

Tropical Convolutional Neural Networks (TCNNs) Based Methods for Breast Cancer Diagnosis

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ABSTRACT

One of the leading causes of mortality for women worldwide is breast cancer. The likelihood of breast cancer-related mortality can be decreased by early identification and rapid treatment. Machine learning-based predictive technologies provide ways to detect breast cancer earlier. Several analytical techniques, such as breast MRI, X-ray, thermography, mammography, ultrasound, etc., may be used to find it. Accuracy metrics are the most extensively used approach for performance evaluation, and the Tropical Convolutional Neural Networks (TCNNs) model for breast cancer detection is the most precise and popular model. The proposed approach was examined using the Kaggle Breast Cancer Datasets (KBCD). The data set is partitioned into training and testing. We suggest a new class of CNNs called Tropical Convolutional Neural Networks (TCNNs), which are based on tropical convolutions and replace the multiplications and additions in traditional convolutional layers with additions and min/max operations, respectively, in order to reduce the number of multiplications. The results of the review demonstrated that the Tropical Convolutional Neural Networks (TCNNs) is the most successful and popular model for detecting breast cancer, and that accuracy metrics is the most popular approach for evaluating performance. It is amazing how deep learning is being used to so many different real-world problems. Additionally, because tropical convolution operators are basically nonlinear operators, we anticipate that TCNNs will be better at nonlinear fitting than

traditional CNNs. The Kaggle Breast Cancer Datasets (KBCD) findings demonstrate that TCNN can reach more expressive power than regular convolutional layers.

Keywords: Machine Learning, Breast Cancer, Malignant, Classification, Tropical Convolutional Neural Networks (TCNNs), Kaggle Breast Cancer Datasets (KBCD).

I. INTRODUCTION

One of these is breast cancer, which has surpassed all other cancers as the leading cause of death in women [1]. Breast cancer is responsible for 15% of deaths among women. Breast cancer is the fourth most common cancer globally by mortality rate. There are several factors at play, all of which contribute to the development of breast cancer. Some of these factors include diet, genetics, hormones, obesity, cell proliferation from aberrant cells, and even radiation therapy. According to earlier studies, roughly half of patients who are diagnosed with breast cancer at an advanced stage pass away [2]. The current techniques for BC classification are no longer sufficient to meet the growing demand for medical photographs due to the population's fast rise and the rapid daily growth of medical photos [3]. Pathologists routinely visually check and investigate the entire pathological image in order to interpret and locate the anomalies within the medical image. Furthermore, it takes a lot of time to use clinical diagnostic [4] methods to determine if a medical image is carcinogenic or not. This process is quite tedious and time-consuming. The human eye is less adept at detecting minute changes in tissue, and each medical professional has a unique subjective mood for determining fatigue. This can cause different medical specialists to get different diagnostic conclusions about the same medical imaging. The human factor, which is not error-free, is significantly relied upon in medical picture diagnosis. The patient may suffer severe effects as a result of the doctor's

little mistake. According to investigations, the situation could become better if women can detect breast cancer early and start treatment at an early stage [5]. To do this, they must precisely predict how the ailment will progress from a benign condition to breast cancer. Machine learning methods provide accurate early forecasting. Machine learning, a subset of artificial intelligence, is crucial in the classification of breast cancer.

Machine Learning (ML) methods made a significant contribution to the early detection of breast cancer. Machine learning techniques, such as linear discriminant analysis (LDA), support vector machines (SVM), and artificial neural networks (ANN) [6], are used in a number of studies to categorize data, build models, or enhance the performance of already-existing models [7]. Convolutional neural networks (CNNs) are a popular tool in the machine learning [8] area of computer vision for problems involving pictures and videos, including as image classification, face recognition, object identification, and image segmentation. However, as CNN layers become deeper, there may occasionally be billions of [11] floating-point multiplications, which greatly increases the convolutional neural network's computing cost. We suggest a brand-new class of CNNs termed Tropical Convolutional Neural Networks (TCNNs) [13], in which the convolution layer employs tropical convolution operators, including both minplus and maxplus operators. As a consequence, a Tropical Convolutional Neural Networks (TCNNs) [14] model

has been proposed by the authors of this study for the classification of breast cancer. The Kaggle Breast Cancer Datasets (KBCD) breast cancer datasets improved by detecting the tumors and classifying them as benign or malignant [15].

II. Background

The literature on the categorization of breast cancer data is covered in this section [16]. Numerous machine-learning techniques have been used to make breast cancer predictions [17]. For the detection of breast cancer, Khuriwal et al developed an adaptive voting ensemble technique [18]. Chi-square feature selection was utilized by the authors. Logistic Regression and ANN [19] are merged and used to the Breast Cancer dataset. Comparing their approach to other ways, they reported high accuracy. Research by Fu et al. [20] examined the use of ML to identify lymphedema in BC patients. Data analysis included both statistical and machine learning approaches. Data on 355 patients in total were gathered for the research. The usage of 8 BC symptom-related characteristics. The authors used RBF to examine five classification algorithms, including DT C4.5, DT C5.0, GBM, ANN, and SVM. There are five cross validations used to optimize the parameters. Among 5 classification methods, ANN had the highest accuracy for spotting lymphedema at 93.75%. The lowest accuracy for DT C4.5 was 76.31% when it came to identifying lymphedema.

A deep learning system [21] has been developed that can more accurately identify breast cancer from mammography pictures [22] by using lesion annotations only during the initial training phase and deleting them during the latter stages.

SVM, Decision Tress [23], Artificial Neural Network [24] [25], Minimum Distance Classifier [26], Fuzzy Classifier [27], Fuzzy Rough Neural Network [28][29], Particle Swarm Optimization [30][31], microRNA and biomarkers [32], and Deep Learning approaches are

just a few of the studies that have been published and are based on various methods that could enable early cancer investigation and prediction. Litejens et al. presented a survey on the application of deep learning in medical image processing in 2017 [33]. Using different datasets of mammography images, contemporary classification methods like CNN, Principal Component Analysis (PCA), and K Nearest Neighborhood algorithms are utilized to identify breast cancer [34]. Meet et al. developed a neural network based on the ICA-RBFNN to discriminate breast cancer, and they were effective in reaching an average precision of 90.49% [36]. Liu [37] presented a categorization system for breast cancer based on mean radius and mean texture. The accuracy of the suggested model was 90.48%. On breast cancer data, logistic regression had a 90.5% accuracy rate. Wadkar et al. suggested ANN and SVM-based breast cancer detection [38]. SVM and ANN, two ML classifiers, are applied on 5000 photos of breast cancer data.

Their suggested approach has an accuracy rating of 91% for SVM and 97% for ANN. A probabilistic perceptron-based machine learning model was suggested by Cowsik and Clark. On WBCD, experiments were conducted. The proposed approach estimates the likelihood that a cancer tumor is malignant or benign [39]. The precision of the model is 97% retrieved, and its deviation from the mean is 2%. Classification model for breast cancer using 3 machines learning algorithms RF, LR, DT was implemented by Murugan et al [40] accuracy obtained using LR is reported as 84.14% whereas for random forest it is 88.14%. Breast cancer classification model combining Three machine learning techniques Murugan et al. applied RF, LR, and DT; accuracy using LR is reported as 84.14%; accuracy utilizing random forest is reported as 88.14% for offering a precise and dependable method of classifying breast cancer into many categories A class structure-based deep convolutional network with hierarchical feature representation was reported by Han et al. [41]. The

accuracy of the multiclass categorization of breast cancer used in this study was 95.9%.

Jiang et al.'s study [42] examined the circumstances of the area under the receiver operating characteristic curves (AUC) using a brand-new dataset called BCDR-F03 (Film Mammography dataset number three). The authors of this work employed the GoogLeNet and AlexNet architectures to categorize breast lesions, with AUC values of 0.88 and 0.83, accordingly.

Hidden patterns are discovered using unsupervised techniques such as Convolutional Neural Networks (CNN), Long-Short-Term Memory (LSTM) [43], and a mix of CNN and LSTM models. SVM was then used to classify the images. M. Abdar et al. recommended an ensemble strategy employing vote/voting classifier to differentiate benign tumors from malignant breast cancer. It produced a two-layer voting classifier for two or three different machine learning algorithms [44]. The results of several voting processes demonstrated that the simple classification algorithm functioned satisfactorily [45]. Toaçar, M. et al. [46] offer the BreastNet convolutional neural network model, which is based on deep learning. The BreastNet's architecture is based on attention modules and is a residual design. Before providing any input to the model, the BreastNet architecture in this study employs the augmentation strategy to produce the synthetic training data. The BreakHis dataset was utilized for the trial, and it performed better than the AlexNet, VGG-16, and VGG-19 systems.

3. Goal

The most prevalent cancer in women, the second-leading cause of cancer mortality for females (behind lung cancer), and the primary killer of females between the ages of 45 and 55. Breast cancer is typically treatable when discovered and treated quickly. Over the past three decades, there has been a reduction of at least one-third of breast cancer

fatalities [47]. This is partly a result of enhanced screening as well as earlier detection and better breast cancer care. Typically, screening finds the disease at an earlier stage, when the likelihood of effective therapy is higher. Because the breast tumour may be removed before it has an opportunity to spread (metastasize), early identification and treatment of breast cancer increase survival. Treatments are also available to stop cancer cells from spreading to other organs once they have left the breast. When a woman or her healthcare professional notices a lump or another alteration in her breast or armpit, it may be breast cancer. A lump may not be the only abnormal change; there may also be dimpling of the skin, an alteration in the size or shape of one breast, retraction (pulling in) of the nipple when it earlier pointed outward, bloody discharge from the nipple, or a yellowing of the skin of the breast that is not caused by an infection or a skin condition like psoriasis or eczema [48]. A mammography and breast ultrasound are often advised to assess a breast lump. A breast biopsy may also be advised if suspected. Even if a mammography is negative, a suspicious lump should never be disregarded. Up to 5 to 15% of newly discovered breast cancers are not detectable by mammography. Holistic treatment goal to eradicate or stop the development of any cancer cells (metastases) that may have fled the breast and may spread to other organs. The lymph nodes in the axilla (under the armpit) are where breast cancer first spreads. The likelihood of curing breast cancer is lower than when it just affects the breast when it has spread to the axillary lymph nodes. Rarely are patients [49] healed if they have metastases or cancerous cells in other organs such the liver, lung, or bone. Systemic treatment, however, may stop metastases in a significant portion of patients, curing many women who might not have been treated. While systemic therapy dramatically lowers the likelihood that a cancer will come back, particularly in cases where the disease has already progressed to the axillary lymph nodes, it has become a crucial part of the treatment of

breast cancer. In turn, this raises the likelihood of beating breast cancer.

4. Kaggle Dataset

Data scientists and machine learning enthusiasts may connect online at Kaggle. Users of Kaggle may work together, uncover and publish datasets, and compete with other data scientists to solve issues in data science. A platform for data science and AI is called Kaggle. Large businesses and organizations post contests with cash rewards on this site. Users can share their datasets and look at others' shared datasets in addition to participating in contests. Kaggle is a [50] platform for crowdsourcing that enables you to draw in, develop, educate, and challenge other data scientists from across the world to tackle challenges in machine learning, predictive analytics, and data science. Kaggle will help you by providing a forum where like-minded enthusiasts may interact and start a friendly competition to address their actual concerns. Additionally, data scientists may discuss these datasets with other data scientists in the discussion area and exchange code snippets that use them. In addition, Kaggle has a discussion board and a few courses where you may learn more about the subject of machine learning and interact with other professionals. Users on the Kaggle platform publish datasets that are known as Kaggle datasets. When you sign up for this platform, you get access to these datasets and may explore and create models using them. More seasoned data scientists utilize the dataset Breast Cancer Wisconsin. Figure 1 depicts information from this Kaggle Dataset regarding Wisconsin breast cancer patients. This dataset's main objective is to provide predictions about a patient's propensity for breast cancer based on their features. For instance, the survival rate is high for patients with tumors that are smaller than 0.5 cm in size, and vice versa.

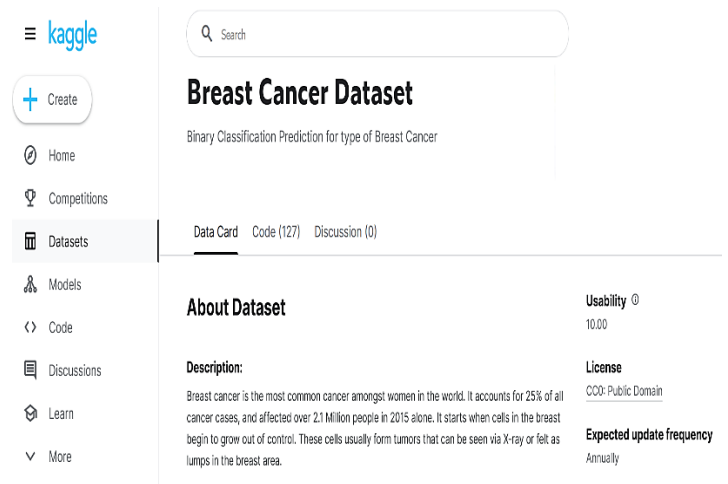


Figure 1. The Breast Cancer Kaggle Dataset

4.1 Dataset

The breast cancer Kaggle dataset [51] was used to perform the research. The dataset was obtained from the well-known machine learning Kaggle dataset and has a simplified size of 56932. The sample count for the dataset is represented by the number 569, whereas

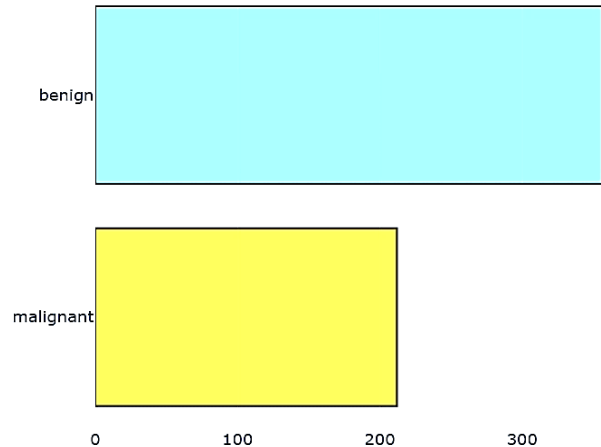


Figure 2: Total Number of Malignant and Benign Data

The integer 32 represents the quantity of characteristics seen in image 2. The example dataset [52] contains the atomic characteristics of fine needle aspirations (FNAs) made from patients' breasts. To get a sample for a diagnosis or illness prediction [53], such as cancer, a tiny needle is inserted into a bodily fluid or tissue that seems abnormal. The entire amount of

malignant and benign data in the Breast Cancer Kaggle dataset is shown in Figure 2. There are no missing attributes in the collection, and there are 357 benign and 212 malignant groups overall.

4.1.1 Attribute Information

- 1) ID number
- 2) Diagnosis (M = malignant, B = benign)
- 3-32)

Ten real-valued features are computed for each cell nucleus:

- a) radius (mean of distances from centre to points on the perimeter)
- b) texture (standard deviation of Gray-scale values)
- c) perimeter
- d) area
- e) smoothness (local variation in radius lengths)
- f) compactness ($\text{perimeter}^2 / \text{area} - 1.0$)
- g) concavity (severity of concave portions of the contour)
- h) concave points (number of concave portions of the contour)
- i) symmetry
- j) fractal dimension ("coastline approximation" - 1)

III. Machine Learning

The rapidly expanding discipline of data science includes machine learning as a key element. Algorithms are taught using statistical techniques to produce classifications or predictions and to find important insights in data mining projects. The decisions made as a result of these insights influence key growth indicators in applications and enterprises, ideally. Data scientists will be more in demand as big data [54] continues to develop and flourish. They will be expected to assist in determining the most pertinent business issues and the information needed to address them. In overall, predictions or

classifications are made using machine learning algorithms. Your algorithm will provide an estimate about a pattern [55] in the input data based on some input data, which can be labelled or unlabeled. The model's prediction is evaluated using an error function. If there are known instances, an error function can compare them to gauge the model's correctness. Weights are changed to lessen the difference between the known example and the model estimate if the model can better match the data points in the training set. This "evaluate and optimise" procedure will be repeated by the algorithm, with weights being updated automatically, until a predetermined level of precision is reached.

5.1 The Convolution Layers

Figures 3 and 4 depict the MinPlus and MaxPlus convolution operators' computation procedures. We choose MinPlus as an example because the two procedures are fairly comparable. (For the convolution operator MaxPlus, simply swap minimum and maximum.) Consider an input picture with dimensions of 7 x 7, 3 x 3 for the convolutional kernel [56] (the size of the sliding window), and 1 for the sliding mechanism. The convolution operation computation in a sliding window may thus be split into two phases.

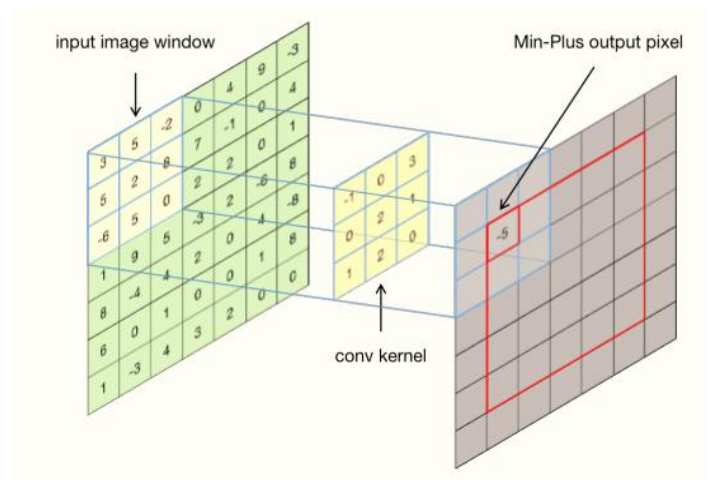


Figure 3. The Convolution Computation Procedures
Min-Plus

Phase 1: To create a new 3 3 matrix, add the 33-sliding window to the matching convolutional kernel components, and use the lowest of the new matrix as the retrieved value of this sliding window.

Phase 2: Slide the window with a stride of 1, and after calculating all the parameters as in Phase 1, we can obtain the final output picture, which is an image with a size of 5 by 5, from Phase 2.

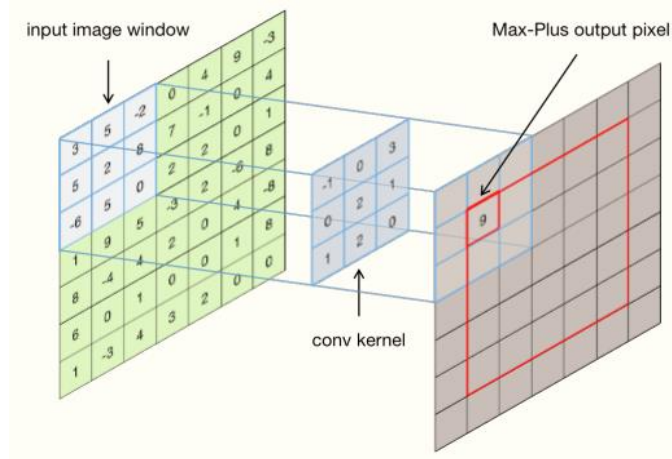


Figure 4. The Convolution Computation Procedures Max-Plus

IV. Suggested System

Let's say we have a picture with many input channels. The first phase of the example in figure 5 can be understood using the operators in figures 3 and 4, where the input picture of size 7 x 7 x 3 (where C_{in} is the number of input channels) is passed through two 3 x 3 convolutional kernels individually to produce a 5 x 5 x 3 intermediate output for each. Then, to get the output result in a single [57] channel, we may either add up the corresponding locations of each channel of the intermediate result or take the highest value of each of them. In this illustration, we successfully complete the forward Min(Max)Plus-Sum(Max)-Conv layer procedure and obtain the feature map of size 5x5x2.

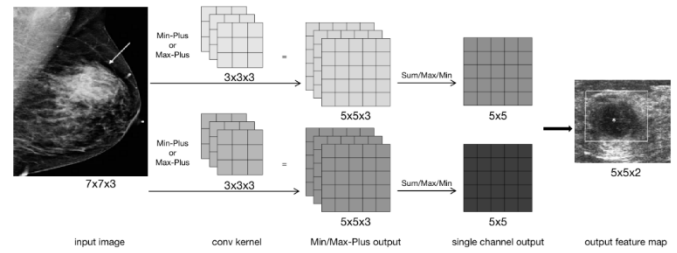


Figure 5. The Suggested Tropical Convolutional for Breast Cancer Classification

Multiplication is not used at all in the tropical convolution layers. Furthermore, tropical convolution layers are effectively nonlinear layers due to the min/max operations they conduct, as opposed to regular convolution layers which are linear, therefore including them in the network can improve its overall non-linear expression capacities. The Kaggle dataset was sent to TCNN [58] as input for the application for classifying breast cancer. After providing them with input, we trained the deep convolutional kernels in the suggested TCNN framework.

i) MinPlus-Sum-Conv Layer (MinP-S)

$$Y(h, w, p) = \sum_{d=0}^{C_{in}} \min_{i,j=0}^k (X(h + i, w + j, d) + K(i, j, d, p))$$

ii) MaxPlus-Sum-Conv Layer (MaxP-S)

$$Y(h, w, p) = \sum_{d=0}^{C_{in}} \max_{i,j=0}^k (X(h + i, w + j, d) + K(i, j, d, p))$$

In the recommended architecture, there are two classes: a benign class and a malignant class. The following weighted loss function was used to train the recommended TCNN classifier.

$$\alpha(\xi, P_n, Q_n) = -\frac{1}{N} \sum_{n=1}^N g_n \sum_{k=1}^K t_{kn} Q_{kn}$$

In more precise terms, P_n denotes the input vector, Q_n the classification result for the n th clinical input data, and t_n the actual clinical sample response. K is the number of classes, and N is the total number of clinical samples. The following layers and settings make up the TCNN architecture that produced the greatest results in our tests.

Convolutional layers employ the output that the input layer generates. It is possible to apply transformations like mean-subtraction and feature-scaling. An output feature map is created for each learnable filter that is convolved with the input picture in a convolution layer. This framework has three convolutional layers. The zero-padding is set to 2, the stride is set to 1, and the receptive fields (kernels) are of size 5 5. The initialization of the first two convolutional layers [59], which each learn 32 filters, is a Gaussian distribution. The spatial dimension of the input is down sampled by the pooling layers. After each convolutional layer, there is one pooling layer. They are all programmed to utilize a spatial extent of 33 and a stride of 2. The most popular max operation across the receptive field is used by the first pooling layer, while average pooling is used by the other min layers [60]. They consider the input as a straightforward vector and generate a single vector as the result. In this framework, there are two inner-product layers. Depending on how many classes are involved in the classification task, the final option a fully linked output layer with Softmax activation is determined [61].

V. FINDINGS AND EVALUATION

The figure 6 shows the contrast between the 1000 photos in the training folder and the 250 images in the validation folder for each category. A matrix of pixel values takes the form [WIDTH, HEIGHT, CHANNELS]. [32x32x3] is what we enter. We often start with a limited number of filters when identifying low-level characteristics [62]. As we

explore the TCNN further, we apply more filters to identify high-level properties. Feature detection relies on "scanning" the input with a filter of a particular size and doing matrix operations in order to produce a feature map. When the pooling-size parameter is set to (2, 2), the pooling layer will scale the output to [16x16x12] along the width and height axes.

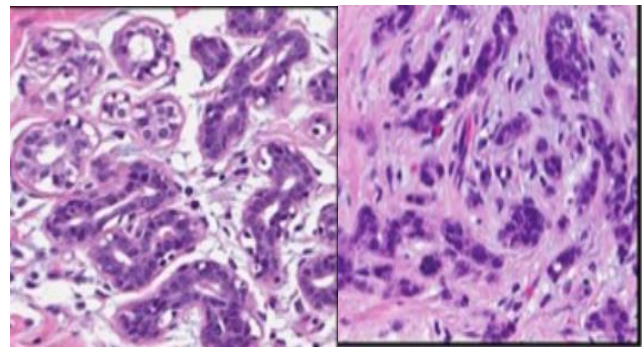


Figure 6. The Benign and Malignant Sample

A training dataset made up of N photos [63][64] that have all been divided into one of two groups serves as our input. The features of each class are then learned by training the classifier using this training set. The classifier's performance is then evaluated by asking it to predict labels for a new set of photographs that it has never seen before. The labels that are really on these images will then be compared to those that the classifier predicted. The proper directories received the photographs and loaded them.

	count	mean	std	min	25%	50%
diagnosis	569.0	0.372583	0.483918	0.000000	0.000000	0.000000
	1.000000	1.000000				
radius_mean	569.0	14.127292	3.524049	6.981000	11.700000	
	13.370000	15.780000	28.11000			
texture_mean	569.0	19.289649	4.301036	9.710000		
	16.170000	18.840000	21.800000	39.28000		
perimeter_mean	569.0	91.969033	24.298981	43.790000		
	75.170000	86.240000	104.100000	188.50000		
area_mean	569.0	654.889104	351.914129	143.500000	420.300000	
	551.100000	782.700000	2501.00000			
smoothness_mean	569.0	0.096360	0.014064	0.052630	0.086370	
	0.095870	0.105300	0.16340			
compactness_mean	569.0	0.104341	0.052813	0.019380	0.064920	
	0.092630	0.130400	0.34540			
concavity_mean	569.0	0.088799	0.079720	0.000000	0.029560	
	0.061540	0.130700	0.42680			
concave points_mean	569.0	0.048919	0.038803	0.000000	0.020310	
	0.033500	0.074000	0.20120			
symmetry_mean	569.0	0.181162	0.027414	0.106000	0.161900	
	0.179200	0.195700	0.30400			
fractal_dimension_mean	569.0	0.062798	0.007060	0.049960	0.057700	
	0.061540	0.066120	0.09744			
radius_se	569.0	0.405172	0.277313	0.111500	0.232400	0.324200
	0.478900	2.87300				
texture_se	569.0	1.216853	0.551648	0.360200	0.833900	1.108000

	1.474000	4.88500				
perimeter_se	569.0	2.866059	2.021855	0.757000	1.606000	2.287000
	3.357000	21.98000				
area_se	569.0	40.337079	45.491006	6.802000	17.850000	
	24.530000	45.190000	542.20000			
smoothness_se	569.0	0.007041	0.003003	0.001713	0.005169	
	0.006380	0.008146	0.03113			
compactness_se	569.0	0.025478	0.017908	0.002252	0.013080	
	0.020450	0.032450	0.13540			
concavity_se	569.0	0.031894	0.030186	0.000000	0.015090	0.025890
	0.042050	0.39600				
concave points_se	569.0	0.011796	0.006170	0.000000	0.007638	
	0.010930	0.014710	0.05279			
symmetry_se	569.0	0.020542	0.008266	0.007882	0.015160	0.018730
	0.023480	0.07895				
fractal_dimension_se	569.0	0.003795	0.002646	0.000895	0.002248	
	0.003187	0.004558	0.02984			
radius_worst	569.0	16.269190	4.833242	7.930000	13.010000	
	14.970000	18.790000	36.04000			
texture_worst	569.0	25.677223	6.146258	12.020000		
	21.080000	25.410000	29.720000	49.54000		
perimeter_worst	569.0	107.261213	33.602542	50.410000		
	84.110000	97.660000	125.400000	251.20000		
area_worst	569.0	880.583128	569.356993	185.200000	515.300000	
	686.500000	1084.000000	4254.00000			
smoothness_worst	569.0	0.132369	0.022832	0.071170	0.116600	
	0.131300	0.146000	0.22260			
compactness_worst	569.0	0.254265	0.157336	0.027290	0.147200	
	0.211900	0.339100	1.05800			
concavity_worst	569.0	0.272188	0.208624	0.000000	0.114500	
	0.226700	0.382900	1.25200			
concave points_worst	569.0	0.114606	0.065732	0.000000	0.064930	
	0.099930	0.161400	0.29100			
symmetry_worst	569.0	0.290076	0.061867	0.156500	0.250400	
	0.282200	0.317900	0.66380			
fractal_dimension_worst	569.0	0.083946	0.018061	0.055040	0.071460	
	0.080040	0.092080	0.20750			
<pre> img = cv2.resize(img, (RESIZE, RESIZE)) IMG.append(np.array(img)) return IMG benign_train = np.array(Dataset_loader('data/train/benign', 224)) malign_train = np.array(Dataset_loader('data/train/malignant', 224)) benign_test = np.array(Dataset_loader('data/validation/benign', 224)) malign_test = np.array(Dataset_loader('data/validation/malignant', 224)) </pre>						

The data collection is then split into two train and test sets, each of which contains 80% benign photos and 20% malignant images, correspondingly.

```

X_train, X_test, y_train, y_test = train_test_split(X, y,
test_size=0.2, random_state=42)
print(f'X_train: {X_train.shape}')
print(f'X_test: {X_test.shape}')
print(f'y_train: {y_train.shape}')
print(f'y_test: {y_test.shape}')
X_train: (455, 30)
X_test: (114, 30)
y_train: (455, 1)
y_test: (114, 1)
    
```

The (M) in this section denotes potentially harmful malignant cells, whereas the (B) denotes benign, or healthy, cells. The relationship between the different qualities is now clear. This heat map shows the degree to which each column effects each other (for instance, radius means have a 34% influence on texture mean) testing and training. The datasets were then divided into dependent (Q) and independent (P) datasets P = df.iloc[:, 2:31].values, and Q = df.iloc[:, 1].values. They

have an array type. While the independent dataset (P) comprises the characteristics that are used to anticipate the result, the dependent data set (Q) contains the malignancy diagnosis for the patient. The dataset is now divided in half, with 20% used for testing and 80% for training. We use a range of machine learning [65] models on the training set, including K-Nearest Neighbor, Convolutional Neural Networks (CNNs), and Naive Bayes Classifier [66]. The properties of the data and training will determine whether a tumor is malignant (M) (hazardous) or benign (B), based on its level of risk. The Kaggle Breast Cancer Datasets (KBBCD) were used to acquire information about breast cancer. The software will assess the datasets using a variety of criteria.

7.1 Attributes

- **diagnosis:** The diagnosis of breast tissues (M=malignant,B=benign)
- **mean_radius:** mean of distances from center to points on the perimeter
- **mean_texture:** standard deviation of gray-scale
- **mean_perimeter:** mean size of the core tumor
- **mean_area mean_smoothness:** mean of local variation in radius length.

7.2 Performance Evaluation

To evaluate the accuracy of forecasts made by a classification algorithm, a classification analysis is utilized. The effectiveness of the suggested framework for categorizing breast cancer [67] using the Kaggle Breast Cancer Datasets (KBBCD) is shown in Table 1. The TCNN is evaluated using the metrics provided below.

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

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

$$FPR = \frac{FP}{FP+TN}$$

$$F - measure = 2 * \frac{Precision*Recall}{Precision+Recall}$$

The accuracy of the TCNN breast cancer classifier was evaluated using the following metrics: True Positive Rate (TPR), True Negative Rate (TNR), False Positive

Rate (FPR), and Precision [68]. True Positives (TP) are clinical samples that the developed classifier correctly classified as benign. Clinical samples that the proposed classifier correctly detected as having malignant clinical data are known as True Negative (TN) clinical samples. Once the suggested design improperly classifies the data into the benign class or the malignant class, respectively, false-negative and false-positive situations happen. It shows the error in categorization. Each sample may be reliably diagnosed by a skilled classifier. A model, however, cannot be used in clinics if it accurately predicts actual negative samples but is unable to identify the real positive ones due to the classifier's uncertainty. Therefore, the built-in classifier needs to be extremely accurate. We employed a range of models after using a lot of classification models to reach the accuracy depicted in figure 7.

Table 1. Performance Assessment of proposed TCNN and Comparison with previously studies (Kaggle Breast Cancer Datasets (KBCD))

Method	Accuracy (%)
K-Nearest Neighbor	97.40
TCNN	99.74
Naïve Bayes Classifier	96.10
CNN	98.86

The TCNN Classification method clearly produces the best outcomes for the data we have after developing our classification model. It isn't relevant to all datasets, though.

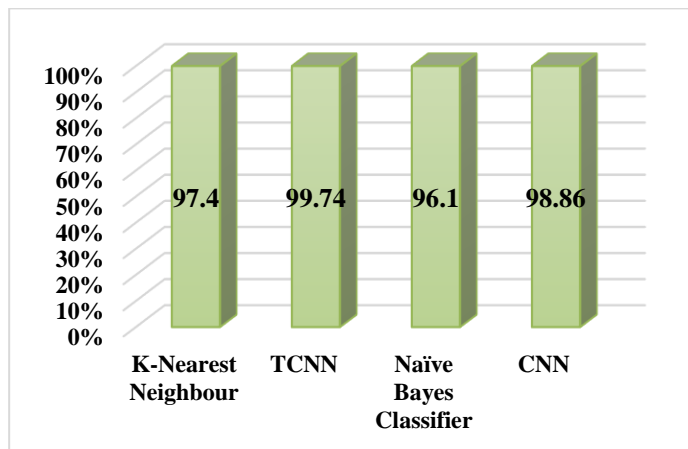


Figure 7. The Accuracies with Different Models

7.3 Confusion Matrix

The performance of a machine learning model on a set of test data is summarized in a matrix called a confusion matrix, as shown in figure 8. It is frequently used to assess how well categorization models work. These models try to predict a category label for each input event [69]. The matrix shows how many true positives (TP), true negatives (TN), false positives (FP), and false negatives (FN) the model generated from the test data. The matrix will have the shape of a 2*2 table for binary classification and n*n for multi-class classification, where n is the number of classes.

```
def plot_confusion_matrix(y_true, y_pred):
    cm = confusion_matrix(y_true, y_pred)
    group_names = ["True Neg", "False Pos", "False Neg", "True Pos"]
    group_counts = ["{0:0.0f}".format(value) for value in cm.flatten()]
    group_percentages = ["{0:.2%}".format(value) for value in cm.flatten()/np.sum(cm)]
    labels = ["{v1}\n{v2}\n{v3}" for v1, v2, v3 in zip(group_names, group_counts, group_percentages)]
    labels = np.asarray(labels).reshape(2,2)
    plt.subplots(figsize = (5,3))
    ax = sns.heatmap(cm/np.sum(cm), annot=labels, fnt="", cmap='Blues')
    ax.set_xlabel('Predicted Class')
    ax.set_ylabel('Actual Class')
    ax.set_title('Random Forest Classification')
    plt.show()
    print("Classification report:\n{classification_report(y_test, y_pred)}")
    print("")
    print("_"*12)
    print("")
    # Plot the confusion matrix as a heatmap
    plot_confusion_matrix(y_test, y_pred)
```

```
y_pred = tcnn.predict(X_test)
y_pred = (y_pred > 0.5)
print(np.concatenate((y_pred.reshape(len(y_pred),1), y_test.reshape(len(y_test),1)),1))
```



Figure 8. The Confusion Matrix

273 samples were chosen as the test data out of the 569 samples used in this experiment, with the other samples being used for training and validation. Total samples are 273, of which 98 are benign and 175 are malignant [70]. Figure 6 displays the confusion matrices for the test data using the Kaggle Breast Cancer Datasets (KBCD). All of the benign and malignant samples could be distinguished with the help of the proposed classifier. The results of this model are shown in Figure 9. It had an overall accuracy of 99.46%, a precision of 99.78%, a recall of 99.66% [71], and an F-measure [72] value of similarly 99.27%.

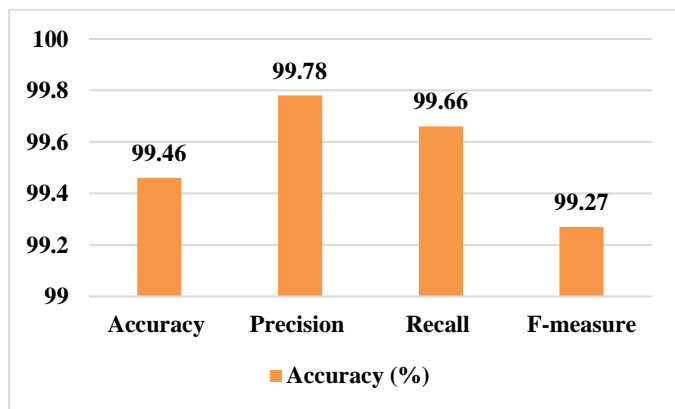


Figure 9. The Overall Accuracy, Precision, Recall, F-measure

VI. Conclusion

Machine learning techniques are often employed and are essential for categorizing health care data. Although several methods for classifying breast cancer data have been established, there are still significant difficulties, such as accuracy. We put out a

methodology for categorizing breast cancer data to solve this. Early breast cancer detection can aid in lowering the mortality rate brought on by breast cancer. The development of automated medical applications has been sparked by the extraordinary success of deep learning and image processing. Carcinomas, masses, lumps, calcification, and asymmetry are just a few of the anomalies in the breast that might be signs of breast cancer. For the purpose of assisting the radiologist in reading a breast picture, a deep learning model has been created. The breast cancer dataset was used in the numerous studies. using the KBCD (Kaggle Breast Cancer Datasets) datasets. The suggested model is evaluated in comparison to various current techniques for categorizing breast cancer data. According to the findings, TCNNs often have greater non-linear expression capabilities than conventional CNNs. From a practical standpoint, this TCNN concept offers us richer opportunities to construct deep neural networks. In the future, we may create networks tailored to individual requirements by choosing the appropriate tropical convolution modules for the job at hand. To perform a more thorough investigation of this novel convolution design in future work, we want to apply the tropical convolution modules to further varieties of deep neural networks. The results of this experiment demonstrate how well the classifier outperforms other state-of-the-art methods. This model generated overall accuracy, precision, recall, and F-measure values of 99.46%, 99.78%, and 99.66%, respectively. Finally, the suggested approach appears to be well suited for managing parameter settings for automated breast cancer diagnostic algorithms.

VII. REFERENCES

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