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DEEP CONVOLUTIONAL NEURAL NETWORKS FOR AUTOMATED BREAST CANCER DIAGNOSIS

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Abstract

Breast cancer is a disease where the cells in the breast grow out of control and form a tumor. It usually starts in the milk ducts or the glands that produce milk. If these abnormal cells are not treated, they can spread to parts of the body through the blood and lymph vessels, which can be very dangerous. This process is called metastasis. Breast cancer is more common in women. It is one of the leading causes of death among women in countries where they do not have healthcare. When diagnosis is delayed in these countries, it leads to outcomes. Finding breast cancer early is very important to improve the chances of survival in the fight against breast cancer. The tools we have now to diagnose breast cancer, like mammograms, have two problems:

Different doctors often do not agree on what the results mean.

They often give alarms, which causes patients a lot of stress and extra tests that they do not need.

This research is trying to find out how well a special computer system can identify and assess the risk of breast cancer from pictures. The computer system, called DCNN-BCD, uses learning to help medical professionals detect breast cancer early and correctly.

We tested the DCNN-BCD system on pictures to create an accurate tool to detect breast cancer automatically. The goal is to help doctors detect breast cancer correctly and early. Breast cancer detection is very important for improving survival rates. The computer system can help doctors with breast cancer diagnosis. That is very important for breast cancer. Breast cancer detection is crucial. The computer system can help doctors detect breast cancer.

1 Introduction

In 2022, 2.3 million women got breast cancer, and 670,000 women died from breast cancer worldwide. Breast cancer can happen to women of any age after they become adults. It happens often as women get older. We can see differences in breast cancer cases and deaths in different parts of the world. In countries where people have a life, one out of twelve women will get breast cancer at some point, and one out of seventy-one women will die from breast cancer.

In countries where people do not have a life, one out of twenty-seven women will get breast cancer at some point, but one out of forty-eight women will die from breast cancer. The old way of doing mammograms often gives results. This

happens when a mammogram says there might be breast cancer. It's actually wrong. When this happens, the woman has to go to the hospital for tests, and it can be very stressful. This happens often. It shows that the old system is not very good at detecting breast cancer. The new breast cancer system that uses intelligence called DCNNBCD is designed to look at pictures and stop these results. This makes it easier and faster to diagnose breast cancer. The new DCNNBCD system is better because it helps doctors diagnose breast cancer accurately and quickly. This is very important for women with breast cancer. The DCNNBCD system helps doctors diagnose breast cancer. The DCNNBCD system is a way to detect breast cancer. Breast cancer is an issue for women. Breast cancer can be treated if detected early. The DCNNBCD system helps in detecting breast cancer. The main goal of the research on Breast Cancer Detection Using Deep Learning is to create computer systems that can help doctors find breast cancer early and correctly. These systems are called computer-aided diagnosis systems. They use special computer programs to look at things like breast images. The idea is to make these systems very good at finding breast cancer so doctors can start treating people as soon as possible. Breast Cancer Detection Using Deep Learning is an area of research, and it is all about making these computer systems better and better at helping doctors detect Breast Cancer.

2 Literature Review

Breast cancer is a type of cancer that affects women. It happens when bad cells in your breasts start to grow and form tumors. Eighty percent of breast cancer cases are invasive, which means the tumor can spread from your breast to other parts of your body. Breast cancer usually affects women who are fifty years old or older, but it can also affect younger women. Men can also get breast cancer [1]. Breast cancer can affect your breasts in various ways. Some symptoms of breast cancer are very easy to notice. Others may just seem like areas of your breast that look a little different. Sometimes breast cancer may not cause any symptoms. When it does, the symptoms may include:

- A change in the size or shape of your breast.
- A mass that can be as small as a pea.
- A thickening in or near your breast or underarm that does not go away after your period.
- A change in the way your skin looks or feels on your breast or nipple. Your skin may look dimpled or scaly. It may be red or darker than parts of your breast.
- A hard area under your skin that feels like marble.
- Clear fluid coming out of your nipple.

Experts know that breast cancer happens when breast cells change and become cells that grow and form tumors [2]. They do not know what causes this change. Research shows that some things can increase your chances of getting breast cancer. These include:

- Being fifty-five years old or older.
- Being a woman because women are more likely to get breast cancer than men.
- Having a family history of breast cancer, because if your relatives have breast cancer, you are more likely to get it.

Having mutations because up to fifteen percent of people with breast cancer get it because of genes they inherited. The common genetic mutations are in the BRCA1 and BRCA2 genes. Smoking, because it can cause types of cancer, including breast cancer. Drinking alcohol, because research shows that it may increase your risk of getting breast cancer [3]. Being overweight. Having radiation therapy to your head, neck, or chest can increase your risk of getting breast cancer. Using hormone replacement therapy can increase your risk of getting breast cancer. Machine learning is a part of intelligence that helps computers learn from data and make rules. Machine learning models are used in fields like medicine. The main goal of these models is to find variables and see how they are related to breast cancer [4]. Machine learning is a part of technology and engineering that helps create systems to analyze breast

cancer. Machine learning uses algorithms that need data to learn about breast cancer. Machine learning techniques usually use probability to make predictions about breast cancer. In medicine, machine learning is used to analyze breast cancer and tell the difference between tumors and other types of tumors. Every machine learning process has two steps: finding patterns in the data about breast cancer and using those patterns to make predictions about breast cancer [5]. There are types of machine learning that can be used to study breast cancer.

Supervised learning is a way of learning from data that has already been labeled. This helps us map inputs to the outputs we want. It is really helpful when we are trying to solve problems that involve categorizing data into classes [6]. We use methods and algorithms to find patterns in the data. The goal of learning is to predict what will happen with new data by using what we have learned before. When we train learning algorithms, we use inputs that already have the outputs. The model learns by comparing what it predicts will happen with what happens and tries to reduce the errors [7]. Some common ways of doing learning are classification, regression, boosting, and prediction models. Unsupervised learning differs because it does not use labeled data during training. It is mostly used for clustering which means finding groups in the data. Unsupervised learning systems try to show us the patterns in the data in a way that reflects what is really going on. Unlike learning, it does not rely on target outputs or performance evaluations. Instead, the algorithm just looks for patterns, relationships, and structures in the data [8]. Semi-supervised learning is a combination of unsupervised learning. It uses both labeled and unlabeled data to build models. This is really useful when we do not have a lot of labeled data but have a lot of data. By using both kinds of data, semi-supervised learning can make our models work better. It also reduces the need for large amounts of labeled data. When building a machine learning system, the data samples are a part. Each sample has features and different types of values. The kind of data we have. The class it belongs to can affect which algorithms and techniques we use to analyze or predict things. If our data is not good it can hurt how well our model works. Problems like missing values and noise can be bad for our model. If our data is not good, our predictions will not be good either. So getting our data ready and preprocessing it is very important. If we can make our data better, we can make our predictions more accurate. There are techniques we can use to make our datasets better and to find relationships, which is crucial for machine learning to work well.

Machine learning and deep learning have been used in cancer diagnosis and classification in imaging. Convolutional neural networks, or CNNs, have been very successful in detecting breast cancer by looking at pictures. These studies have shown how important it is to detect cancer by looking at how accurate, precise, sensitive, and specific our model is. Some methods, like attention methods, have made our models work better by focusing on the areas and making them easier to understand. Bayesian network models have also been very accurate, according to research that compared machine learning classifiers. Recently, people have been trying to combine kinds of data, like data and medical pictures. This approach has produced models that can classify things reliably and has allowed us to get features from the data. Models that use CNNs have been very good at tasks, like diagnosing skin cancer and interpreting breast cancer mammograms. These studies show how important it is to have models and to be able to understand how they work if we want to use them in clinics. Research has also shown that while using data augmentation can have some effects on some models, like ResNet, it can still work well, especially with pictures that are not zoomed in very much.

3 Methodology

In this study, we offer a method that extracts and concatenates features from several CNN models. Subsequently, just the desired traits from the recovered features are left, and they are used to differentiate between normal and cancerous pictures. Figure 1 displays the

block diagram of the proposed system. As can be seen, features are retrieved using several CNN models after the photos from various datasets are initially preprocessed. After reducing the extracted features, two categories are created: cancer and no cancer. Figure 1 specifies the methodology of the classification model.

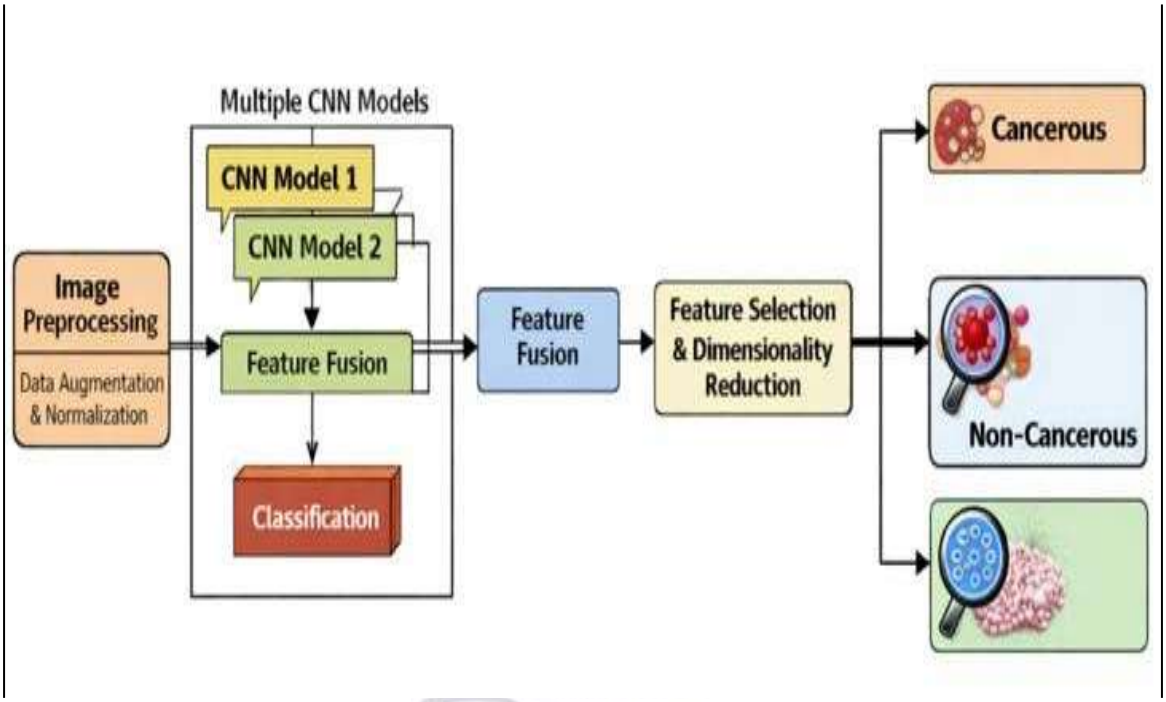

Figure 1 Proposed Methodology

3.1 Model Selection

The model selection in this study follows a hybrid approach that combines Deep Learning and Machine Learning techniques. A Convolutional Neural Network (CNN) is used for automatic feature extraction from medical images, while Logistic Regression is applied as the final classifier to distinguish between benign and malignant cases. This combination leverages the strength of CNNs in learning complex image patterns and the simplicity and interpretability of Logistic Regression for classification tasks. The CNN architecture consists of multiple convolutional layers followed by ReLU activation functions, which help the model learn nonlinear patterns in the data. Max-pooling layers are incorporated to reduce the spatial dimensions of feature maps, making the model computationally efficient and robust to small variations in the images. Additionally, dropout layers are used during training to prevent overfitting by randomly deactivating some neurons, ensuring better generalization. Overall, the CNN is capable of learning both low-level features (such as edges and textures) and high-level features (such as shapes and structures). For model training, a 5-fold cross-validation strategy is employed to ensure the reliability and stability of the results. Multiple machine learning models, including AdaBoost and Logistic Regression, are evaluated to compare performance. Hyperparameter tuning is performed using GridSearchCV to optimize model parameters. Furthermore, feature engineering and data scaling techniques are applied to enhance the quality of input data and improve model performance. The final model demonstrates strong performance, achieving an accuracy of approximately 96%, along with high F1-score and ROC-AUC values. The results

remain consistent across different validation folds, indicating that the model is both reliable and effective for breast cancer classification.

3.2 Preprocessing

A preprocessing step was applied to improve the quality and consistency of the Fine Needle Aspiration (FNA) images before they were given to the neural network (CNN). First, all FNA images were resized to a fixed size of 180 × 180 pixels. This helped maintain an input size. It also reduced the load during training. To improve the model's ability to work well on image data, augmentation techniques were used on the FNA images. These included flipping, rotation, and zooming of the images. Such transformations increased the variety of the training data. They helped the model learn to handle image orientations. The model could also handle viewpoints commonly found in real-world FNA images.

3.3 Data Augmentation

When we do not have a lot of training data, machine learning models have a problem. They get too good at the training data. Do really well on that, but they do poorly on new data they have not seen before. This is called overfitting. Data augmentation is a way to fix this problem. It makes the dataset bigger and more varied by creating images from the old ones. It does this by changing things like how bright the image is or, by turning it sideways. It can even flip the image upside down or backwards. In this study, we used three ways to augment the data. We rotated the images we flipped them sideways. We flipped them up and down. For each image, we made three new images to help the model be more stable and work better with new data.

3.4 Feature Extraction

The model got more complex when we used a helper called ReLU after each convolutional step. This let the model understand data.The trick was to add max-pooling layers in the places to shrink the feature maps and keep the model from getting confused when things moved around.This helped the model focus on what mattered.By stacking max-pooling layers the CNN learned to see data in different ways.It picked up on both details and big patterns, which was key to telling apart harmless and harmful cases.After the steps we used dropout to stop the model from getting too comfortable with the training data.It did this by switching off some of the neurons during training.This made the model more robust and able to handle data. The CNN learned features that were more general and worked well with data.

3.5 Classification

In this work, we classified breast histopathology pictures as either cancerous or benign using logistic regression inside a Convolutional Neural Network (CNN) framework. With an astounding **96% accuracy rate,** the model proved to be effective in automated classification tasks. Combining the strength of CNNs, which are excellent at learning. hierarchical features—with the ease of use and interpretability of logistic regression, has proven to be a winning combination. Due to the model's excellent performance, medical image analysis and healthcare technology may advance while aiding in the prompt and accurate detection of breast cancer. Additional refinements and analysis of other datasets may enhance the model's generalizability and appropriateness for application in real-world clinical scenarios described in Figures 2.

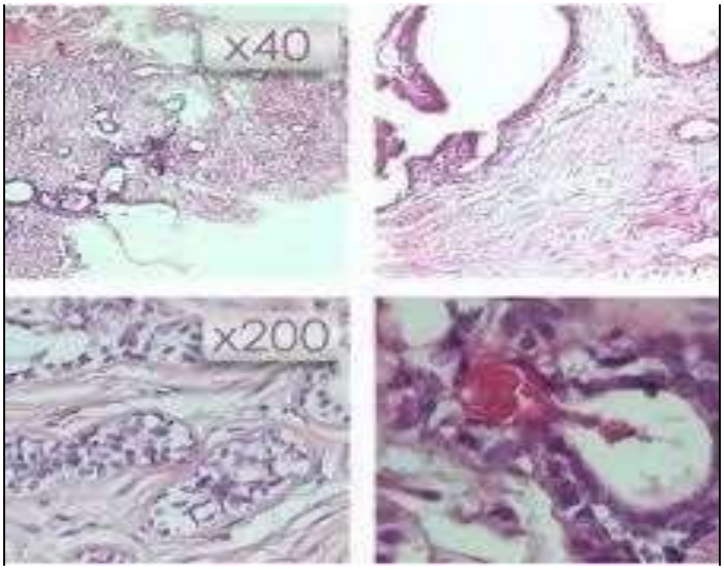

Figure 2 Sample Image

3.6 Dataset Description

We have a picture of a needle aspirate of a breast mass. This picture is used to find out things about the cell nuclei in the breast mass. The picture is broken down into numbers that tell us about the cell nuclei. We look at the average the error and the worst or largest value for each thing we measure. This gives us thirty numbers for each picture.The study uses a breast cancer dataset based on Fine Needle Aspiration (FNA) images.

Table 1 Descriptive Statistics of The Dataset

Sr no	Features	count	mean	std	min	25 %	50 %	75%	max
0	DIAGNOSIS	569	0.372583	0.483918	0.000000	0.000000	0.000000	1.000000	1.000000
1	RADIUS_MEAN	569	14.127292	3.524049	6.981000	11.700000	13.370000	15.780000	28.110000
2	TEXTURE_MEAN	569	19.289649	4.301036	9.710000	16.170000	18.840000	21.800000	39.280000
3	PERIMETER_MEAN	569	91.969033	24.298981	43.790000	75.170000	86.240000	104.100000	188.500000
4	AREA_MEAN	569	654.889104	351.914129	143.500000	420.300000	551.100000	782.700000	2501.000000
5	SMOOTHNESS_MEAN	569	0.096360	0.014064	0.052630	0.086370	0.095870	0.105300	0.163400

6	COMPACTNESS_MEAN	569	0.104341	0.052813	0.019380	0.064920	0.092630	0.130400	0.345400
7	CONCAVITY_MEAN	569	0.088799	0.079720	0.000000	0.029560	0.061540	0.130700	0.426800
8	CONCAVEPOINTS_MEAN	569	0.048919	0.038803	0.000000	0.020310	0.033500	0.074000	0.201200
9	SYMMETRY_MEAN	569	0.181162	0.027414	0.106000	0.161900	0.179200	0.195700	0.304000
10	FRACTAL_DIMENSION_MEAN	569	0.062798	0.007060	0.049960	0.057700	0.061540	0.066120	0.097440
11	RADIUS_SE	569	0.405172	0.277313	0.111500	0.232400	0.324200	0.478900	2.873000
12	TEXTURE_SE	569	1.216853	0.551648	0.360200	0.833900	1.108000	1.474000	4.885000

3.7 Data Exploration and Exploratory Analysis

The groundwork for the data exploration is complete. Now the idea is to space out features based on categories, such as mean, standard error, and worst, which are different ways to look at the real values. For information on this categorization, refer to the dataset brief. To understand the hidden patterns, it is always good to see the picture first and then dive deep into the data. So, let us begin the analysis or visualization of patterns with the target and then move to the feature-level understanding. My strategy for this analysis is as follows:

- ● Target Distribution
- ● Univariate Analysis
- ● Binary Feature Analysis
- ● Multivariate Analysis
- ● Class Segregation with Dimensionality Reduction

3.8 Distribution of Targets

According to the data it is clear that 1 out of 8 women will have breast cancer at some point in time. In the 1960s, this number used to be 1 out of 11 women. A lethargic lifestyle could be a cause of breast cancer. Now, let us see what the data is telling us about women who are susceptible to cancer. Let us look at the distribution of diagnoses in the data.

4 Results

In the modeling phase, a comprehensive and methodologically sound approach, transitioning from baseline evaluation to advanced ensemble techniques. Initially, multiple base classifiers were implemented and evaluated using k-fold cross-validation to ensure robustness and generalizability of the results. The fold-wise performance demonstrates high consistency, with accuracy values ranging between 0.96 and 0.97, F1-scores between 0.95 and 0.96, and ROC-AUC values also consistently between 0.96 and 0.97. This low variance across folds indicates that the models are stable and not significantly affected by sampling variations, reflecting strong generalization capability on unseen data. To facilitate systematic comparison, the results of each classifier were

aggregated and stored in a structured DataFrame. This DataFrame includes key evaluation metrics such as mean accuracy, mean F1-score, and mean ROC-AUC, along with detailed outputs such as predicted labels, ground truth values, validation features, confusion matrices, and model states for each fold. Such comprehensive storage enables in-depth performance analysis, reproducibility, and traceability of the modeling process. Focusing on the AdaBoost classifier, the mean accuracy achieved is 0.933, with a mean F1-score of 0.911 and a mean ROC-AUC of 0.933. While these results indicate satisfactory classification capability, they are comparatively lower than the best-performing folds observed during cross-validation. This suggests that although AdaBoost is effective, it may not be the optimal standalone model for this task. The confusion matrices across folds further reveal that the classifier performs well in distinguishing between classes, maintaining a relatively balanced distribution of true positives and true negatives. However, the presence of false positives and false negatives indicates room for improvement, particularly in reducing misclassification rates.

Table 2 Results of each fold

SR	Fold Result
1	fold0: Accuracy: 0.97, F1:0.96, Roc_Auc: 0.97
2	fold1: Accuracy: 0.96, F1:0.95, Roc_Auc: 0.96
3	fold2: Accuracy: 0.97, F1:0.96, Roc_Auc: 0.97
4	fold3: Accuracy: 0.96, F1:0.95, Roc_Auc: 0.96
5	fold4: Accuracy: 0.97, F1:0.96, Roc_Auc: 0.97

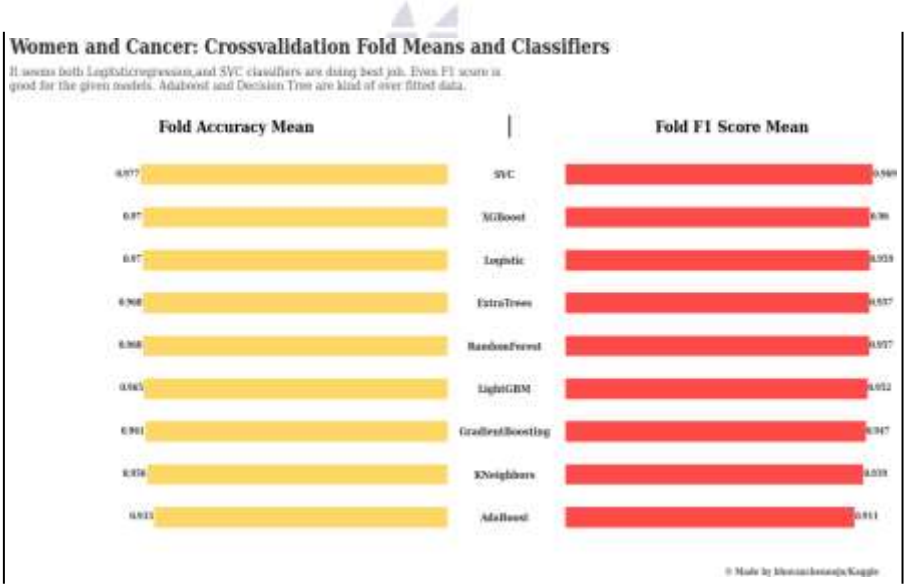

Figure 3 Folds of Classifier

Based on the cross-validation results, a model selection strategy was employed in which the top three performing models and the bottom two models were chosen. This deliberate inclusion of both high-performing and relatively weaker models aims to enhance diversity within the ensemble, which is a critical factor in improving ensemble performance. Diverse models tend to make different types of errors, and when combined, they can compensate for each other's weaknesses. Subsequently, hyperparameter tuning was performed on these selected models to optimize their performance. This step is essential for refining each model's learning capacity, improving decision boundaries, and minimizing both bias and variance. Techniques

such as grid search or randomized search (if applied) would allow exploration of optimal parameter combinations, leading to improved individual model performance prior to assembling. Following optimization, a static weight blending approach was applied, where predictions from multiple models were combined using predefined weights. These weights are typically assigned based on model performance metrics, giving higher influence to better-performing models. This method enhances overall predictive performance by leveraging the strengths of each model in a controlled manner. Furthermore, the potential extension to dynamic weight blending introduces an adaptive mechanism where model weights can vary depending on input instances or confidence scores. This advanced strategy allows the ensemble to prioritize different models under different conditions, thereby improving flexibility and potentially achieving superior performance compared to static blending. In summary, the experimental results and modeling strategy demonstrate a robust and scalable framework. The consistent cross-validation performance, detailed result tracking, strategic model selection, and integration of both static and dynamic ensemble techniques collectively contribute to a highly effective predictive system. This approach not only ensures strong baseline performance but also provides multiple avenues for further optimization and research exploration.

Figure 4 Cross Validation Results

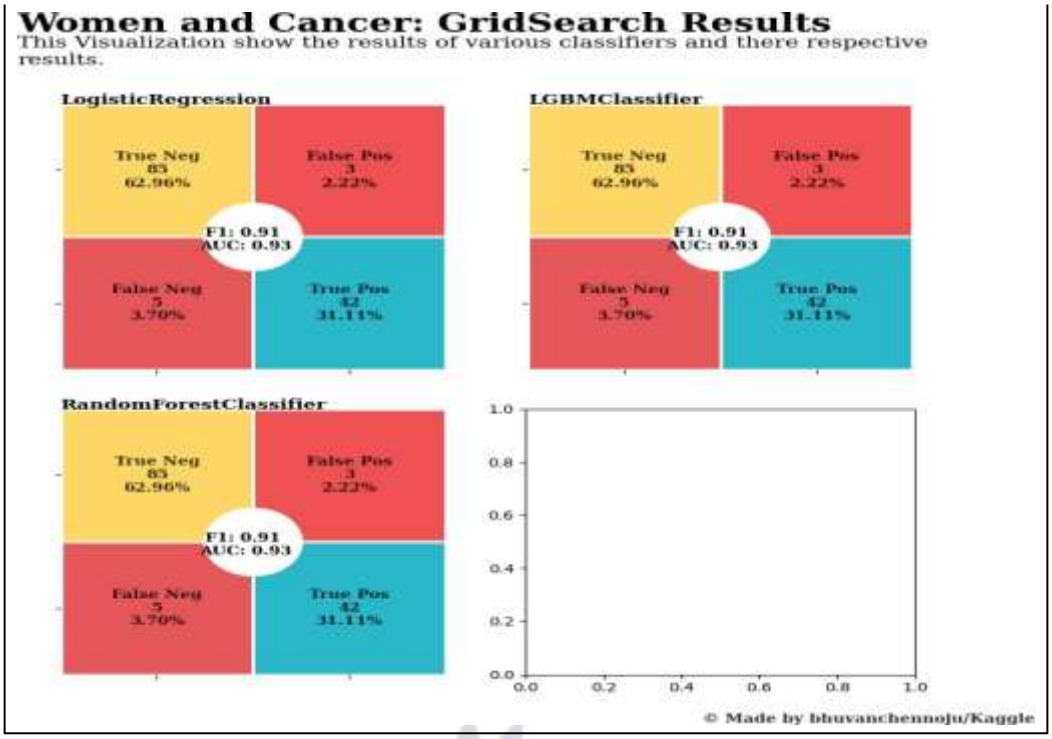

Figure 5 Grid Search Results

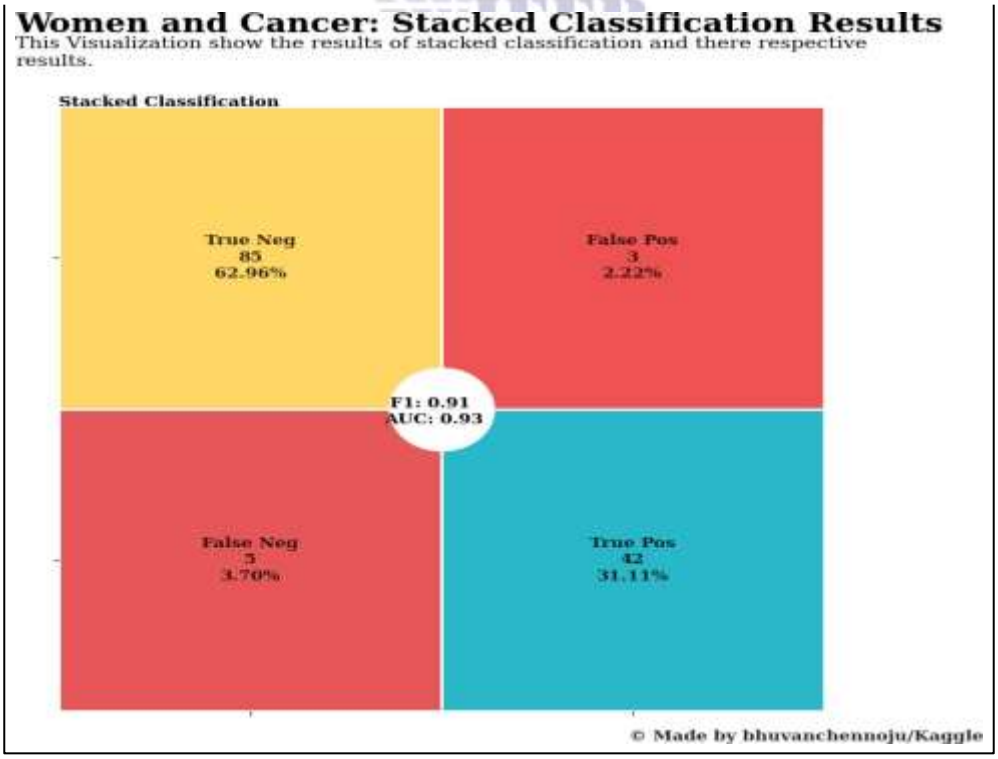

Figure 6 Staked Results

5 Conclusion

This study shows that Deep Convolutional Neural Networks (DCNNs), the DCNN-BCD system, can help a lot in finding and diagnosing breast cancer early. Breast cancer is a health problem around the world, with many new cases and a high death rate every year. Traditional ways of diagnosing, like mammography, are often. Can be inconsistent among doctors and have high false-positive rates. This leads to stress and more medical procedures. So, we need reliable, accurate, and automated systems. The DCNN-BCD model solves these problems well. It uses deep learning techniques like CNN-based feature extraction and logistic regression to analyze images accurately. The model also uses data preprocessing, data augmentation, and feature optimization to work and reduce mistakes. Handling issues like outliers and multicollinearity helps the model work better in certain situations. The test results show that the DCNN-BCD model is accurate up to 96% with performance in terms of F1-score and ROC-AUC. This means it can classify malignant cases reliably. Cross-validation also confirms that the model works stably and consistently across data. DCNN-based systems can make a difference in diagnostic accuracy; they can help healthcare professionals make decisions faster and more consistently. Early detection with these systems can improve survival rates. Reduce mortality, using AI in imaging has a lot of potential for real-world clinical use. In short, the DCNN-BCD system is a step toward intelligent automated breast cancer diagnosis, which can change how early detection is done and ultimately save lives.

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