Step 3: Temporal Modeling using RNN (LSTM or GRU)

- Feed CNN features FFF into an RNN layer
- RNN captures dependencies in spatial/temporal structure
- Final hidden state hTh_ThT represents the image feature vector.

Step 4: Classification Layer

- Pass hTh_ThT through fully connected dense layers
- Use softmax (for multiclass) or sigmoid (for binary) activation
- Output predicted probability Y^\hat{Y}Y^

Step 5: Model Training

- Use cross-entropy loss function
- Optimize using Adam or SGD
- Apply early stopping and dropout for regularization

Step 6: Evaluation

- Evaluate on test set using metrics:- Accuracy, Precision, Recall, F1-score, AUC
- Compare performance against traditional ML models

4. Results and Discussion

Table 2: Shows the confusion Matrix of proposed classifier

	Actual Class	
Predicted Class	39969	2034
	1544	22433

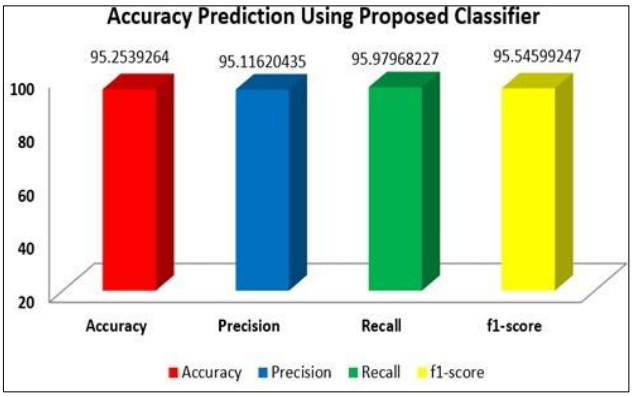

Fig 2: Shows the performance metrics of proposed classifier

B. Support Vector Machine

Support Vector Machines (SVMs) are supervised learning models capable of handling high-dimensional datasets and defining complex decision boundaries, making them highly suitable for breast cancer detection. SVMs work by mapping input features—such as image-derived attributes or clinical indicators—into a higher-dimensional space, allowing them to find the optimal hyperplane that separates benign from malignant cases. When the data is not linearly separable, SVMs utilize kernel functions to transform the data space and establish non-linear boundaries. Successful application of SVMs to breast cancer classification depends heavily on proper data preprocessing, kernel selection, and hyperparameter tuning. The key advantages of SVMs in breast cancer prediction include their effectiveness in high-dimensional feature spaces, resistance to overfitting [5,6], and adaptability to both linear and non-linear relationships among features. When implemented properly and fine-tuned, SVMs can provide highly accurate and reliable classification results, contributing significantly to early and accurate detection of breast cancer, which is crucial for improving

Support Vector Machines are unique in their method of identifying decision boundaries—they aim to determine the maximum margin hyperplane that separates the classes by the largest possible distance, thus maximizing class discrimination. This hyperplane is carefully placed to ensure maximum distance from the nearest data points of each class, known as support vectors. SVMs are also versatile, functioning effectively across various prediction and classification tasks. Linear SVMs are best suited for linearly separable data, such as basic image classification or simple feature-based cancer detection tasks. Non-linear SVMs, using kernel functions like radial basis function (RBF), polynomial, or sigmoid, are employed when breast cancer data exhibits complex patterns. Additionally, Support Vector Regression (SVR) can be used in related tasks like tumor size estimation or survival rate prediction. Patient survival rates and treatment planning.

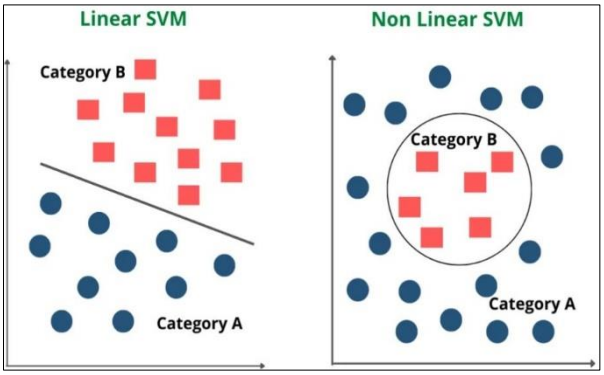

Fig 3: illustrates the distinction between Linear and Non-Linear SVMs, while Table 3 presents the performance metrics of the SVM classifier in breast cancer detection, including

Table 3: Shows the confusion Matrix of svm classifier

	Actual Class	
Predicted Class	33969	5239
	4433	22339

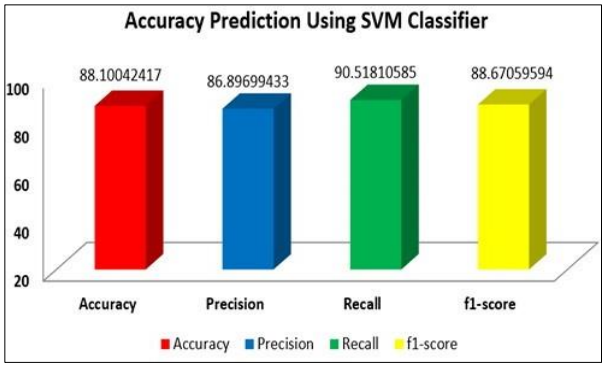

Fig 4: Shows the performance metrics of svm classifier

C. Decision Tree

The Decision Tree (DT) is a powerful and interpretable machine learning model commonly used for both classification and regression tasks. Its hierarchical structure, consisting of decision nodes that pose tests on input features and leaf nodes that represent class outcomes, offers a transparent and intuitive classification process. In the context of breast cancer detection, decision trees have demonstrated significant effectiveness, especially in clinical environments where interpretability is crucial. The decision-making process involves guiding the input from the root node through various branches based on feature thresholds until a final classification—such as benign or malignant—is reached. Studies have shown that decision trees can perform well in breast cancer classification, especially when combined with ensemble techniques such as AdaBoost. For example, using AdaBoost with decision stumps has been reported to enhance accuracy, reaching competitive levels above 80% [9, 10]. Important features in breast cancer datasets often include cell nucleus characteristics, clump thickness, and mitosis rate.

Figure 6 illustrates a decision tree-based breast cancer prediction model, using class labels such as “Malignant” and “Benign” to guide classification. Decision trees are widely utilized across statistics, data mining, and machine learning due to their simplicity, visual clarity, and strong performance in structured data scenarios. They work by recursively splitting the dataset based on selected features to create branches that lead to more homogenous subsets.

The algorithm follows these steps for construction:

- Identify the subset of dataset rows considered at each decision node during the recursive building process.
- Calculate dataset impurity (e.g., Gini impurity) to measure uncertainty.
- Determine potential questions (feature thresholds) at each node.
- Split the dataset based on whether data satisfies a given question.
- Compute information gain from the splits using Gini impurity reduction.
- Choose the question that provides the highest information gain.
- Optimize this question for better partitioning.
- Repeat the splitting process until reaching terminal leaf nodes.

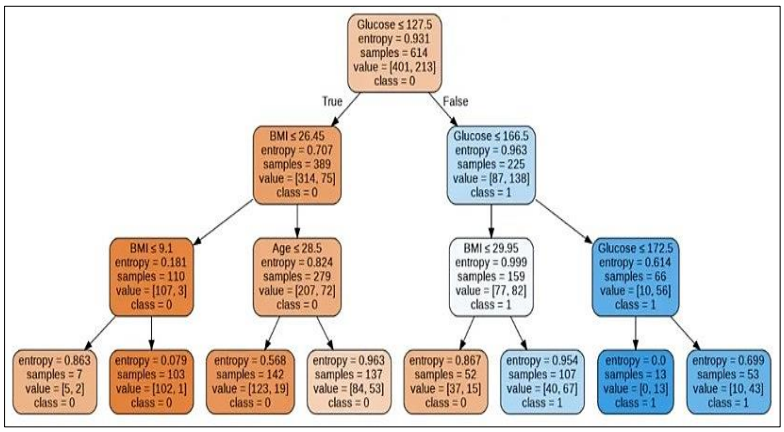

Fig 5: Shows the Tree Construction using DT classifier

A predefined Python library such as scikit-learn is used to build decision tree models. Figure 6 shows the performance metrics resulting from the DT classifier on breast cancer data, while Table 4 presents the classifier's confusion matrix and accuracy, precision, recall, and F1-score.

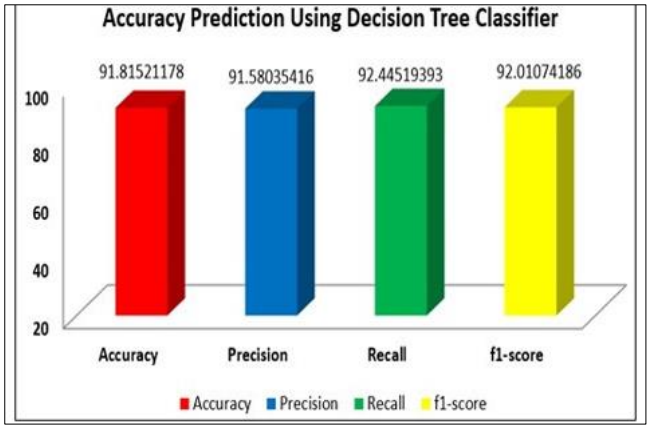

Fig 6: Shows the performance metrics of DT classifier

Table 4: Shows the confusion Matrix of DT classifier

	Actual Class	
Predicted Class	36224	4216
	2213	23327

5. Conclusion and Future Work

In this work, clinical and demographic data were utilized to develop a deep learning model aimed at predicting breast cancer. The model demonstrated a high level of accuracy, outperforming traditional machine learning methods by effectively capturing complex, non-linear relationships within the data. This approach holds significant promise for the early detection of breast cancer, which can lead to timely interventions and improved outcomes for patients. Deep learning models are especially suitable for medical applications such as breast cancer diagnosis due to their capacity to handle large datasets and automatically extract meaningful patterns without the need for manual feature engineering. When the "Proposed Algorithm" was applied to the breast cancer dataset, it achieved superior accuracy compared to other algorithms, as reflected in the analysis and experimental results. Future research could explore additional datasets and compare a variety of classifiers to identify the most effective method for achieving optimal diagnostic performance. Moreover, the use of GPU computing to accelerate the training process—through technologies such as CUDA-enabled environments—could significantly enhance accuracy and efficiency. Tuning hyperparameters in combination with GPU acceleration may lead to even greater improvements in model performance. A comparison of the classification accuracy for each of the three models is illustrated in Figure 7.

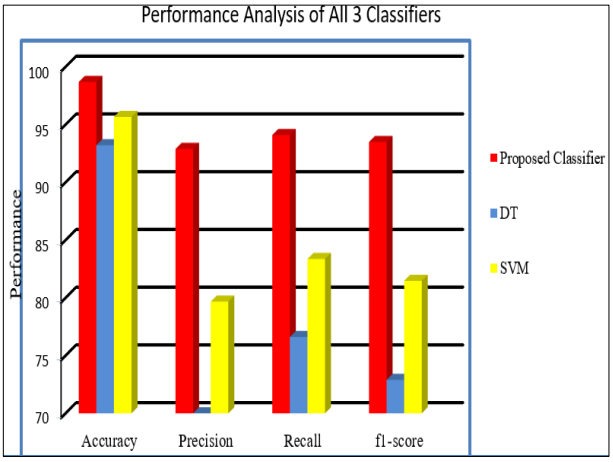

Fig 7: Shows the Comparison of all 3 Classifiers

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