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OPTIMIZED DEEP CONVOLUTIONAL NEURAL NETWORK FOR THE PREDICTION OF BREAST CANCER RECURRENCE

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ABSTRACT
Breast cancer affects 2.1 million individuals each year, maintaining its status as a prominent women's disease. Its alarming 30% recurrence rate within ten years poses a significant threat to lives, solidifying its formidable impact. This study addresses the imperative need for improved recurrence prediction through the development and evaluation of a groundbreaking Deep Convolutional Neural Network (DCNN) algorithm. The primary purpose is to harness Artificial Intelligence (AI) for automatic breast cancer recurrence classification, offering clinicians a robust tool for forecasting and enabling personalized treatment strategies. Methodologically, the study leverages the Wisconsin Breast Cancer dataset for training and validation, employing various dataset combinations to assess the performance of the proposed DCNN model. The algorithm's accuracy, precision (98.57%), recall (96.84%), and F1-score (97.89%) demonstrate its efficacy in predicting breast cancer recurrence, marking a significant advancement in prognostic capabilities. The practical implications of this research are profound, as the proposed DCNN model equips clinicians with a precise tool to anticipate recurrence, potentially minimizing ineffective overtreatment. This has direct applications in clinical decision-making, guiding personalized treatment plans and improving patient outcomes. Theoretical implications extend to the broader field of cancer research, demonstrating the transformative potential of AI in enhancing prognostic accuracy and contributing to the evolution of personalized medicine. This study's value is underscored by its dual contribution to both theory and practice. The novel DCNN algorithm represents a theoretical advancement, pushing the boundaries of AI application in cancer research. On a practical level, the study introduces a tangible solution for clinicians, providing a new dimension in the management of breast cancer by bridging the gap between prediction and personalized treatment. Overall, this research represents a significant stride towards integrating advanced AI methodologies into clinical practice, fostering more effective and tailored approaches to breast cancer treatment.
Keywords: *Breast Cancer, Recurrence, Prediction, Deep Learning, DCNN, Classification.*

1. Introduction

Breast cancer is one of the top causes of mortality for women globally. In order to improve survival rates, early detection is crucial. Hence, extensive research endeavours focus on enhancing the early detection of these cancers through the utilization of existing technology, such as diverse image processing methods and general Machine Learning (ML) approaches, as suggested by (Chouhan et al., 2021). Even if breast cancer has a high 5-year survival rate, recurrence is a common phenomenon (20% to 30% based on stage), and metastasis is frequently involved. Proper risk grouping of patients after initial diagnosis for the best course of treatment and follow-up is a challenge in this cancer supervision (including risk of recurrence). Risk classification is crucial for enhancing patient monitoring, providing high-quality care, and making better use of available medical resources. The reported accuracy for many of these studies, however, was frequently below the desired level. An approach that shows promise for the early detection of breast cancer is Deep Learning (DL)-based methodology. Highly effective method for the early discovery of cancerous breast tumours is mammography combined with ultrasound. MRI is also employed on occasion. According to (Wu et al., 2020), using deep neural networks is believed to enhance the performance of radiologists when it comes to screening for breast cancer.

Recent developments in earlier diagnosis and better therapeutic options have reduced cancer mortality rates. A breast cancer diagnosis affects a person's health, way of life, career, and family life. In addition to the risk of serious mortality and morbidity, it carries the possibility of long-lasting psychological and physical effects. Economic hardship brought on by lost wages and

medical expenses may also be a result of this illness. According to (Anderson et al., 2009), women diagnosed with early-stage breast cancer face the risk of experiencing recurrences either locally, regionally, or in other areas. Though 80% of these cases happen within five years of diagnosis, 30% of patients experience cancer again within ten years. It is currently challenging to distinguish between those who will experience a recurrence and those who won't. The risk of distant recurrence after years of occurrence is depicted in Figure 1.

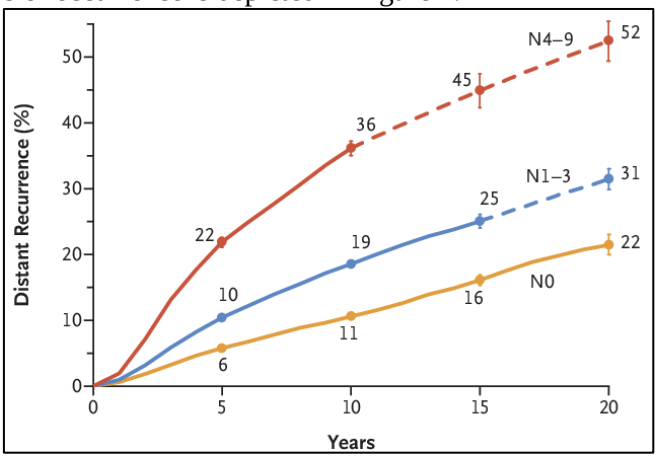

Fig.1. Chance Of Distant Recurrence Over Time

The application of DNN for medical data classification has become increasingly popular in recent years. These networks have demonstrated high accuracy in tasks such as image analysis, signal processing, and clinical decision-making. The ability of DNN to learn complex patterns and relationships in data has made them an attractive tool for medical researchers and practitioners. The development of these networks requires a large amount of annotated medical data and specialized expertise, but the potential benefits in improving diagnosis, treatment, and patient outcomes make it a worthwhile investment. DL techniques are being developed to address problems in various medical specialties, including diagnosis, prognosis, drug design, and testing. In their review, (Tufail et al., 2021) outlined a clear roadmap concerning the application of DL methods in detecting and prognosing breast cancer, offering valuable guidance in this area. A general DL framework for the classification of medical data is depicted in Figure 2.

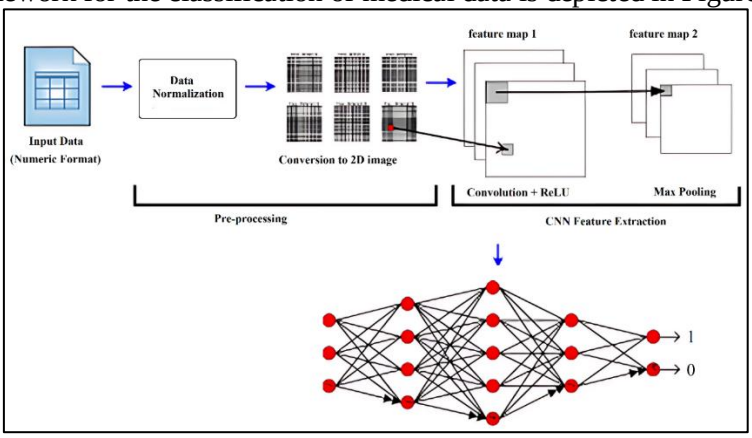

Fig. 2. Deep Learning Model for Medical Data Classification

At the heart of the current state-of-the-art in breast cancer research lies a pivotal problem: the accurate prediction of cancer recurrence. This precision is not merely an academic pursuit but a clinical imperative, essential for tailoring effective treatment plans that maximize patient outcomes and resource allocation. The prevailing limitations of existing methods (Hassan et al., 2023), encompassing both imaging and prognostic models, signal a clarion call for a more robust and nuanced approach. Beyond the technical intricacies, there exists a pressing need for an approach that transcends the limitations of conventional risk classification, addressing the dynamic nature of breast cancer progression and recurrence risk. This study represents a major advancement in predicting breast cancer recurrence through the introduction of an innovative system based on a pioneering DCNN algorithm. Analysing the Wisconsin Breast Cancer (WBC)

dataset revealed remarkable average metrics, including accuracy reaching 97.63%, precision at 98.57%, recall at 96.84%, and an F1-score of 97.89%. Moreover, it demonstrates a distinct superiority over traditional ML methods, as proposed by (Wang et al., 2020) and (Phan et al., 2021).

Our study addresses multifaceted challenges (Cheung & Rubin, 2021) by introducing a groundbreaking DL approach. This study uses the Wisconsin Breast Cancer dataset, consisting of 569 samples with 30 features each from biopsy images, to predict breast cancer recurrence. Employing the DCNN algorithm as the primary method, the dataset's labelled ground truth data facilitates model training. Pre-processing techniques like data encoding and normalization prepare the dataset for optimal model training, followed by fine-tuning within specified parameters for accuracy. The model, trained using this dataset, predicts the likelihood of breast cancer recurrence and undergoes rigorous evaluation using diverse metrics to gauge its predictive efficacy based on clinical data. To firmly situate our work within the broader context, we draw upon a comprehensive review of relevant studies. These citations intricately map the current contours of breast cancer research, emphasizing the imperatives of early detection, recurrent challenges, and the escalating significance of DL methodologies in the intricate domain of medical data analysis.

2. Literature Review

In crafting the literature review, a rigorous and systematic selection method was employed to ensure alignment with the research questions and emphasize key points relevant to the study. The selection criteria prioritized studies that specifically addressed the timely prediction of breast cancer recurrence, focusing on time-based models, and incorporated the latest advancements in the field. Additionally, the review covered recent journal articles from the last five years. This included the latest research findings and methodologies to ensure it was thorough and current. The inclusion of diverse studies employing various machine learning and deep learning techniques was integral to providing a holistic understanding of the current state of the art in predicting breast cancer recurrence timelines.

Using medical records, (Alzu’bi et al., 2021) created a Natural Language Processing (NLP) algorithm to extract crucial information about breast cancer. They combined these elements and created a medical glossary for breast cancer. On the information that was extracted, they ran a number of Machine Learning (ML) algorithms to forecast patients' chances of developing breast cancer again. The creation of the medical dictionary included the validation of the data's accuracy by specific users (physicians, researchers). Personalized medicine can benefit from the use of this dictionary. Each ML algorithm performed well and the OneR algorithm has the best sensitivity to specificity ratio.

An EHR-based predictive model was created by (Wang et al., 2020) to calculate the likelihood that breast cancer patients will experience distant recurrence. Data processing tools were used to map clinical notes to Concept Unified Identifiers (CUI). Words and CUI sequences were vectorized using embedding. These features were down streamed to traditional ML classifiers and CNN along with clinical features from structured data (K-CNN). Our model's optimal setup produced F1-score of 0.5 and AUC of 0.892. This research offers an automatic scheme that combines DL and data processing to forecast recurrence. (Macías-García et al., 2020) developed a method for synthesising DNA methylation by utilising AI. This approach generates new features from CpG site values of patients. A limited number of relevant genes are then proposed to explain breast cancer recurrence by the use of survival analysis and a well-considered ranking of genes according to the distribution of their CpG sites. All of the genes identified by our experiment were linked to breast cancer recurrence, according to the literature and enrichment analysis done on them.

In order to precisely analyse the risk of recurrence, (Yang et al., 2022) proposed multimodal DL approach by incorporating clinical data and whole slide HE images. These images were subjected to DCNN in order to extract features, which were then combined with medical information based on the fusion of features. In the two-fold cross-validation, a novel multimodal model that was created to predict the prognosis had an AUC of 0.76. (S. H. Huang et al., 2017) compared the predictive abilities of ANN model to predict 5-year mortality of patients following

surgery. In order to distinguish clinical data, (Chatterjee & Krishna, 2019) proposed methodology uses DCNN to identify the presence of invasive ductal carcinoma. The seven-channel image matrix created from the microscopic RGB images is fed to the network. With an ROC score of 0.9996, the proposed model achieves a prediction accuracy of 99.29%. For the purpose of predicting breast cancer and its recurrence, (Jalal et al., 2021) suggested four different ML algorithms were implemented. This was done to demonstrate how each algorithm performs differently on different datasets with various sets of attributes or features while maintaining same data samples. Results showed that KNN performed best at predicting breast cancer and SVM performed best at predicting breast cancer recurrence.

(Chang & Chen, 2019) created a classification method based on ML for identifying risk in cancer survivors. To increase the training accuracy, the proposed scheme combined XGBoost classifier with ensemble learning, clustering, resampling, and transformation. XGBoost is associated with clustering and resampling strategies. (Boeri et al., 2020) introduced a preliminary assessment of ML to forecast the recurrence of breast cancer. 1021 patients that underwent surgery for breast cancer were included in the analysis. Cancer death within 32 months and recurrence were the two outcomes that were selected. For every outcome, they created two different ML models (Artificial Neural Network and Support Vector Machine). Accuracy obtained is 95.53 %, sensitivity is 94.82 %, specificity is 96.13 %, and AUC is 91.6 %. These models can be used as an additional tool to assess breast cancer patients' prognoses in routine clinical practise. In order to classify patients as being at low or high risk for distant recurrence within five years of diagnosis, (Bakre et al., 2019) suggested CAB that uses an SVM trained algorithm that takes into account the expression levels of five biomarkers (CD44, ABCC4, ABCC11, N-Cadherin, and Pan-Cadherin) as well as three clinical parameters (tumour size, grade, and node status). To determine the hazard ratios, multivariate analysis was used. The Distant Metastasis-Free Survival (DMFS) was significantly different (P0.002), according to the findings.

Using PAM50 gene structure to define subtypes of breast cancer, (Cespedes Feliciano et al., 2017) investigated whether there were differences in BMI at diagnosis with survival and recurrence. Age, menopause, race/ethnicity, stage, and chemotherapy were taken into account when creating Cox regression models. When subtype was taken into account, BMI was generally not linked to breast cancer survival or recurrence. Even though ML-based prediction models perform very well, they are not frequently used because they lack the ability to elucidate their choices and are not been written down in the clinical way of presentation. The primary aim of (Kim et al., 2016) was to generate mammogram-based data for predicting breast cancer recurrence using the Naive Bayesian model. They used a data set of 679 patients and seven prognostic variables were chosen as independent variables for the model. The model's AUC was 0.81 and its accuracy was 80%.

(Alwohaibi et al., 2022) introduced a comprehensive multi-stage technique, integrating statistical feature selection methods and a modified Brain Storming Optimization algorithm, effectively refining breast cancer recurrence datasets and demonstrating improved classification accuracy through a rigorous evaluation process involving three main stages. Addressing the critical need for individual prognosis prediction, (Yang et al., 2022) introduced a groundbreaking multimodal DL methodology. By seamlessly integrating whole slide Haematoxylin and Eosin (H&E) images with clinical information, the proposed approach leverages a DCNN to extract nuanced image features, resulting in a robust model that attains an impressive area under curve (AUC) of 0.76 in a two-fold cross-validation. The model's efficacy is further underscored by its consistent performance, achieving an AUC of 0.72. (Rabinovici-Cohen et al., 2022) developed an integrative approach using clinical history, immunohistochemical markers, and multiparametric magnetic resonance imaging to predict post-neoadjuvant chemotherapy breast cancer recurrence within five years. Analysing data from 1738 patients through classical machine learning and deep learning, the results demonstrate standalone predictive capabilities for each modality and improved outcomes through their combined use. This multimodal model, evaluated on holdout data, achieves a promising AUC of 0.75 with 0.57 specificity at 0.90 sensitivity, while further stratification reveals exceptional accuracy (AUC > 0.89) for specific high-risk cohorts.

Analysing sentinel lymph node (SN) biopsies from a sizable cohort of 4757 breast cancer patients, (Osako et al., 2022) employed the OSNA (One-step nucleic acid amplification) assay and a randomized 2:1 training-to-validation ratio to establish a robust model for predicting 5-year distant recurrence-free survival. Utilizing Youden's index on the training cohort, the study identified a prognostic cutoff value of 1100 copies/μL for SN tumour burden, revealing significant associations with distant recurrence. The constructed prediction model demonstrated compelling predictive performance in the validation cohort, boasting an area under the curve of 0.83, sensitivity of 63.4%, specificity of 81.7%, and an overall accuracy of 81.1%. (Gupta, 2022) introduced innovative ML models capable of predicting the precise time of breast cancer recurrence, achieving remarkable accuracy, with 40% of analysed patients predicted to experience recurrence within the first year. Utilizing classification models like SVM and Random Forest, the study unveils a nuanced understanding of tumour recurrence timelines, with SVM showcasing the highest accuracy at 78.7%. This population-based approach, relying on multivariate real attribute data, offers patients valuable insights into their recovery timeline, aiding informed decisions on timely medical interventions.

3. Research Methods

In this work, a novel DCNN algorithm is utilized for the prediction of breast cancer recurrence from clinical data. The pre-processing of the data and the development of prediction models make up the two essential parts of this research. This research made use of the publicly accessible Wisconsin Breast Cancer (WBC) dataset (Kaggle, 1995). The database, which has 569 samples and 30 features, was created using biopsy images. Figure 3 outlines the steps required to develop a framework for predicting breast cancer recurrence, from start to finish. The dataset is labelled with ground truth data for training the proposed DCNN. The dataset is downloaded from the internet in .csv format. During the pre-processing stage data is encoded and normalized. The model is then optimized for the dataset to fit within the given parameters. The proposed DL model is then developed and trained using protocols as per (S. C. Huang et al., 2020). The trained model can them be used to predict the chance of recurrence. Finally, the performance of proposed model is evaluated using various metrics.

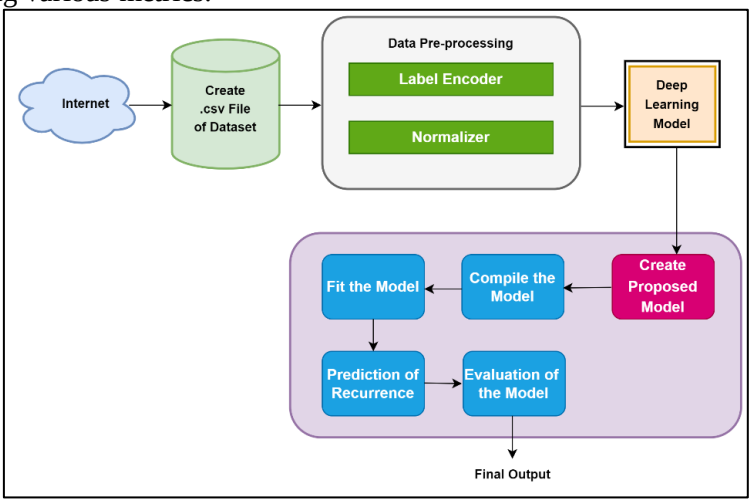

Fig. 3. Proposed Framework for Breast Cancer Recurrence Prediction

DCNN algorithm was chosen as the method for predicting breast cancer recurrence due to its proven effectiveness in learning complex patterns and relationships within data, particularly in image analysis. Given that the Wisconsin Breast Cancer (WBC) dataset utilized in this study was created from biopsy images, the DCNN algorithm aligns well with the visual nature of the data. The selection of the WBC Data Set is based on its comprehensive composition, comprising detailed attributes obtained from breast cancer biopsies. Moreover, its ample size and the availability of labelled data render it well-suited for effectively training and validating the DCNN model. The WBC Data Set mainly consists of tumour characteristics obtained from breast cancer biopsies. However, it lacks specific demographic information about participants, such as age,

ethnicity, or personal traits. The dataset predominantly highlights tumour-related attributes like cell size, shape, uniformity, nuclei presence, mitosis count, and other tumour-specific features.

The WBC dataset has 569 samples with 30 features each. The features encompass various aspects derived from biopsy images, allowing the DCNN algorithm to learn and predict breast cancer recurrence patterns. The WBC dataset does not directly specify instruments used for data collection. Instead, it emphasizes attributes extracted from examining cell features within biopsy samples observed under a microscope. The dataset, labelled with ground truth data, is crucial for training the model. Pre-processing techniques such as data encoding and normalization are employed to prepare the dataset for optimal model training. The model is then fine-tuned and optimized to fit within specified parameters, contributing to its accuracy in predicting breast cancer recurrence. The ultimate evaluation of the model's performance involves various metrics to gauge its effectiveness in making accurate predictions based on the given clinical data.

3.1. Dataset

This experiment used the WBC dataset, that is freely downloadable by the general public. The dataset was pre-processed in the subsequent phase. The dataset was structured and pre-processed using alternative techniques. Data pre-processing is used to filter data and put it in a format that can be utilised. Since the dataset from the actual world is generally always available in numerous formats, it must better fit the dataset in a comprehensible manner. Data pre-processing is a tried-and-true approach of dealing with such problems. (Latchoumi et al., 2019) utilized a methodology for data transformation, crafting the dataset into a format perfect for streamlined operations.

The Irvine UC ML repository, which has 569 cases, one class characteristic called "outcome" with 2 major values (R = recurring, N = non-recurring), and 34 additional attributes, contained the information utilised in this work. 47 recurrences per class, 151 non-recurrences. Each entry contains follow-up information for instances of breast cancer. patients with invasive breast cancer and no signs of remote metastasis at the point of diagnosis are included in this list. The first 30 characteristics are calculated from a digitised image of a breast lump obtained by a Fine Needle Aspiration (FNA). They characterise the features of the visible cell nuclei in the image.

3.2. Data Pre-processing

A useful tool for encoding categorical feature levels into numerical values is the label encoder. Label values between classes 0 and 1 are encoded using the Label Encoder. Encoding is performed on the features of all category. Recurrence and No-recurrence are categorised in this research using the numbers 1 and 0 respectively. This work applied DL to the datasets after encoding them to attain better accuracy. However, the acquired accuracy is evaluated using various metrics of (Li et al., 2020). The practise of scaling one or more parameters to lie between 0 and 1 is known as data normalisation. As a result, each attribute's maximum value is 1 and its lowest value is 0. If the researcher doesn't have knowledge about the distribution of data, normalisation is a useful approach to apply. The entire dataset is transformed into a numerical dataset in lieu of the Label Encoder technique as suggested by (Ali et al., 2020). The normalising method for numeric datasets is explained using Equation 1.

$$\left|x_i\right| = \frac{x_i}{\sqrt{x_i^2 + y_i^2 + z_i^2}}$$

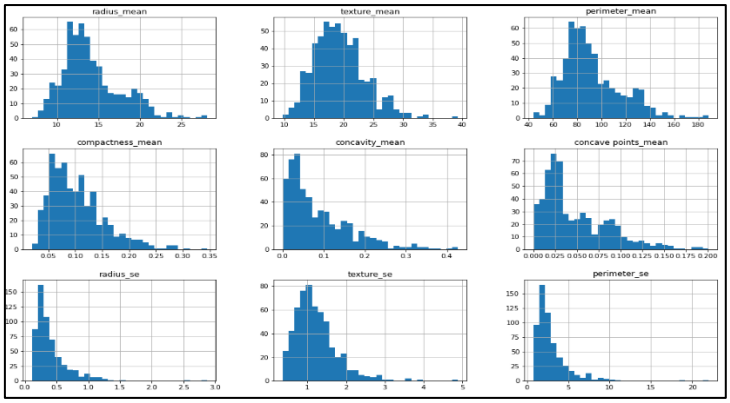

Fig. 4. Distribution Of Geometrical Features

Following data pre-processing, 30 distinct features were obtained with named linked relationships among them. Figure 4 shows the distribution of geometrical features in the form of histogram. This data has been used for training the proposed Deep Convolutional Neural Network (DCNN) model. The structure and size of cancer affected tissues can be described by geometric features such as perimeter, area, and shape. In image analysis, geometric features are often used to describe and quantify the features of objects in the image. Extracting these features from mammogram is crucial as they provide valuable information about the cell's geometric shape.

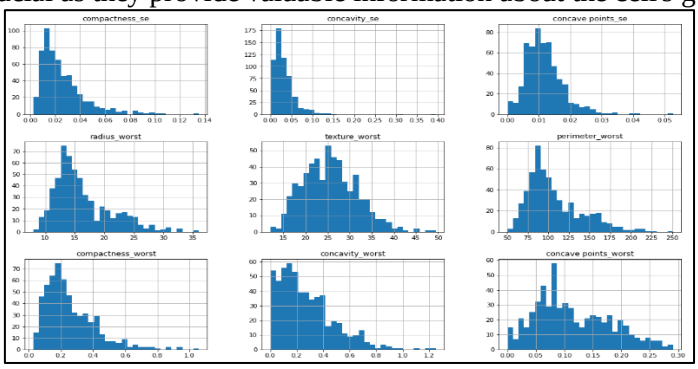

Fig. 5. Distribution of Structural Features

Structural features in image analysis capture the spatial relationships between pixels within an object to describe its texture, pattern, and shape. The distribution of structural features in the dataset is illustrated in Figure 5. These features represented in numerical values enable the analysis of the inter-component relationships within an object. It encodes texture by analysing the binary patterns within a circular neighbourhood around each pixel. Other structural features include Gabor filters, which determine the orientation and frequency of texture patterns, and shape context descriptors, which characterize object shapes by comparing the distribution of their contour points with those of a reference shape.

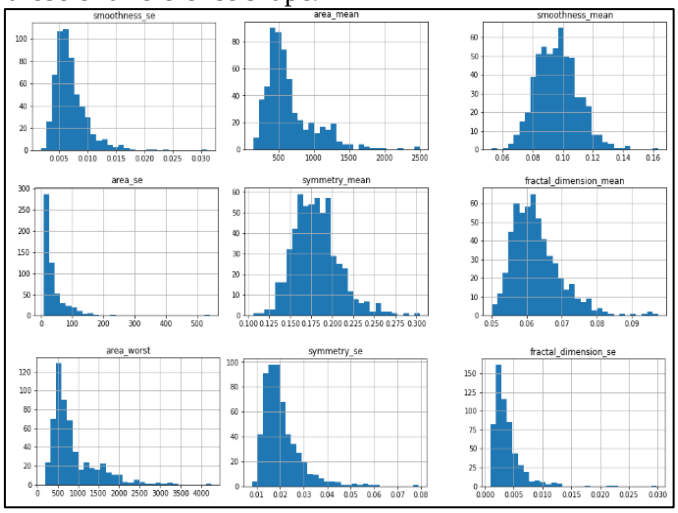

Fig. 6. Texture Feature Distribution

Texture-based features are a type of feature that describe the spatial variations in pixel intensities within an image. The distribution of these features is depicted in Figure 6. These features are used to capture information about the texture or surface characteristics of an object. Texture-based features can be computed using a variety of techniques such as frequency analysis, and transform-based analysis. These features can be used to characterize the texture of an image by quantifying the distribution of Gray-level or binary patterns.

The dataset consists of the records of 569 patients. The correlation between data indicates the ability of the dataset to predict breast cancer recurrence in an efficient way. The correlation factor is computed on a range between +1 to -1. The full relationship between two variables is represented either by + 1 or -1. When one variable decline while the other grows, the correlation is negative; when both variables increase, it is positive. 0 shows a correlation having total absence. The feature having perfect correlation (1) is dropped and the remaining features are considered. The correlation analysis of the given dataset is depicted in Figure 7. Highest correlation is obtained for “diagnosis” and lowest correlation is obtained for “smoothness_se”. The correlation of remaining features falls in between these two features.

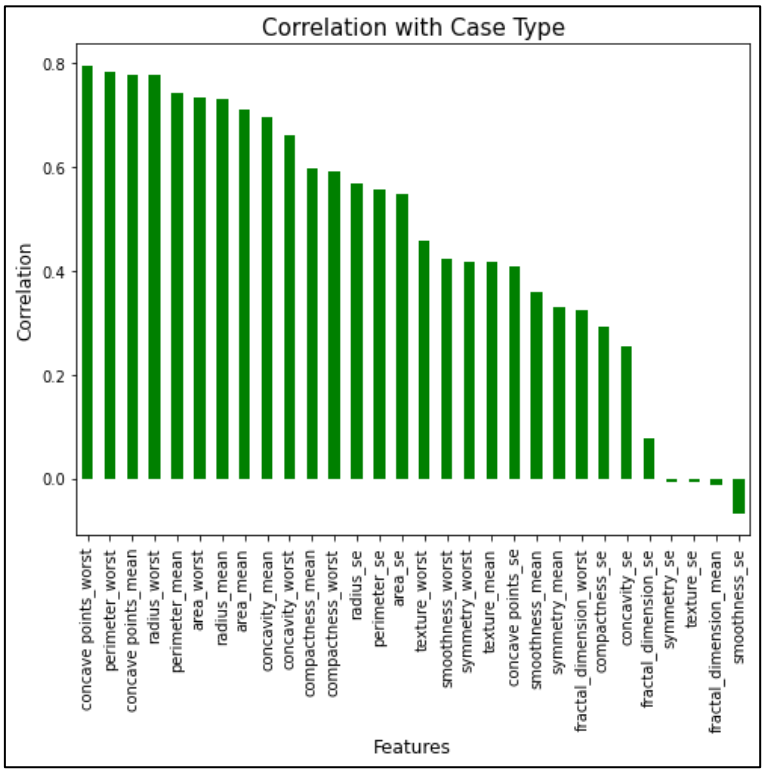

Fig. 7. Correlation of Features

The correlation of features refers to the extent to which two or more features in a dataset are related or have a similar pattern. It is a crucial aspect of feature selection and deep learning algorithms since highly correlated features can negatively affect the model's performance and accuracy. If two features have a high correlation, it means that they carry similar information and can potentially cause redundancy, leading to overfitting. Therefore, it is important to analyse and identify the correlation between features to select the most relevant and independent features for a given task. This process is achieved using statistical methods such as Pearson's correlation coefficient or mutual information. By identifying and removing correlated features, the model's performance can be improved, and it can also lead to faster and more efficient computations.

Heat map is a graphical representation of data that uses color-coding to indicate the magnitude of values. It is a way of visualizing the relationship between two variables by showing how one variable changes as the other variable changes. Heat maps are commonly used to represent large datasets and to identify patterns or trends. The heat map displays data in a matrix format, with rows and columns representing different categories, and the colours indicating the intensity of the values. The intensity of the colours is usually based on a gradient scale, with darker colours indicating higher values and lighter colours indicating lower values. Heat maps is

used to identify correlations, clusters, or outliers in the given data, and to provide insights that are difficult to obtain from other types of visualizations. The correlation between the features in the dataset is illustrated using a heat map as depicted in Figure 8.

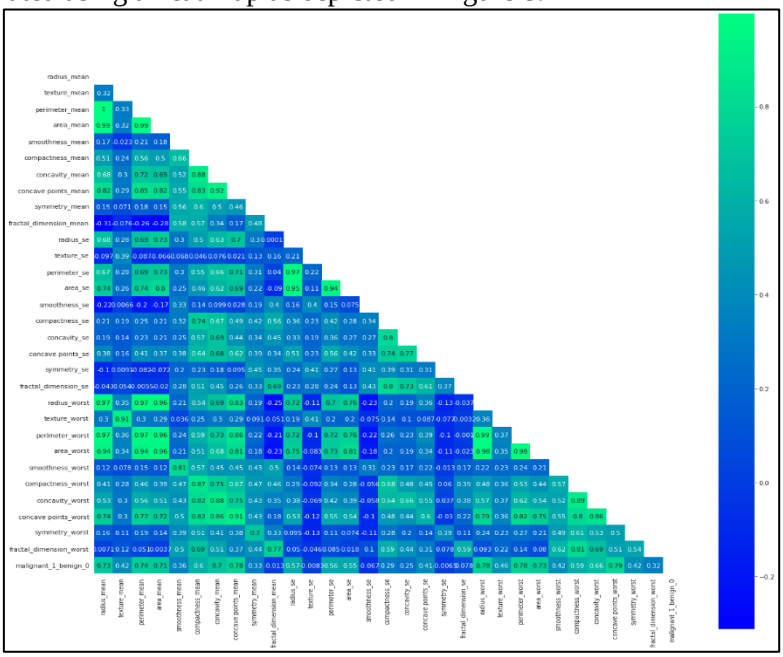

Fig. 8. Correlation Heatmap Of The Dataset

3.3. Deep Learning Model

This work proposed data wrangling technique to obtain image data from numerical data. To represent a certain class, the transformed image has to exhibit particular patterns. The WBC dataset from the UCI library is used for numerical data classification. Initial step is the formation of a distance matrix *[d x d]*. Here d represents the sum of all features present in the WBC dataset. Matrix elements can be obtained by considering the difference of 2 features represented by Equation 2.

$$x_{ij} = x_i - x_j$$

Here, x_i and x_j characterize the quantity of a provided features with $i, j \in [1, d]$. Euclidean distance is utilized in this experiment and normalization is performed on the matrix for values between 0 and 1. This generates an image having size *[d x d]* with 3 folds gain. Selected data samples of WBC dataset are transformed to normalized distance matrix. These images can easily be scaled in the dimension *[3d x 3d]*. Figure 9 displays the output of first convolutional layer, which consist of six features resembling bar graphs. The layers in the DCNN are capable of processing image data only. The data must be in the form of a 2D array. So, the numerical data is converted into 2D array and are represented in the form of an image.

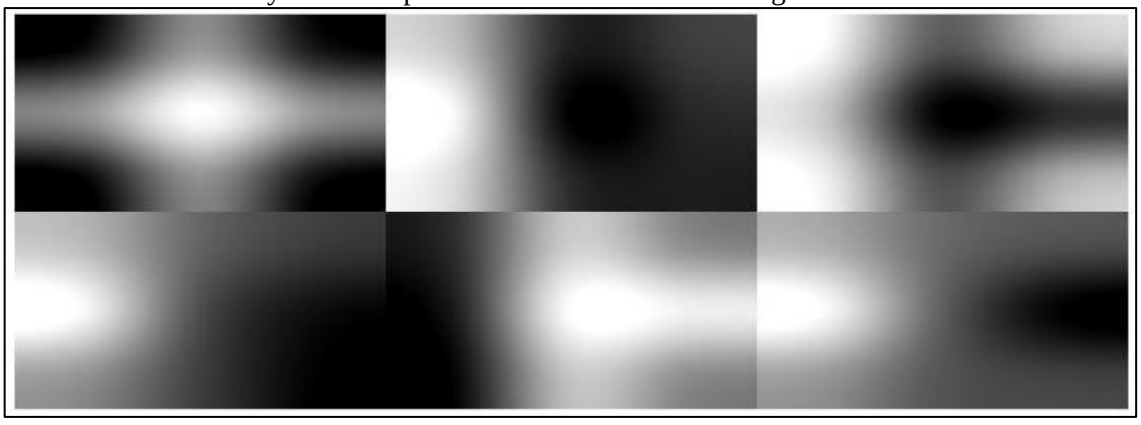

Fig. 9. Features Trained By Initial Convolutional Layer Of DCNN

On the WBC dataset, a DCNN-based data classification system is put into practise. The final result is computed using extra processes in addition to input, output, and hidden layers. These extra steps include bias, the insertion of a few hidden layers, and the computation of an activation function before the output is generated. The neural network input layer stores the input data that will be processed. It is composed of input neurons that put forward the initialization data so that later the neuron layers can process it. Following the input layer is the convolution layer, which is one of CNN's fundamental layers as suggested by (Ali et al., 2020). The whole input volume depth receives the dot product, and this layer (filter or kernel) has a constrained receptive field. The operation of a filter in the convolution layer is shown in Figure10.

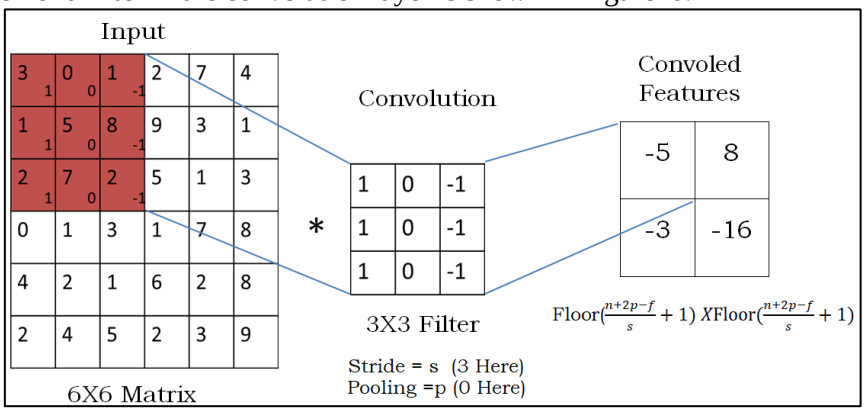

Fig.10. Convolution Operation on Input Data

This technique produces an output data volume integer called a feature map. The same input data's next accessible region is crossed by the kernel after which the previous accessible region and the same kernel are again used to calculate the dot products. A feature map is then created from the input. The density layer down samples the feature map to lessen the computational load and spatial dimension of the input. This avoids overfitting and operates separately on every segment of the input. According to (Maniruzzaman et al., 2020), in a densely linked layer, each neuron connects individually to neurons in the layer above it. In DCNN, this dense layer is the one that is most frequently utilised. The maximum value present in the obtained feature map is considered and the dense layer is based on the filter size. The output of neural network is decided using the activation function. The obtained values are mapped between [0 and 1] or [-1 and 1] (depending upon the function). The work is ideally suited for sigmoid activation function since it is based on a binary classification issue as suggested by (Stephen et al., 2019). The curve of a sigmoid activation function, which has an S-shaped appearance. The slope of sigmoid plot may be calculated at any 2 places since the function is differentiable. The training time of a neural network can be sped up by using the logistic sigmoid function. The sigmoid function is expressed in Equation 3.

$$\phi(x) = \frac{1}{1+e^{-x}}$$

This work introduces an innovative approach to classify tabular data utilizing CNN. The key innovation involves transforming tabular data into images by convolving a pre-defined base image with input feature vectors regarded as filters or kernels. The resulting filtered images are then classified using CNN. This method has significant relevance in the field of medicine, and could have a significant impact. First, we introduce a kernel method that is able to convert tabular data into images for use in classification tasks. This is a novel approach that has not been widely explored before. Second, we apply this method to real-world data in order to classify medical. The steps involved in the proposed tabular convolution method are explained in Algorithm 1.

Algorithm 1: Tabular Convolution
Input: $X^i = \left[x_r^i \right]_{1\times d}$ (Training Set), $V^j = \left[v_r^j \right]_{1\times d}$ (Validation Set) Output: Features for DCNN Classifier.
Step 1: Initialize the values of $1 \le i \le X; 1 \le j \le Y;$ and $1 \le r \le d$

Step 2: Compute the closest square having odd values: $S_o = e(d)$; $S_o = k^2$
Step 3: Trim or perform padding on the feature vectors to n dimension and compute $X^{'i}$ and $V^{'i}$
Step 4: for i=1to X, perform
Step 5: $Z = x_k^{'}(a-1) + b^i - \overline{X^{'i}}$
Step 6: $T^i = M * Z$
Step 7: end for
Step 8: for i=1to $\lvert V \rvert$, perform
Step 9: $Z = v_k^{'}(a-1) + b^i - \overline{V^{'i}}$
Step10: $W^i = M * Z$
Step 11: end for
Step 12: Train the DCNN using W and T.

The proposed method, begins by transforming the feature vector into a kernel through rearrangement into a square matrix and subtracting the mean value. The convolutional kernels are square matrices with an odd number of rows and columns, such as 3x3, 5x5, or 7x7. Therefore, if the number of features is an odd square (9, 25, 49, etc.), feature vectors can be directly converted to kernels. However, if the number of input features is not an odd square, the feature vectors must be padded or trimmed to the nearest odd square. Padding can be done by adding zeros, random noise, or engineered features such as products and fractional polynomials. Trimming is done by removing features in an unsupervised manner to avoid bias, such as removing features with the least variance. The decision to pad or trim depends on the number of features to be added or removed. Usually, the nearest odd square is selected and the feature vectors are trimmed or padded to the nearest one. The nearest odd square of d is denoted as e(d). In this context, f_i and ki represent the number of filters and kernel size, respectively, in the i_{th} convolutional layer, while r_i denotes the dropout rate. The Fully Connected (FC) layers contain nd_1 and nd_2 nodes, with nd_2 corresponding to the number of classes in the output layer. Since the hyper-parameters are chosen manually, we can compute the number of trainable parameters. The total count of trainable parameters in the first convolution layer of the proposed algorithm is represented in Equation 4.

$$N_{p1} = C * f_1 * k_1 + b_1$$

The total count of trainable parameters in other convolution layers of the proposed algorithm is represented in Equation 5.

$$N_{pn} = f_{i-1} * f_1 * k_1 + b_1$$

The total count of trainable parameters in the dense layers of the proposed algorithm is represented in Equation 6.

$$N_{pd} = nd_{i-1} * nd_i + b_i$$

The first layer serves as the input layer for a four-layer convolutional model. Convolutional, hidden, and fully connected layers are the next levels. These layers are all constructed on top of one another. To achieve improved categorization results, we use the Adam optimizer. According to (Khan et al., 2019), it performs exceptionally well, especially with large datasets. Hyper-parameters are often easy to tune and have an obvious denotation. Binary cross-entropy is utilized to compute the amount of loss (error) occurred during training and validation. Binary Cross Entropy (BCE) is used to compare each predicted probability to the original class output (either 0 or 1). The probabilities are then given a score based on how much they deviate from the projected value. The count of parameters employed in the model for the prediction of breast cancer recurrence is displayed in Table 1.

Table 1 - Proposed DCNN Model Summary

Layers	Type	Output Shape	Parameters
Input Layer	Dense	30	-

Convolution Layer	Dense	30	930
Hidden Layer	Dense	30	930
Fully Connected Layer	Dense	1	31
		Total	1891
		Trainable	1891
		Non-Trainable	0

Figure 11 shows the proposed DCNN model for WBC dataset that initialize with 30 features. After the processing in convolutional and hidden layers, final output is generated with two classes (Recurrence=1, No-Recurrence=0). In this model 512 neurons and 600 epochs were utilized for training and validation. 600 epochs were used because it is the best value at which the DCNN model converges and the loss and accuracy are stable providing best results.

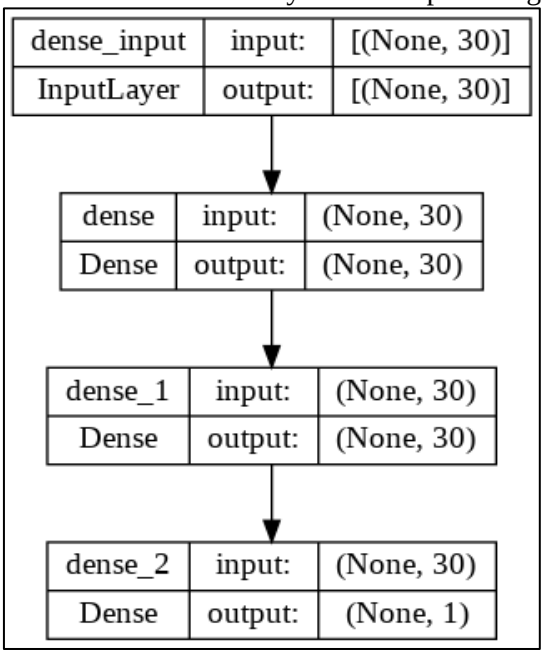

Fig.11. Proposed DCNN Model for Breast Cancer Recurrence Prediction

4. Results and Discussions

Training loss is the loss amount relative to the training data at the end of each epoch. With training, the optimization process seeks to decrease this, therefore the lower the number, the better. The ratio of correct predictions to all other predictions in the training data is known as accuracy. Normally, but not always, the loss is inversely connected with this. The validation counterparts are the same notions as the training counterparts, but they are computed using validation data instead of training data, making them invisible to the model. The BCE is used to calculate the loss (error) that happens during each iteration and is compared according to (Battineni et al., 2020). In this computation, y denotes the output label (1 for recurrence and 0 for no-recurrence) and p(y) is the prediction probability for all N points. The expression for BCE is given in Equation 7.

$$H_p(q) = -\frac{1}{N}\sum_{i=1}^{N} y_i.\log[p(y_i)] + (1-y_i).\log[1-p(y_i)]$$

Identifying relevant features that accurately represent the case type is crucial in breast cancer recurrence prediction. These relevant features are usually selected based on their correlation with the target variable and their ability to discriminate between different categories. The selected features can then be used to build predictive models that can effectively predict the outcome of new cases. Identifying relevant features is an essential step in many data-driven applications and can significantly impact the performance and accuracy of the final model. The relevant features corresponding to the case type is depicted in Figure 12.

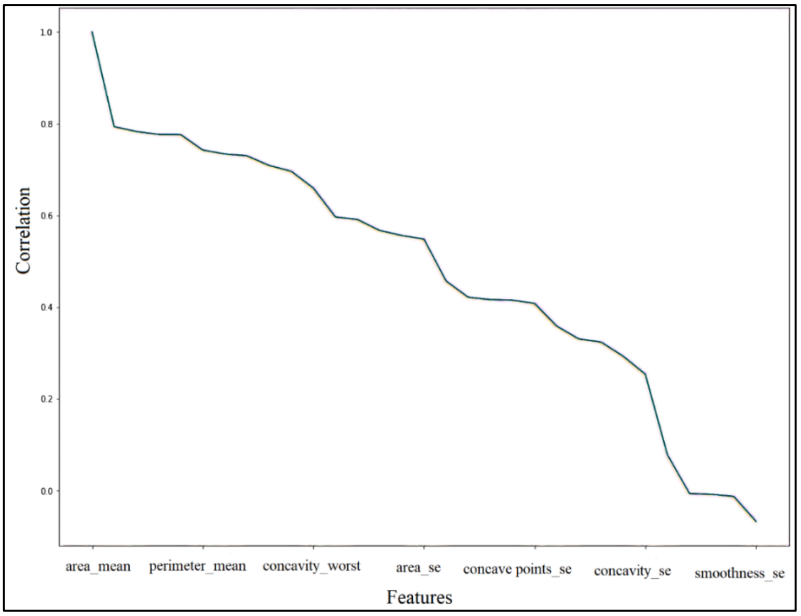

Fig.12. Correlation Of Features With Case Type

This formula indicates that, for all correct prediction points (y=1), it performs addition of log(p(y)) to the loss, for the correction of log probability. Similarly, the sum of log(1-p(y)) is obtained to find the log probability of result being incorrect, for the wrong prediction point (y=0). The model is overfitting if the training loss and accuracy are good but the validation equivalents are poor because it cannot generalise to new data. In order to properly assess the behaviour of breast cancer recurrence prediction, these measurements are typically plotted combined into a training and validation loss as depicted in Figure 13.

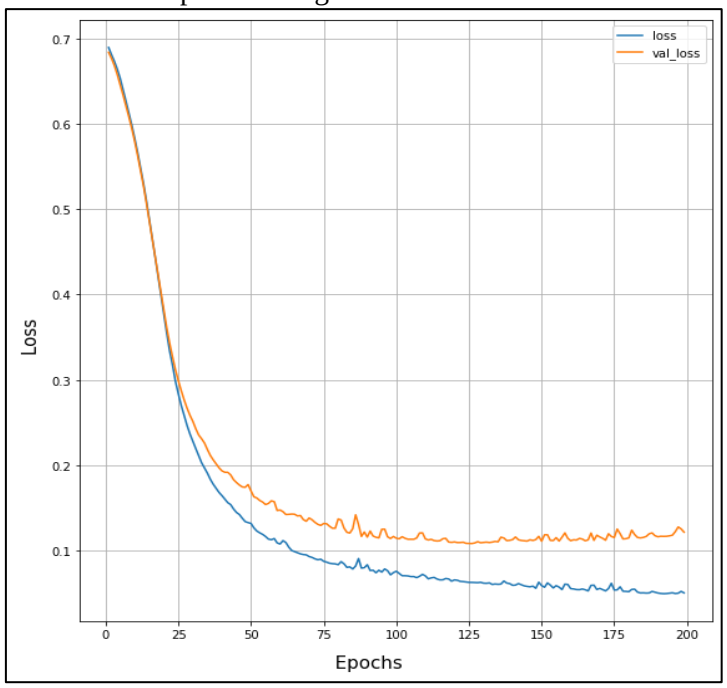

Fig. 13. Average Loss Per Epoch

There is a change in the accuracy of the model as it is trained over a series of epochs or iterations. During training, the model is presented with a set of labelled data, and it tries to learn the underlying patterns and features in the data that are associated with each label. As the model is trained over multiple epochs, it adjusts its parameters and weights to better fit the data and improve its accuracy. Analysing the variation of accuracy with epochs it can be identified that overfitting is eliminated due to the introduction of novel feature optimization scheme. For analysing the efficiency of breast cancer recurrence prediction algorithm, training and validation accuracy are evaluated over various epochs and it is depicted in Figure 14.

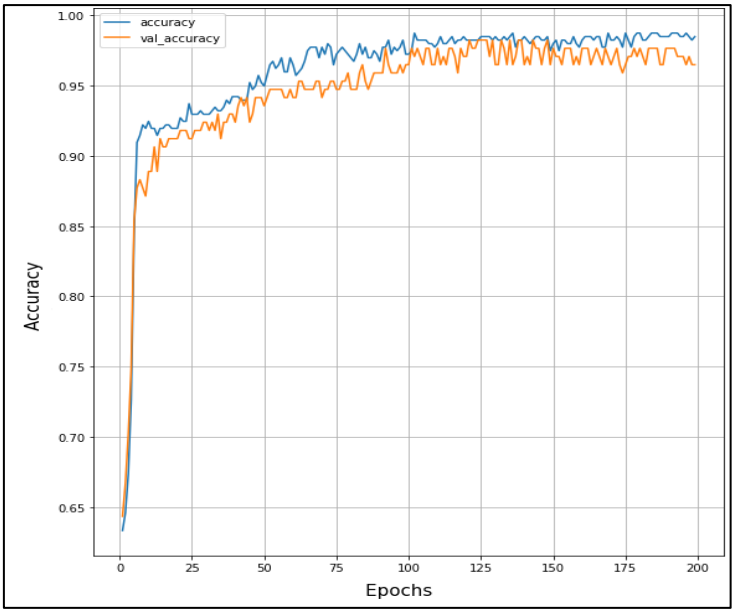

Fig. 14. Average Accuracy Per Epoch

For the accuracy analysis, the entire dataset is divided into two categories such as validation data and train data. Precision, accuracy, recall and F1-score declines as the percentage of validation data rises. The value of these performance matrices increases as the percentage of train data rises. Various combinations of train and validation data are considered in the experiment. Optimum result is obtained for (train=30% and validation=70%). This finding is clear from Table 2 and the associated Figure 15.

Table 2 - Performance Analysis of Breast Cancer Recurrence Prediction Algorithm

Validation Data (%)	Train Data (%)	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
10	90	91.45	92.17	90.85	91.37
15	85	93.21	93.75	91.96	93.84
20	80	95.78	96.32	94.38	95.37
25	75	96.11	97.36	95.13	96.25
30	70	97.63	98.57	96.84	97.89
35	65	95.84	96.84	94.37	95.29
40	60	93.15	94.98	92.63	93.11
45	55	92.74	93.26	91.44	92.67
50	50	90.80	91.59	90.03	91.35

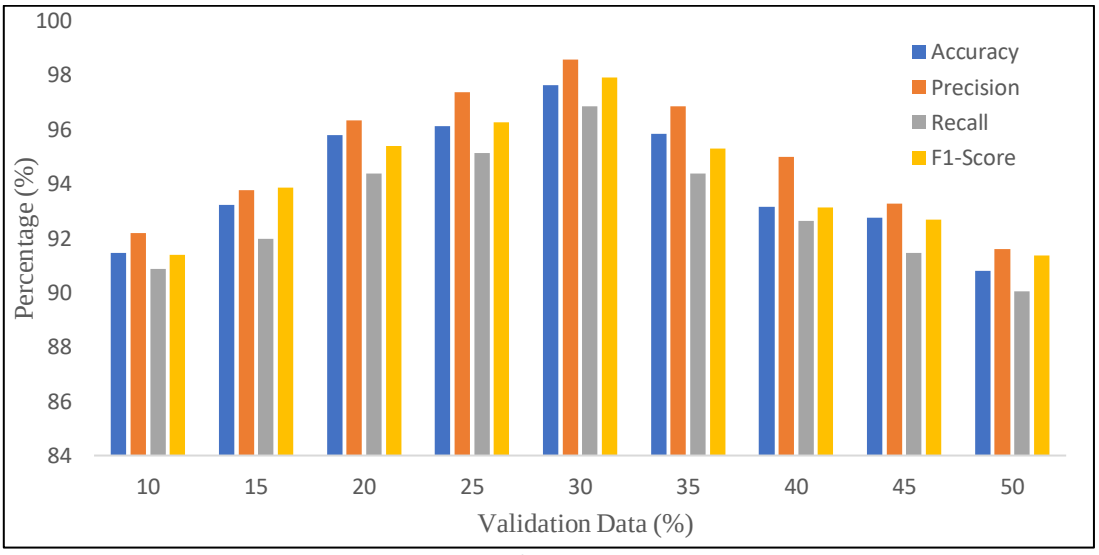

Fig. 15. Performance Analysis

By incorporating 30 features maps and cross validation different performance parameters are computed. The beast performance was obtained for 30% validation data and 705 training data.

All the results are obtained for 10-fold cross validation and the highest accuracy is 97.63%. After various attempts on the dataset, the proposed DCNN model is optimized and average classification results were obtained. Specially designed DCNN algorithm is chosen because of the improvement in performance parameters. Moreover, this implementation of DL technique is accurate and faster.

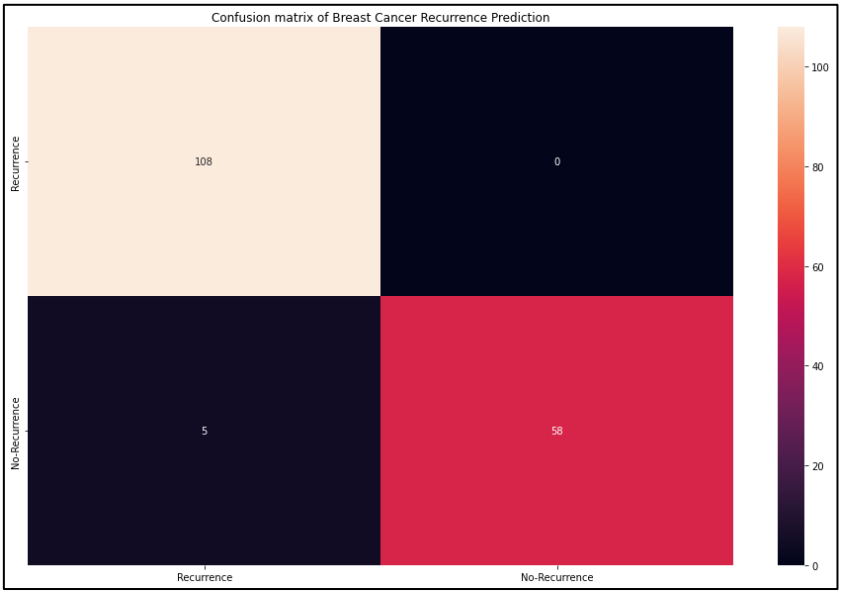

Fig. 16. Confusion Matrix Of Breast Cancer Recurrence Prediction

The confusion matrix depicted in Figure 16 provides a clear idea about the performance of proposed DCNN algorithm in discriminating various classes in the validation data. The total number of patients considered for validation is 171. In this validation dataset, 63 patients belong to class 0 (No-Recurrence) and 108 patients belong to class 1 (Recurrence). All the 108 patients with recurrence are correctly categorized. In the case of no-recurrence, 58 patients are correctly categorized and 5 patients are wrongly categorized. This indicates that, the proposed algorithm is able to discriminate between both classes in an efficient way.

The Receiver Operating Characteristic (ROC) curve provides a graphical representation of the performance of this binary prediction algorithm. It plots the true positive rate (TPR) on the y-axis against the false positive rate (FPR) on the x-axis, as the discrimination threshold is varied. The area under the curve (AUC) is a measure of the algorithm's overall performance, with a value of 0.5 indicating random guessing and a value of 1.0 indicating perfect classification. A higher AUC suggests better discrimination between positive and negative classes. The ROC curve and AUC of the proposed prediction algorithm is depicted in Figure 17 and is in accordance with (Phan et al., 2021).

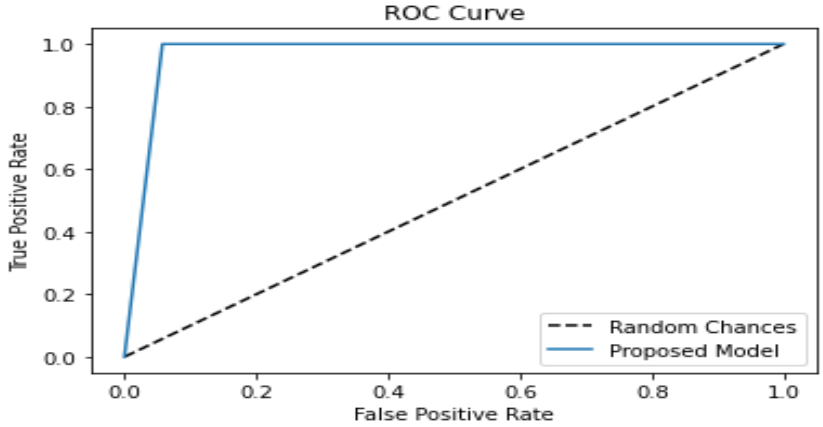

Fig. 17. ROC Curve of Proposed Prediction Algorithm

The performance of the proposed breast cancer recurrence prediction scheme is compared with existing schemes. The accuracy, precision, recall and F1-score are higher for the proposed

scheme. The mean of accuracy, precision, recall and F1-score were computed as 97.63 %, 98.57 %, 96.84 % and 97.89 % respectively. The reason for obtaining good performance is due to the incorporation of additional dense layers to enable DL. The performance comparison of proposed DCNN scheme with existing schemes is presented in Table 3 and depicted in Figure 18.

Table 3 - Performance Comparison

Methodology	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
Naïve Bayes (S. C. Huang et al., 2020)	92.94	93.85	90.89	92.63
Random Forest (Quist et al., 2021)	96.71	96.77	95.14	94.36
KNN (Magboo & Magboo, 2021)	95.03	95.24	94.18	95.52
SVM (LG & AT, 2013)	95.70	96.28	93.48	95.83
Decision Tree (Guo et al., 2017)	90.46	91.34	90.18	90.89
Logistic Regression (Witteveen et al., 2018)	95.74	96.83	95.32	95.10
General CNN (Desai & Shah, 2021)	85.83	87.34	83.13	86.38
Proposed DCNN	97.63	98.57	96.84	97.89

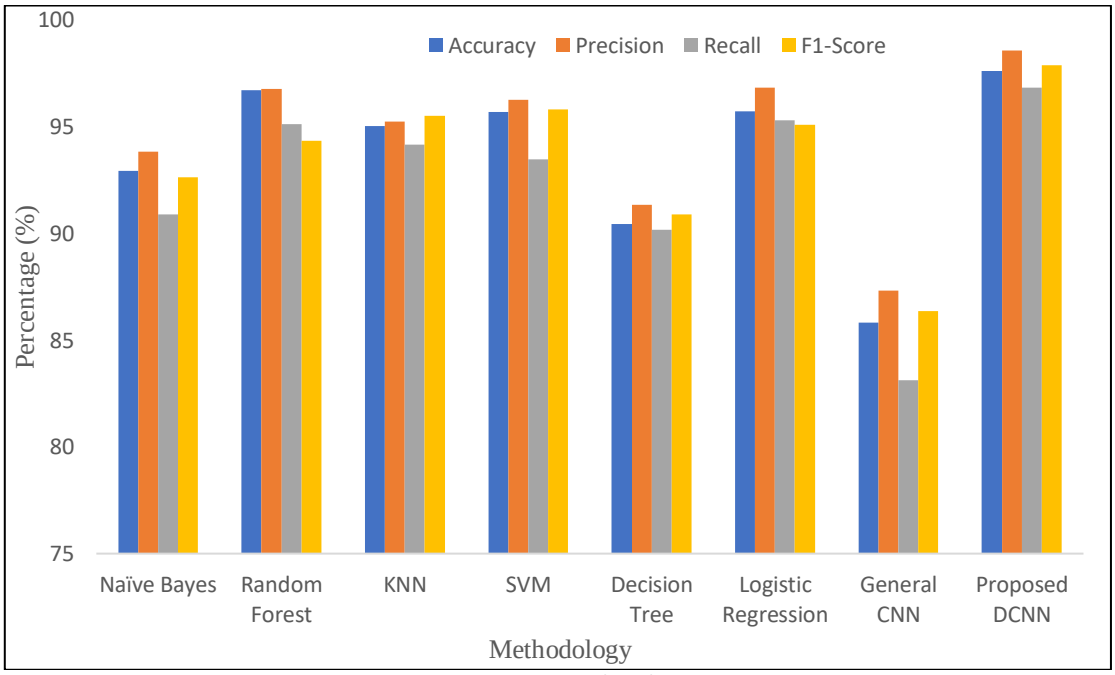

Fig. 18. Comparison of Performance

The average performance of WBC dataset is compared with seven existing techniques. From the above comparison the accuracy for proposed DCNN method is 11.8 % higher than general CNN algorithm and 0.92 % higher than Random Forest. The precision measure of proposed DCNN method is 10.88 % higher than CNN and 1.74 % higher than Logistic Regression. The measure recall for proposed DCNN method is 13.71 % higher than CNN and 1.52 % higher than Logistic Regression. By selecting the optimum number of layers, overfitting problem is reduced and the performance of the network is boosted. The optimum features are identified through correlation analysis and heatmaps. These features contributed more in improving the performance of the proposed DCNN. The F1-score for DCNN scheme is 11.51 % higher than CNN and 2.06 % higher than SVM. From this comparison, it is evident that proposed DCNN is capable of achieving good classification and prediction performance with lowest error rate and better accuracy.

The proposed breast cancer recurrence prediction model shows exceptional performance when compared to existing methods, like that of (Gianni et al., 2022), demonstrating substantial advantages in accuracy, precision, recall, and F1-score metrics. In comparison to the result of (Zeng et al., 2023), the infusion of additional dense layers into DCNN emerges as a pivotal element contributing to the observed superiority. A meticulous comparison with other schemes (as outlined in Table 3) shows that the DCNN method excels across various performance measures, affirming its efficacy in classification and prediction tasks. Furthermore, the discussion underscores the importance of mitigating overfitting through the strategic optimization of layers

and the identification of optimal features using correlation analysis and heatmaps in context of (CK Chan et al., 2023). This nuanced approach not only minimizes overfitting risks but also accentuates the critical role of feature selection in augmenting the predictive capabilities of the model.

In a broader context, the findings suggest that the proposed DCNN method holds significant promise as a robust and accurate tool for breast cancer recurrence prediction. Its superior performance, demonstrated through diverse metrics and comparative analyses, signifies its potential to surpass conventional methodologies and contribute meaningfully to the field of medical prognostics. The strategic integration of DL techniques, coupled with meticulous feature selection, emerges as a key strategy for enhancing the accuracy and reliability of breast cancer recurrence predictions. These outcomes encourage further exploration and application of advanced ML approaches in medical research, particularly for refining predictive models in the domain of oncology.

5. Conclusion

This research work marks a significant step in breast cancer recurrence prediction by introducing a groundbreaking system anchored by a novel DCNN algorithm. The comprehensive evaluation on the Wisconsin Breast Cancer (WBC) dataset showcases not only impressive mean metrics (accuracy at 97.63%, precision at 98.57%, recall at 96.84%, and F1-score at 97.89%), but also a clear superiority over conventional ML approaches. The transformative aspects in this research, like converting numerical data into a 2D image format and strategically applying dense layers, highlight the strength of the predictive model. Moving forward, fine-tuning strategies and structural adjustments, such as adding more layers, offer opportunities for further optimization. Beyond the technical nuances, the research holds profound implications for clinical practice, offering a pioneering tool for clinicians to navigate the complexities of breast cancer recurrence prediction. This not only aids in tailoring personalized treatment plans but also holds the promise of mitigating unnecessary interventions. This research encourages further exploration into advanced neural networks in medical research, paving the way for a new era of predictive modelling that could significantly improve patient outcomes.

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