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Review Article

Exploring AI Algorithms for Cancer Classification and Prediction Using Electronic Health Records

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Abstract: Cell division that is not controlled leads to cancer, an incurable condition. An early diagnosis has the potential to lower death rates from breast cancer, the most frequent disease in women worldwide. Imaging studies of the breast may help doctors find the disease and diagnose it. This study explores an effectiveness of DL and ML models in a classification of mammography images for breast cancer detection, utilizing the publicly available CBIS-DDSM dataset, which comprises 5,000 images evenly divided between benign and malignant cases. To improve diagnostic accuracy, models such as Gaussian Naïve Bayes (GNB), CNNs, KNN, and MobileNetV2 were assessed employing performance measures including F1-score, recall, accuracy, and precision. The methodology involved data preprocessing techniques, including transfer learning and feature extraction, followed by data splitting for robust model training and evaluation. Findings indicate that MobileNetV2 achieved a highest accuracy99.4%, significantly outperforming GNB (87.2%), CNN (96.7%), and KNN (91.2%). The outstanding capacity of MobileNetV2 to identify between benign and malignant instances was shown by the investigation, which also made use of confusion matrices and ROC curves to evaluate model performance.

Keywords: Breast cancer, Mammography, MobileNetV2, CBIS-DDSM Dataset, Electronic Health Records (EHR)

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1. Introduction

Histology was vital in determining cancer prognosis and diagnosis over a century ago. Anatomic pathologists evaluate and rank lesions by examining histology for characteristics such nuclear atypia, mitotic activity, cellular density, and tissue architecture, as well as by combining cytologic details and higher-order patterns. Prognostication is increasingly reliant on genomic biomarkers that evaluate genetic alterations, gene expression, and epigenetic alterations; yet, histology remains an invaluable tool for predicting the future course of a patient's illness [1]. On one hand, histology gives a visual representation of disease aggressiveness via its phenotypic data, which reflect the cumulative impact of molecular changes on cancer cell behaviour. As a result of the inherent subjectivity and lack of repeatability in human histology evaluations, computer analysis of histology images has garnered considerable interest. Recent developments in computer power and slide scanning microscopes have allowed for the creation of many image processing algorithms that can grade, classify, and identify lymph node metastases in a variety of cancers [2].

It is critical to precisely identify hospitalised patients' diseases or conditions in real-time before producing direct patient treatment, enhancing quality, developing in-hospital registries, and adopting EHR interventions such as clinical decision support. Theoretically, issue lists allow for easy patient identification of conditions like heart failure; thus, documenting of problem lists has been linked to better treatment quality [3]. A large proportion of people with a particular ailment go unrecognized since issue lists are often lacking in detail [4].

Breast cancer is the second leading cause of cancer-related deaths among women, behind lung cancer. The United States is projected to have 246,660 new instances of invasive breast cancer in women in 2016, with an anticipated 40,450 deaths from the disease. Among female malignancies, breast cancer accounts for 25% and accounts for around 12% of all new cases. Potential use of information and communication technologies (ICT) in cancer treatment are being explored. Big data has revolutionized business intelligence (BI) by expanding the scope of reporting and decision-making to include prediction outcomes, and it has also increased the bulk of data and the value that can be extracted from it. The use of data mining techniques in the medical field, for example, is on the increase because of the many benefits it offers, including better health prediction, lower healthcare costs, more efficient use of resources, enhanced healthcare quality and value, and the ability to make life-saving decisions in real time [5].

The performance standards in several difficult applications have been smashed by deep CNNs, which have become an essential tool for image processing. The ability of CNNs to acquire predictive traits from raw visual data signifies a paradigm shift, opening up exciting new avenues for medical imaging. Medical image analysis has made extensive use of the feature engineering technique to train models capable of predicting patient outcomes. Employing segmentation algorithms to clearly define structures of interest and then establishing a reputation for accuracy via measurements is the essence of this strategy [6].

A purpose of this paper is to explore the effectiveness of various ML and DL models in classifying mammography images from the CBIS-DDSM dataset to enhance breast cancer detection. This project intends to assess different models' performance by using cutting-edge methods including feature extraction and transfer learning. Its ultimate goal is to help enhance breast cancer diagnosis accuracy and patient outcomes. The CBIS-DDSM dataset research on cancer classification and prediction using electronic health records contributed the following:

- Provides a detailed methodology for data collection, preprocessing, and classification model implementation, establishing a clear roadmap for future research in medical image analysis.
- Compares the performance of multiple classification models, including Gaussian Naïve Bayes, CNN, K-Nearest Neighbors, and MobileNetV2, highlighting an efficacy of DL approaches in cancer diagnosis.
- Employs comprehensive performance metrics, like F1-score, recall, accuracy, and precision, to evaluate and validate the effectiveness of the models, ensuring robust and reliable results.
- Demonstrates that MobileNetV2 achieves superior accuracy compared to other models, underscoring the potential of DL to enhance the accuracy of breast cancer detection through advanced image analysis techniques.

A. Structure of the paper

The following is the structure of the study: Methods currently used for analysing mammography images are reviewed in Section 2. Data gathering and preparation are detailed in Section 3, which also contains the study methodology. The outcomes of the experiments are detailed and discussed in Section 4. Finally, Section 5 presents the most important results and suggests avenues for further study.

2. Literature Review

This section provides an overview of important ML and DL research related to similar datasets and challenges, limitations, results and emphasizing notable methods and studies. The important literature in this field is briefly outlined in Table 1.

In this study, Naveen, Sharma and Ramachandran Nair, (2019) to accurately forecast an occurrence of breastcancer based on cancer characteristics. With the help of the breast cancer Coimbra dataset from the University of California Irvine (UCI), the best ensemble ML models were created. Our primary procedures here include feature scaling, cross validation, and a number of ensemble ML models that make use of the bagging technique. The most accurate methods are decision trees and KNN, which provide a 100% record. Our nearest neighbours are denoted by k. Along with it, we assess its forecast using the categorisation report, confusion matrix, and accuracy. Constructing the best possible machine learning model is our primary objective. As a consequence of the prognosis, the patient may begin therapy at an earlier stage [7].

The purpose of this study, Badriyah et al., (2018) aims to help patients understand their cervical cancer risk factors, so that they may seek additional treatment if necessary, in the event that a high-risk level is detected. The study's data came by a RSI Jemursari Hospital in Surabaya, Indonesia, and the application was built employing the LR approach. The data was collected from August 1, 2017, to December 1, 2017. According to the findings, vaginal bleeding, vaginal lumps, and lower abdominal or waist discomfort all significantly increase the chance of cervical cancer. Patients may use this application to determine their estimated risk of developing cervical cancer. As compared to two other approaches, the LR method yields superior outcomes, according on the findings of studies conducted using NB and DT. Approximately 95% of the data can be classified accurately using the LR approach, and the classification precision on both precision and recall is very high. This indicates that the performance of the method is quite strong [8].

This paper, Mercan et al., (2018) highlights our possible approaches to overcoming these obstacles via the use of pathologists' viewing records and their comments at the slide level in poorly supervised learning situations. To begin, they analyze the pathologists' image screening logs for suitable ROIs based on several behaviors, including zooming, panning, and fixation. The next step is to use the pathology forms' extracted class labels and a bag of instances representing the possible ROIs to model each slide. Finally, for diagnostic category predictions in whole-slide breast histopathology pictures, they apply four distinct multi-instance multi-label learning methods at the slide level and at the ROI level. Various poorly labelled learning situations revealed average accuracy values of 69% and 81% for slide-level assessment utilizing 14-class setups, respectively. Classifier performance was shown by ROI-level predictions inside entire slide pictures chosen to include all difficult diagnostic categories, demonstrating good multi-class localization and classification [9].

In this study, Harrell, Levy and Fabbri, (2017) in order to get an AUC of 0.74, the RFC was used in conjunction with variables pertaining to medical appointments, demographics, and health. Our RF model finds that patient age, median income by zip code, and total drug counts to be the strongest predictive factors for follow-up. Our findings imply that the frequency with which patients visit VUMC for treatment (i.e., primary care) may be associated with more accurate follow-up prediction. Patients undergoing adjuvant endocrine treatment had their follow-up dates reasonably predicted using data from their electronic health records in this research. Interventions to increase follow-up rates and patient care for adjuvant endocrine treatment groups may be facilitated by follow-up prediction. The capacity to identify areas for EHR data-driven patient care improvement is shown by this research [10].

In this paper, Khuriwal and Mishra, (2018) selected a technique for adaptive ensemble voting based on the Wisconsin Breast Cancer database for breast cancer diagnoses. The purpose of this work is to use ensemble ML approaches to compare and explain the better results provided by ANN and logistic algorithms for breast cancer detection, even when variables are reduced. Wisconsin Diagnosis Breast Cancer was the dataset used in this research. In comparison to other relevant material. It has been shown that an alternative ML method yielded an accuracy of 98.50% when applied to an ANN strategy using a logistic algorithm [11].

Table 1. Comparative research table for cancer classification and prediction using electronic health records

Ref	Methodology	Dataset	Result	Limitations and Future Work
[7]	Ensemble learning with bagging (Decision Tree, KNN)	Breast Cancer Coimbra dataset (UCI)	100% accuracy (Decision Tree and KNN)	High accuracy may be dataset-specific; results not generalizable
[8]	Logistic Regression, Naïve Bayes, Decision Trees	RSI Jemursari Hospital, Surabaya (Cervical Cancer Data)	Logistic Regression achieved 95% accuracy	Limited dataset and period; focused on specific risk factors
[9]	Multi-instance multi-label learning	Pathologists' viewing records, slide-level annotations	Average precision of 81% (5-class), 69% (14-class)	Weakly supervised learning scenarios
[10]	Random Forest Classifier	Electronic Health Records (EHR)	AUC of 0.74, predictive features: medication count, age, income	Moderately accurate, limited predictive ability for follow-up
[11]	Adaptive ensemble voting (ANN, Logistic Algorithm)	Wisconsin Breast Cancer dataset	98.50% accuracy (ANN with logistic algorithm)	Limited comparison with other methods; dataset reduction effects unknown

A. Research gaps

According to the research being examined, a number of different machine learning algorithms are helpful in predicting illnesses such as breast cancer and cervical cancer, as well as in providing follow-up treatment for patients. There are, however, a number of holes. To begin, the specificity of the datasets used in many research is a limitation that may impair the capacity of the models developed to be generalized to larger populations. Additionally, the dependence on limited or localized datasets hinders the possibility for rigorous model validation across varied healthcare systems. Furthermore, although ensemble approaches and sophisticated classifiers like artificial neural networks (ANN) and logistic regression all provide high levels of accuracy, there is still a lack of study into hybrid or innovative deep learning architectures. Finally, there is a need for more research into enhancing weakly supervised learning and multi-instance learning techniques, particularly for increasingly complicated and large-scale medical datasets. This is necessary in order to attain improved predicted results and application of real-time diagnostic algorithms.

3. Research Methodology

The main goal of this study is to evaluate several AI algorithms for cancer classification and prediction using EHR. By leveraging ML and DL techniques, the study seeks to identify key patterns and predictive markers within EHR data that can aid in early cancer diagnosis, risk assessment, and personalized treatment recommendations. The end objective is to improve clinical decision-making and patient outcomes by making cancer prediction models more accurate and reliable. For this used CBIS-DDSM dataset, which contains 5,000 publicly accessible mammography pictures and serves as a vital resource for training and assessing algorithms in mammography image interpretation, is the first stage in the technique for this work. Through methods like feature extraction and transfer learning (with and without fine-tuning), data pre-processing converts the raw pictures into a format that can be used to adapt pre-trained models to the dataset. Data splitting is used to partition the dataset into training and test sets after pre-processing, which allows for model hyperparameter adjustment and generalisation performance estimate. Lastly, a variety of classification models are used and contrasted based on performance criteria to see how well they identify mammography data: Gaussian Naïve Bayes, CNNs, KNN, and MobileNetV2. The process flow diagram for detecting financial fraud is shown in Figure 1.

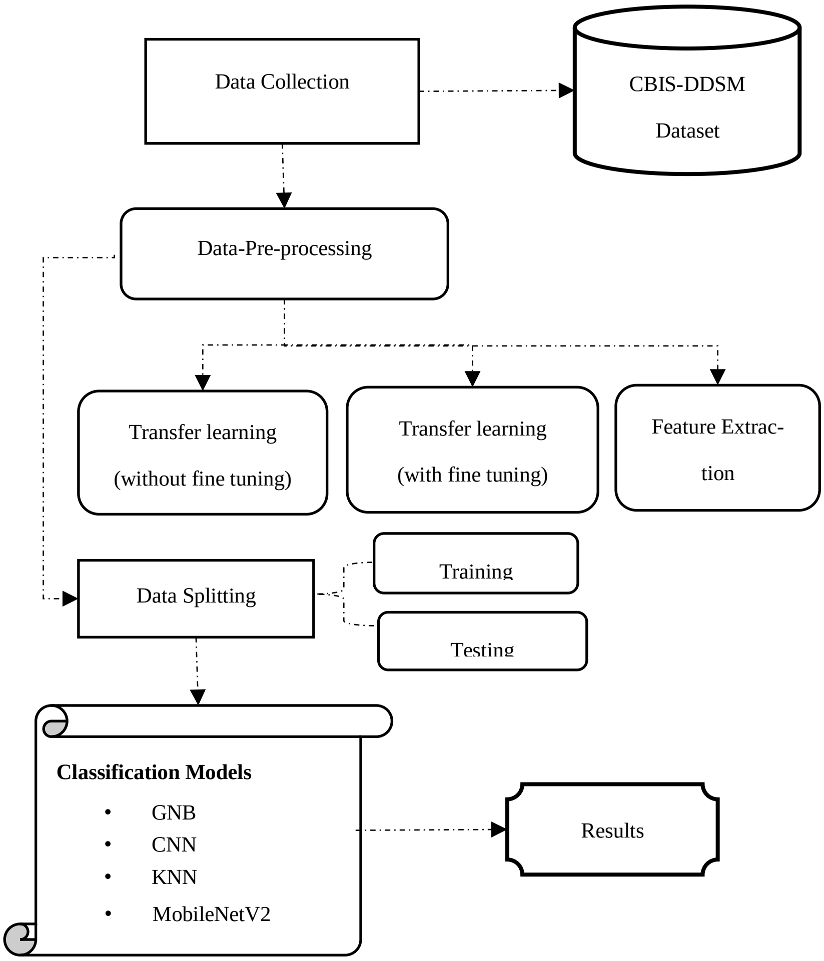

Figure 1. Brief diagram of the Methodology.

The following steps outline the data flow diagram, with each stage of data processing within the system thoroughly detailed.

A. Dataset Description

Digital Database for Screening Mammography (CBIS-DDSM) is a publicly accessible dataset that is extensively used for mammography image processing; it was used to construct the BCD (Breast Cancer Detection) model. The dataset contains a total of 5000 mammography images, with an equal distribution between two classes: 2500 benign images and 2500 malignant images. For model development, 80% of the images were utilized for training a CNN (Convolutional Neural Network) architecture, while a remaining 20% were set aside for evaluating a performance of a trained model.

B. Data preprocessing

Transformation of raw data into a more understandable format is all that is involved in data preprocessing. Sometimes data from the real world is lacking information, is inconsistent, repeats itself, or is noisy. In order to transform raw data into a processed and reasonable format, data preparation comprises a number of processes. These are the key pre-processing techniques:

- **Transfer learning (Without Fine-tuning):** This involves using a pre-trained model directly without altering the learned weights. The model is applied as-is, leveraging the knowledge gained from its original training on a large dataset to make predictions on the target dataset.
- **Transfer learning (With Fine-tuning):** In this approach, a pre-trained model is adapted to the new dataset by allowing the weights of the top layers, or sometimes the entire network, to be adjusted. This helps the model fine-tune its features to better suit the specific characteristics of the target data.
- **Feature Extraction:** Feature extraction identifies key data attributes, transforming raw data into useful features to enhance model performance and efficiency.

C. Data Splitting

The data is often divided into a train set and a test set with a ratio of 80% to 20% using data splitting, which is a popular practice in ML. Finding the model hyper-parameter and estimating the generalization performance are both made possible by this method.

D. Classification Models

In this section, comparison of classification models using CBIS-DDSM dataset. Compare these models' performance using their attributes.

1) Gaussian Naïve Bayes (GNB)

Bayes' theorem is the foundation of GNB, a classification technique that relies on the characteristics being conditionally independent given the class and following a normal (Gaussian) distribution.

2) Convolutional Neural Network (CNN)

DL algorithms like CNNs may distinguish between distinct parts of an input image by giving them varying amounts of weight and bias that can be learnt. In contrast to other classification techniques, ConvNets rely on far less pre-processing. In contrast to basic methods that need hand-engineered filters, a ConvNet can acquire these attributes and filters via training.

3) K-Nearest Neighbors (KNN)

KNN is a lightning-fast technique for regression and classification. Working with train-test sets, this non-parametric technique doesn't assume anything. It takes into account both positive and negative examples in the training sets and produces results as either a classification or a regression. Because it can generalise without training data points, this technique is referred to as a lazy algorithm.

4) MobileNetV2

The MobileNetV2, which is a modified version of MobileNetV1, serves as the convolutional base in all three TL variants for performing mammography image classification tasks. The low-powered and lightweight structure of MobileNetV2 makes it suitable to deploy the trained model on a smart embedded platform with low memory and computation capabilities.

MobileNetV2 consists of three layers: the expansion layer, depth-wise convolution layer, and projection layer. There are fewer channels accessible at the projection layer due to the MobileNet architecture's residual bottleneck connection. "Bottleneck" describes the situation when the number of channels at the output of the projection layer is reduced. In the standard MobileNet architecture, a 3x3 depth-wise convolutional layer extracts features from input channels, while a 1x1 point-wise convolutional layer combines a feature maps generated by the depth-wise convolutional layer to efficiently decrease a dimensionality of input channels. This feature makes depth-wise separable convolution filters faster than standard convolutional filters and reduces the network training time. The MobileNetV2 network Figure 2 is shown below:

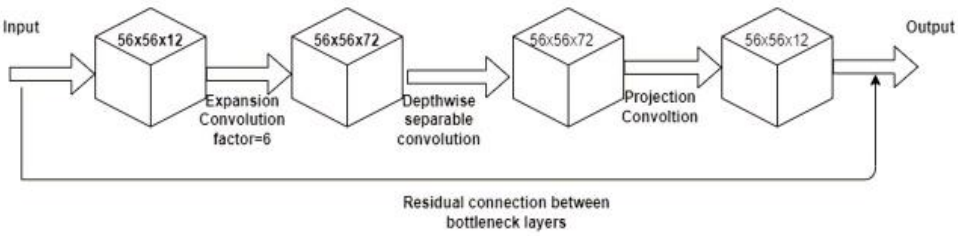

Figure 2. MobileNetV2 Network.

The classification model provides a comprehensive overview of each deep learning model relied on to enhance predictive performance for optimal outcomes.

4. Result Analysis and Discussion

The performance metrics for the models used in the comparison results are presented in this section. For the purpose of assessing AI models' efficacy using the Accuracy and AUC metrics. These assessment factors are outlined below:

A. Confusion Matrix

An essential tool for evaluating the effectiveness of classification algorithms is the confusion matrix. It details the correspondence between model predictions and actual labels, reflecting the model's accuracy and types of misclassifications in each category. The TP and TN in the matrix reflect the number of correct predictions, while FP and FN represent a number of misclassifications. The confusion matrix depiction in Figure 3 is shown below:

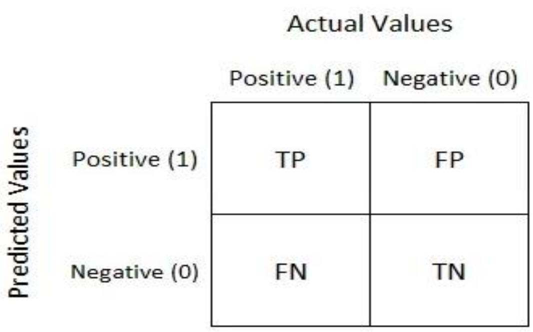

Figure 3. Confusion matrix

B. Accuracy

According to Equation (1), accuracy is calculated as follows: number of properly identified samples divided by total number of samples.

$$Acuracy = \frac{TP+TN}{TP+TN+FN+FP} \quad (1)$$

C. AUC

The AUC is a useful metric for describing the intrinsic validity of diagnostic tests as it combines the sensitivity and specificity measures. Mathematically, it is represented as in the Equation (2):

$$AUC = \int_0^1 TPR()FPR\, d(FPR) \tag{2}$$

1) Experiment Results

Table 2 below displays the outcomes of experiments performed using DL models on the CBIS-DDSM dataset.

Table 2. Results of MobileNetV2 model for Accuracy.

Model	Accuracy
MobileNetV2	99.4

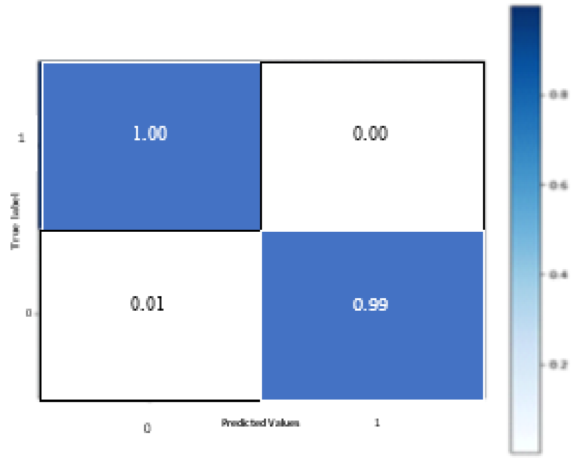

Figure 4. Confusion matrix obtained using MobileNetV2.

Figure 4 shows the confusion matrix classification model's performance for two classes: class 0 (negative) and class 1 (positive). The horizontal axis displays anticipated labels, while the vertical axis displays true labels. The model performs excellently, with a true positive rate of 1.00 for class 0 and a true negative rate of 0.99 for class 1, indicating high accuracy and minimal errors.

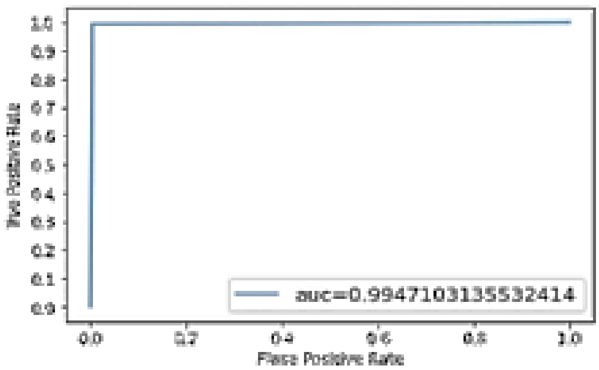

Figure 5. Fixed feature extraction with MobileNetV2.

Figure 5 displays a ROC curve, which has an AUC value of around 0.9947. When evaluating a model's discriminatory power, the ROC curve is useful since it shows the

TPR versus the FPR. The model does exceptionally well of differentiating among positive and negative instances if the AUC is near to 1.

2) Comparative analysis

Using the CBIS-DDSM dataset, this section compares and contrasts DL models for cancer categorisation and breast cancer prediction. It provides the results for different models in the below Table 3.

Table 3. Comparison between different models using CBIS-DDSM dataset using deep learning models.

Models	Accuracy
GNB[12]	87.2
CNN[13]	96.7
KNN[14]	91.2
MobileNetV2	99.4

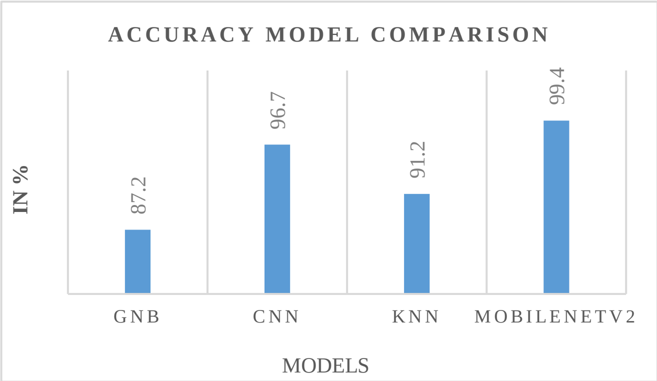

Figure 6. Accuracy model comparison

Figure 6 shows a comparison of accuracy for four models: GNB (87.2%), CNN (96.7%), KNN (91.2%), and MobileNetV2 (99.4%). MobileNetV2 has the highest accuracy, followed by CNN, KNN, and GNB. The vertical axis indicates accuracy in percentages, highlighting MobileNetV2's superior performance.

Table 3 and Figure 6 represent a comparative analysis of cancer classification models using the CBIS-DDSM dataset. MobileNetV2 stands out with the highest accuracy of 99.4%, significantly outperforming other models such as Gaussian Naive Bayes (GNB) with 87.2%, K-Nearest Neighbors (KNN) with 91.2%, and the Convolutional Neural Network (CNN), which achieved 96.7%. Figure 6 visually highlights the superiority of MobileNetV2 in terms of accuracy, clearly showing its dominance over the other models. AUC of 0.9947, which indicates MobileNetV2's great capacity to distinguish among positive and negative cancer cases, further supports its remarkable performance. This combination of high accuracy and minimal classification errors makes MobileNetV2 the best model for cancer prediction in this study.

5. Conclusion and Future Work

Mammograms are important but sometimes insufficient instruments in early identification of breastcancer, which is mostly responsible for a disease's high death rate. We used the CBIS-DDSM dataset's mammography pictures to illustrate in this research how well different ML models perform in that regard. According to our results, MobileNetV2 achieved a remarkable 99.4 percent accuracy, well beyond that of competing models. The comparison research demonstrated that DL methods excel in improving diagnostic accuracy for breast cancer diagnosis by learning complicated characteristics from raw picture data. The results indicate that computational analysis of histological images can effectively complement traditional diagnostic methods, providing more reliable prognostic information.

To enhance model generalization, future studies should concentrate on growing the dataset to include a wider variety of cancer kinds and different image quality. Additionally, incorporating advanced techniques such as ensemble learning and transfer learning with larger pre-trained models may further enhance classification performance. It would also be beneficial to explore real-time applications of these models in clinical settings, including integration with electronic health records (EHR) for automated decision support. Investigating the interpretability of model predictions could help bridge the gap between computational results and clinical practice, ensuring that healthcare professionals can confidently rely on AI-assisted diagnostics.

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