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RESEARCH ARTICLE

Optimizing Breast Cancer Detection: Deep Transfer Learning Empowered by SVM Classifiers

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Abstract

Objectives: The research aims to enhance breast cancer detection accuracy and effectiveness using deep transfer learning and pre-trained neural networks. It analyses breast ultrasound images and identifies important characteristics using pre-trained networks. The goal is to create a more efficient and accurate automated system for breast cancer detection. **Methods:** The study uses breast ultrasound cancer image data from the Kaggle Data Repository to extract informative features, identify cancer-related characteristics, and classify them into benign, malignant, and normal tissue. Pre-trained Deep Neural Networks (DNNs) extract these features and feed them into a 10-fold cross-validation SVM classifier. The SVM is evaluated using various kernel functions to identify the best kernel for separating data points. This methodology aims to achieve accurate classification of breast cancer in ultrasound images. **Findings:** The study confirms the effectiveness of deep transfer learning for breast cancer detection in ultrasound images, with Inception V3 outperforming VGG-16 and VGG-19 in extracting relevant features. The combination of Inception V3 and the SVM classifier with a polynomial kernel achieved the highest classification accuracy, indicating its ability to model complex relationships. The study demonstrated an AUC of 0.944 and a classification accuracy of 87.44% using the Inception V3 + SVM polynomial. **Novelty:** This research demonstrates the potential of deep transfer learning and SVM classifiers for accurate breast cancer detection in ultrasound images. It integrates Inception V3, VGG-16, and VGG-19 for breast cancer detection, demonstrating improved classification accuracy. The combination of Inception V3 and SVM (polynomial) achieved a significant AUC (0.944) and classification accuracy (87.44%), outperforming other models tested. This research underscores the potential of these technologies for accurate breast cancer detection in ultrasound images.

Keywords: Breast Cancer; Deep Learning; Feature Extraction; Inception-v3; SVM; Transfer Learning

1 Introduction

Breast cancer (BC) is a highly suspicious disease characterized by the uncontrollable growth of abnormal cells in the breast, primarily occurring in the lobules or milk ducts that supply milk to the epithelial duct [(1)]. In 2020, the American Cancer Society reported 2.3 million new cases, accounting for 11.7% of all new cancer diagnoses. The disease has increased by nearly 0.5% from 2008 to 2017. BC is the most common cancer-causing death in women, with the leading cause being among women aged 35-54. The World Health Organization reported that 685,000 people died in 2020 due to breast cancer, affecting millions of women. As of 2020, 7.8 million women had been diagnosed with breast cancer in the previous five years [(2)]. To combat this, women should start getting annual mammograms between 40 and 44, every two years for those aged 45 to 54, and every two years for those over 55. Screening should continue if a woman is in good health and expected to live at least another ten years [(3)]. An ultrasound is a diagnostic tool used to identify breast cancer, detecting solid masses like tumours and benign cysts [(4)]. Mammograms are the most common imaging tests for breast cancer detection, with annual mammograms performed on women over 40 [(5)]. Other recommended tests include breast biopsy or MRI [(6)]. The table provides a detailed analysis of breast cancer stages, diagnosis systems, prevention, and treatment, and affected breast area. The Table 1 shows the Stages of BC, Diagnosis, Prevention, and treatments.

This research aims to develop a breast cancer identification system using deep transfer learners and SVM classifier models. The system will extract features from ultrasound images and classify them into benign, malignant, or average. The system will be trained on a 10-folder cross-validation dataset and tested on a separate dataset. The performance of the models will be evaluated using accuracy, precision, recall, and F1 score metrics. The system aims to accurately identify breast cancer in ultrasound images and provide a reliable diagnosis.

This research explores breast cancer research using breast cancer images, highlighting the increasing use of Computer Aided Detection Systems (CAD) for medical image analysis. The study also discusses the significant variation in breast anatomy and tumour growth probability based on race. Alsolami et al. (2021) [(7)] examined the KAU-BCMD dataset, re-examining 1416 cases of images 5662 and 405 ultrasound images from 205 patients, with three radiologists annotating the data set. Zhu et al. (2020) [(8)] analyzed deep learning methodologies in cancer diagnosis and prediction, focusing on accuracy, cost reduction, and application issues in cancer diagnosis systems. Tufail et al. (2021) [(9)] reviewed research papers on cancer predictions, diagnosis challenges, and trends in deep learning, highlighting the importance of data argumentation in cancer diagnosis. Kourou et al. (2021) [(10)] compared reinforcement learning, deep learning, and AI/ML cancer-related applications. Tang et al. (2019) [(11)] reviewed computational biology and bioinformatics for deep learning methodologies, examining model similarities, basic structures, and applications and discussing the disadvantages and advantages of suicide and failure models. Table 2 presents a comprehensive overview of the various models and datasets used by researchers in their studies on breast cancer, providing a comprehensive overview of their diverse methodologies and approaches.

Table 1. Stages of Breast Cancer, Diagnosis, Symptoms, Protection and Treatment

Stages	Affected area of Breast	Diagnosis	Precautions and Treatment
Stage 0	The disease doesn't hurt. This indicates that it has not emerged from our breast ducts.	Regular Self-testing. As per Symptoms, Family history and Age consult the doctor.	Avoid using any tobacco materials. Maintain a healthy weight Engage in regular exercise. Fruits and vegetables for a healthy diet [12].
Stage 1	The cells of cancer have reached the breast tissue nearby.	Regular Self-testing. Make an appointment with your doctor if you notice spot or an unusual lump in your breast or other signs of breast cancer. Other imaging tests.	Chemotherapy, hormone therapy, radiation, or targeted therapy. Beware of ourselves, your family's past, and your dangers. Get cancer screening tests and check- ups.
Stage 2	At this stage, tumours can be anywhere from 2 to 5 centimeters across and may or may not affect the lymph nodes in the vicinity.	Symptoms, Imaging tests like Ultrasound, Magnetic resonance (MRI) imaging, Mammogram	Surgery is the most utilized therapy for breast cancer. Many individuals get supplemental therapies like as chemotherapy, hormone therapy, radiation, or targeted therapy [13].
Stage 3	The cancer has spread beyond its original location at this point. Typically, breast cancer at stage III is referred to as locally advance [14].	Symptoms, Mammogram, Magnetic resonance (MRI) imaging, and Breast biopsy. Some other essential tests prescribed by doctors.	Surgery, Chemotherapy, hormone therapy, radiation, or targeted therapy. Avoid using any tobacco materials. Maintain a healthy weight. Engage in regular exercise. Fruits and vegetables for a healthy diet.
Stage 4	Breast cancer tumours can be of any size. Cancer cells from it have migrated to local and regional lymph nodes, in addition to lobules [15].	Symptoms, Mammogram, Magnetic resonance (MRI) imaging, Ultrasound, and Breast biopsy. Some other essential tests prescribed by doctors.	Surgery, Chemotherapy, hormone therapy, radiation, or targeted therapy. Avoid using any tobacco materials. Maintain a healthy weight. Engage in regular exercise. Fruits and vegetables for a healthy diet. Avoid drinking. alcohol at all costs

Table 2. Comprehensive Review of The Different Research Works With Various Models And Various Datasets

Ref.	Author & year	Description	Data set and Methodologies	Highlights
[16]	**Lee et al. (2010)**	The study examined breast imaging techniques such as ultrasound, mammography, and MRI for cancer screening.	Imaging analyzing and screening Models	Screening breast cancer with all imaging methodologies
[17]	Wu et al. (2013)	Analysis and classification of ultrasound breast images using SVM and Genetic Algorithms	The study utilized 210 breast images, including 120 benign and 90 malignant images, using PCA for feature selection and SVM and SVM+GA for classification.	The proposed model SVM + GA outperforms other experimental models.
[18]	Houssein et al. (2021)	The study examined 760 recent breast cancer detection and classification studies using machine learning and deep learning strategies across five image modalities.	The study utilized various machine learning models, including SVM, DT, KNN, NB Network, ANN, and Transfer learner, on Mammograms, Ultrasound, and MRI datasets.	A study of 760 breast cancer research papers found that deep learning models are highly effective for image classification.
[19]	Rezaei, (2021)	The study analyzed various breast cancer image datasets and examined various methodologies such as segmentation, classification, and detection.	Utilize breast cancer imaging datasets including mammograms, ultrasound, and MRI for analysis, and use ML and DL models for classification.	The text introduces public datasets and discusses the main gaps and issues in current methods for diagnosing breast cancer.

Continued on next page

Table 2 continued

[20]	MurtiRa Wat et al. (2020)	The study focuses on the use of machine learning models for classification in diagnosing breast cancer.	ML algorithms like KNN, Logistic Regression, and Ensemble learning are widely used in this.	The proposal proposes a model that outperforms other models in terms of ensemble learning accuracy.
[21]	Vakanski et al. (2020)	This study focuses on the segmentation analysis of Breast Ultrasound images.	The 510 Ultrasound employs a U-Net architecture to image breast tissue and acquire feature representations.	The U-Net model demonstrated high accuracy.
[22]	Luo et al. (2022)	Tumor region segmentation and Classification based analysis on Breast Ultrasound images	Deep Learning methodologies.	DCNN is the best classifier for Breast. Cancer dataset
[23]	Fei et al. (2021)	New deep transfer learning models have been applied to imbalanced breast ultrasound images.	The Deep Transfer Learner novel models, such as the doubly supervised parameter (DSPTC) transfer classifier, are being applied.	The DSPTC model exhibits high accuracy in analyzing the imbalance image dataset compared to other models.

2 Methodology and Materials

The proposed model and methodologies for breast cancer identification utilize transfer learning models like Inception V3, VGG-16, and VGG-19 for feature extraction, and SVM classifiers for classification of malignant, benign, and normal breast cancers.

2.1 Proposal Model

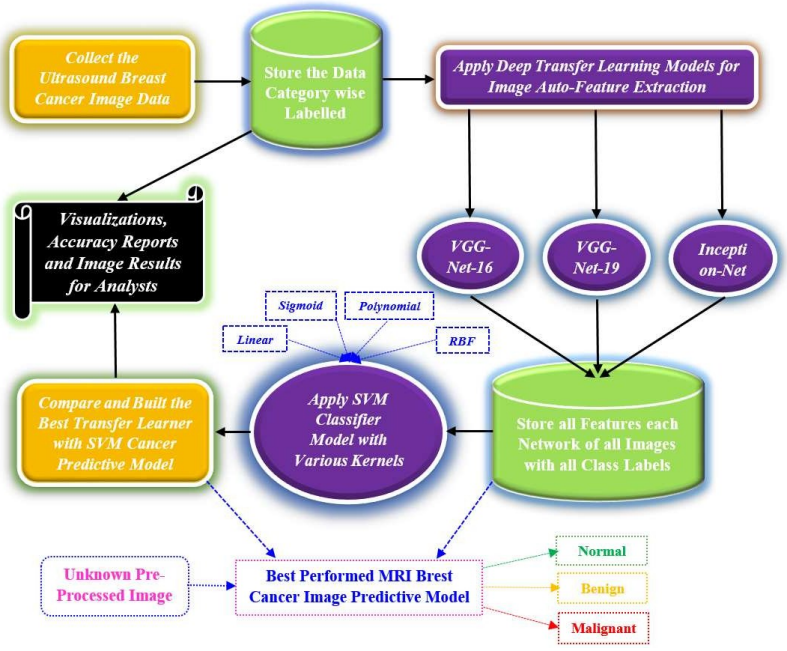

Fig 1. Proposal model for Breast cancer identification using Transfer Learners + SVM Classifier

The proposed model (Figure 1) for detecting breast cancer using ultrasound breast cancer image data involves collecting and storing the data in categories like benign, malignant, and normal. Deep transfer learning models are used to extract features and store their values for classification using an SVM classifier. The data is then split using a 10-folding method and the best-performing model is chosen for prediction. The results are then sent to analysts for analysis.

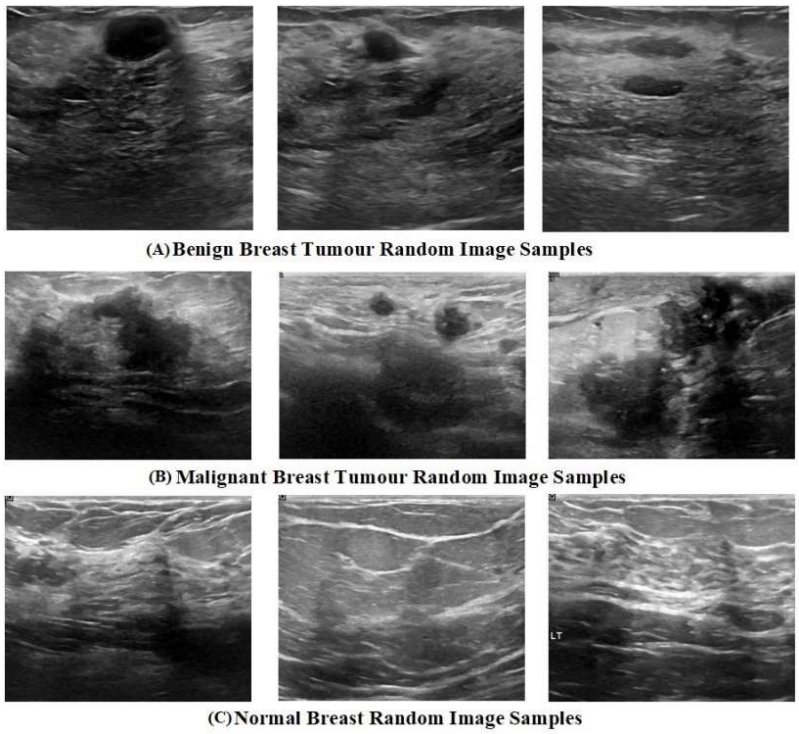

Fig 2. Categories of Breast cancer Images Benign, Malignant and Normal

2.2 Data Set Description

The Breast Cancer Ultrasound imaging data from Kagle's repository includes 780 images in three categories: Benign (440), Malignant (210), and Normal (130). Figure 2 visually categorizes these images into benign, malignant, and regular classes, aiding in precise classification and diagnostic analysis. Figure 2 (A) and (B) depict benign and malignant categories, while Figure 2 (C) represents normal.

2.3 Transfer Learners

Transfer learning (TL) is a technique that reuses a previously trained model for another task, with pre-training being the initial step. It teaches the conceptual framework's general features, while the end stage notifies specific features for the data. TL Networks are useful for processing large image datasets, as they are faster and more accurate than other custom models. The working process of pre-trained networks and saved networks is illustrated in Figure 3.

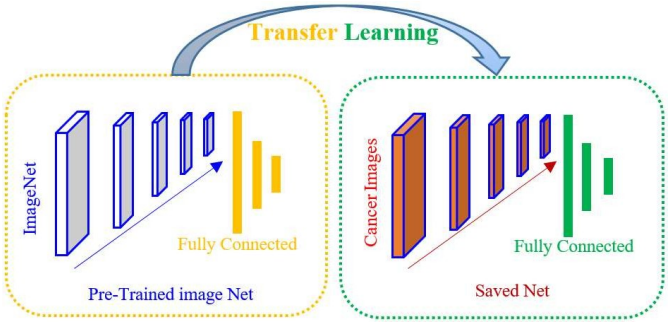

Fig 3. Transfer learning working process

VGG network structures are deep networks with smaller filter sizes, such as 3 by 3 convolution. VGG-16 (Figure 4 (A)) architecture is a variant of VGG-Net, consisting of 16 layers and built with convolution, pooling, and fully connected layers. It scans a small portion of surrounding pixels, resulting in detailed feature representations for different image sets. VGG-19 architecture (Figure 4(B)) is a deep CNN with 19 layers, including convolutional layers, pooling layers, and fully connected layers. The input layer accepts 224x224 pixels, with 16 convolutional layers extracting features from the input image. The pooling layers, which follow the convolutional layers, are five max pooling layers that down-sample feature maps and reduce data dimensionality. Both VGG-16 and VGG-19 architectures have their advantages and disadvantages.

Image Input	224x224x3 images with 'zero-centre' normalization
Convolution	64 3x3x3 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Convolution	64 3x3x64 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Max Pooling	2x2 max pooling with stride [2 2] and padding [0 0 0 0]
Convolution	128 3x3x64 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Convolution	128 3x3x128 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Max Pooling	2x2 max pooling with stride [2 2] and padding [0 0 0 0]
Convolution	256 3x3x128 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Convolution	256 3x3x256 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Convolution	256 3x3x256 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Max Pooling	2x2 max pooling with stride [2 2] and padding [0 0 0 0]
Convolution	512 3x3x256 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Convolution	512 3x3x512 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Convolution	512 3x3x512 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Max Pooling	2x2 max pooling with stride [2 2] and padding [0 0 0 0]
Convolution	512 3x3x512 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Convolution	512 3x3x512 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Convolution	512 3x3x512 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Max Pooling	2x2 max pooling with stride [2 2] and padding [0 0 0 0]
Fully Connected	Connected 4096 fully connected layer
ReLU	ReLU
Dropout	50% dropout
Fully Connected	Connected 4096 fully connected layer
ReLU	ReLU
Dropout	50% dropout
Fully Connected	Connected 4096 fully connected layer
Softmax	softmax
output	Classification Output cross-entropies with 'tench' and 999 other classes

(A) VGG-16 Net

Image	Input 224x224x3 images with 'zero centre' normalization
Convolution	64 3x3x3 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Convolution	64 3x3x64 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Max	Pooling 2x2 max
Convolution	128 3x3x64 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Convolution	128 3x3x128 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Max	Pooling 2x2 max
Convolution	256 3x3x128 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Convolution	256 3x3x256 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Convolution	256 3x3x256 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Convolution	256 3x3x256 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Max	Pooling 2x2 max
Convolution	512 3x3x256 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Convolution	512 3x3x512 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Convolution	512 3x3x512 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Convolution	512 3x3x512 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Max	Pooling 2x2 max
Convolution	512 3x3x512 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Convolution	512 3x3x512 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Convolution	512 3x3x512 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Convolution	512 3x3x512 convolutions with stride [1 1] and padding [1 1 1 1]
ReLU	ReLU
Max	Pooling 2x2 max
Fully	Connected 4096 fully connected layer
ReLU	ReLU
Dropout	50% dropout
Fully	Connected 4096 fully connected layer
ReLU	ReLU
Dropout	50% dropout
Fully	Connected 1000 fully connected layer
Softmax	softmax
Out-Put	1000 features

(B) VGG-19 Net

Fig 4. Transfer Learners VGG-16 and VGG-19 Structures

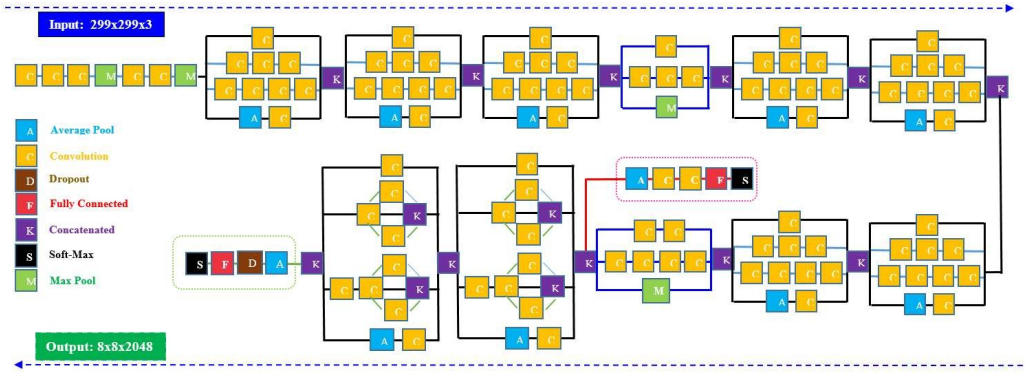

Fig 5. Detailed model of Inception V3 Transfer Learner

2.4 SVM Classifier

The Support Vector Machine (SVM) is a machine learning model used in classification and regression analysis. It aims to find the best hyperplane to separate data into different classes, maximizing the margin. The model uses kernel functions like linear, polynomial, Gaussian, and sigmoid. Training involves finding the hyperplane and minimizing classification errors. Hyperparameters like kernel type, regularization parameter, and kernel bandwidth can affect performance. After training and tuning, the model can be tested by mapping new data points to the same hyperplane.

2.5 Performance Parameters

Accuracy is the overall accuracy of a model's predictions, calculated as the ratio of correctly predicted instances to the total number of instances. The F1 score balances precision and recall by considering both FPs and FNs, making it suitable for imbalanced class distribution scenarios. Precision measures the model's accuracy by comparing true positive predictions to the total number of positive predictions, while recall measures the model's capacity to accurately represent all positive instances.

$$Accuracy = (TP + TN) / (TP + TN + FP + FN) \tag{1}$$

$$F1 = 2 * (Precision * Recall) / (Precision + Recall) \tag{2}$$

$$Precision = TP / (TP + FP) \tag{3}$$

$$Recall = TP / (TP + FN) \tag{4}$$

3 Results and Discussions

The research on "Optimizing Breast Cancer Detection" shows the effectiveness of deep transfer learning and SVM classifiers in improving accuracy and transparency in breast cancer detection, highlighting the synergistic power of advanced technologies.

Inception V3 (IV3) + SVM classification analysis:

SVM (RBF)		Predicted			Total
Class		Benign	Malignant	Normal	
Actual	Benign	396	39	5	440
	Malignant	41	161	8	210
	Normal	20	5	105	130
Total		457	205	118	780

(A) Inception V3+SVM(RBF)

SVM (Linear)		Predicted			Total
Class		Benign	Malignant	Normal	
Actual	Benign	396	36	8	440
	Malignant	54	148	8	210
	Normal	18	5	107	130
Total		468	189	123	780

(B) Inception V3+SVM(Linear)

SVM (Sigmoid)		Predicted			Total
Class		Benign	Malignant	Normal	
Actual	Benign	364	68	8	440
	Malignant	49	154	7	210
	Normal	25	12	93	130
Total		438	234	108	780

(C) Inception V3+SVM(Sigmoid)

SVM (Polynomial)		Predicted			Total
Class		Benign	Malignant	Normal	
Actual	Benign	407	29	4	440
	Malignant	43	160	7	210
	Normal	12	3	115	130
Total		462	192	126	780

(D) Inception V3+SVM(Polynomial)

Fig 6. Inception V3 + SVM Confusion matrix Analysis

InceptioV3+SVM 10-fold cross-validation models (Figure 6) were used to classify extracted features from Inception V3 transfer learning into Normal, Malignant, and Normal. The IV3+SVM with the polynomial kernel (Figure 6 (D)) performed

well for all classes, with a near-accuracy of 97% for Normal category images and 89% for Malignant images. The IV3+SVM with kernel RBF (Figure 6 (A)), Linear, and Sigmoid kernels (Figure 6 (B) and (C)) also correctly classified Normal, Malignant, and Normal categories. The performance parameters of IV3+SVM were analyzed, showing high accuracy in the average cancer class and higher classification accuracy for polynomial kernel models. However, the SVM+Sigmoid model performed poorly compared to other models. The analysis provides valuable insights into the effectiveness of IV3 transfer learning in breast cancer classification (Table 3).

Table 3. Inception v3+SVM (Kernel) Performance Parameters Analysis on target class

Inception V3 + SVM (Kernel)	Target Class	CA	F1	Precision	Recall	AUC
SVM (RBF)	Benign	0.8654	0.8829	0.8665	0.9000	0.9366
	Malignant	0.8808	0.7759	0.7854	0.7667	0.9187
	Normal	0.9513	0.8468	0.8898	0.8077	0.9724
	All (Avg.)	**0.8487**	**0.8481**	**0.8486**	**0.8487**	**0.9359**
SVM (Polynomial)	Benign	0.8872	0.9024	0.8810	0.9250	0.9400
	Malignant Normal	0.8949 0.9667	0.7961 0.8984	0.8333 0.9127	0.7619 0.8846	0.9281 0.9775
	All (Avg.)	**0.8744**	**0.8731**	**0.8734**	**0.8744**	**0.9440**
SVM (linear)	Benign	0.8513	0.8722	0.8462	0.9000	0.9199
	Malignant	0.8679	0.7418	0.7831	0.7047	0.9094
	Normal	0.9500	0.8458	0.8699	0.8231	0.9621
	All (Avg.)	**0.8346**	**0.8327**	**0.8331**	**0.8346**	**0.9252**
SVM (Sigmoid)	Benign	0.8077	0.8292	0.8311	0.8272	0.8077
	Malignant Normal	0.8256 0.9333	0.6937 0.7815	0.6581 0.8611	0.7333 0.7154	0.8256 0.9333
	All (Avg.)	**0.7833**	**0.7847**	**0.7895**	**0.7833**	**0.7833**

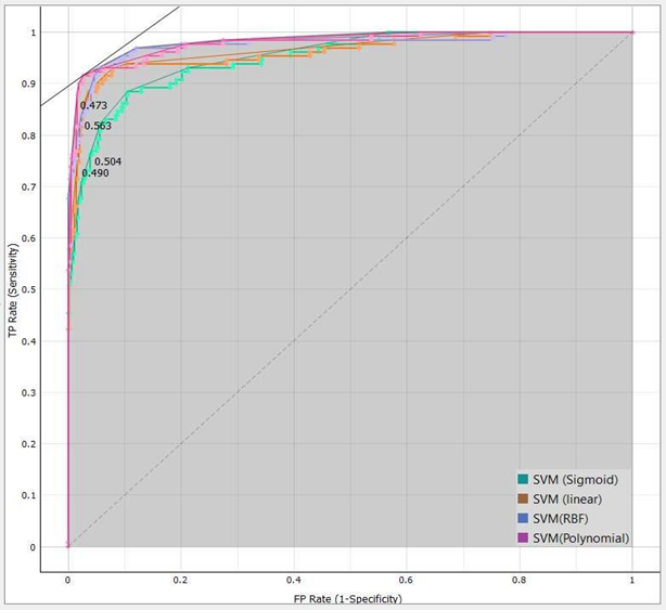

Fig 7. Inception V3 + SVM (Kernels) AUC under ROC Analysis

Figure 7 displays various SVM models' AUC (Area under the ROC Curve), with blue representing RBF, violet representing polynomial, brown representing linear, and green representing sigmoid. All kernel SVM models perform well, except for

sigmoid SVM mode, with a polynomial model showing the highest performance.

3.2 VGG-19 +SVM classification analysis:

The VGG-19+SVM (Figure 8) classification analysis reveals that the extracted features from VGG-19 transfer learning were classified using various SVM classifiers. The VGG-19 + SVM with the polynomial kernel (Figure 8 (D)) performed well for all classes (Benign, Malignant, and Normal), with the 'normal' class having the highest accuracy at 87%. The class' typical' was classified correctly in 95 out of 130 images, with a 90% accuracy rate. The class' was classified correctly in 154 out of 210 images, with an 83% accuracy rate. The class' normal' was classified correctly in 80 out of 130 images, with the sigmoid classifier classifying the class 'malignant' in 163 out of 210 images. Figure 8 (A) presents the VGG-19 +SVM with kernel RBF, Figure 8 (B) shows the VGG-19 +SVM with kernel Linear, and Figure 8 (C) shows the VGG-19 +SVM with kernel sigmoid classifies the class 'normal' correctly 80 out of 130, 348 benign class images out of 440, and 163 images out of 210.

SVM (RBF)		Predicted			Total
Class		Benign	Malignant	Normal	
Actual	Benign	370	39	31	440
	Malignant	60	144	6	210
	Normal	41	10	79	130
Total		471	193	116	780

(A) VGG-19+SVM(RBF)

SVM (Linear)		Predicted			Total
Class		Benign	Malignant	Normal	
Actual	Benign	310	69	61	440
	Malignant	93	105	12	210
	Normal	41	7	82	130
Total		444	181	155	780

(B) VGG-19+SVM(Linear)

SVM (Sigmoid)		Predicted			Total
Class		Benign	Malignant	Normal	
Actual	Benign	198	158	84	440
	Malignant	33	163	14	210
	Normal	23	27	80	130
Total		254	348	178	780

(C) VGG-19+SVM(Sigmoid)

SVM (Polynomial)		Predicted			Total
Class		Benign	Malignant	Normal	
Actual	Benign	348	57	35	440
	Malignant	47	154	9	210
	Normal	27	8	95	130
Total		422	219	139	780

(D) VGG-19+SVM(Polynomial)

Fig 8. Inception V3 + SVM Confusion matrix Analysis

The study (Table 4) analyzes the performance parameters of IV3+SVM (RBF, polynomial, linear, and sigmoid kernels) for breast cancer classes normal, malignant, and benign. The results show that IV3 transfer learning features are highly accurate for the "normal" cancer class, with all SVM kernel models performing above 90% accuracy. The polynomial kernel classifies all classes more favourably than other kernels+SVM models, with SVM+sigmoid performing particularly poorly.

The VGG-19+SVM (Figure 9) classifier with the polynomial kernel (Figure 9 (D)) performs well for all classes (Benign, Malignant, and Normal), with the class 'normal' classified correctly in 95 out of 130 images with near accuracy of 90%. The least performed class is benign, with only 80% accuracy. The VGG-19 +SVM with kernel RBF (Figure 9 (A)) classifies the class 'normal' with 87% accuracy, while the class 'normal' is typed correctly in 82 out of 130, 348 benign class images out of 440 and 163 images out of 210. The malignant class classifies 163/210 more than the SVM sigmoid classifier (Figure 9 (C)), while the SVM-polynomial classifier highly classifies benign and normal class images. Figure 9 (B) shows a detailed analysis of SVM kernel Linear.

3.3 VGG-16 + SVM classification analysis:

The VGG-16+SVM classifier (Figure 10) was used to classify extracted features from VGG-16 transfer learning. The polynomial kernel (Figure 10 (D)) performed better for all classes (Benign, Malignant, and Normal) than other kernels. The Normal class category images were classified with 93 out of 130 images with an 89% accuracy and 154 out of 210 with an 84% accuracy. The VGG-16+SVM with a kernel RBF (Figure 10 (A)) and linear (Figure 10 (B)) classified the class "Normal" with 88% accuracy, while the kernel sigmoid classified the class "normal" with 69 out of 130 images. Figure 10 (C) shows the VGG-16+SVM with a kernel sigmoid detailed analysis.

Figure 11 displays the AUC (area under the ROC curve) of various SVM models, with the polynomial model performing the best with an AUC of 0.8747, outperforming the linear model with an AUC of 0.7639, and the sigmoid model with an AUC of 0.7711.

Table 4. VGG-19+SVM (Kernel) Performance Parameters Analysis

VGG-19+ SVM (Kernel)	Target Class	CA	F1	Precision	Recall	AUC
SVM (RBF)	Begin	0.7513	0.7770	0.786	0.7682	0.8592
	Malignant	0.8385	0.6986	0.7019	0.6952	0.8856
	Normal	0.8795	0.6544	0.6268	0.6846	0.9112
	All (Avg.)	**0.7346**	**0.7355**	**0.7369**	**0.7346**	**0.8684**
SVM (Polynomial)	Begin	0.8013	0.8229	0.8276	0.8182	0.8713
	Malignant Normal	0.8538 0.9013	0.7299 0.7072	0.7264 0.6992	0.7333 0.7154	0.8960 0.9215
	All (Avg.)	**0.7782**	**0.7785**	**0.779**	**0.7782**	**0.8884**
SVM (linear)	Begin	0.7295	0.7561	0.7694	0.7432	0.7768
	Malignant	0.7923	0.6087	0.6176	0.6000	0.8333
	Normal	0.8526	0.5907	0.5497	0.6385	0.8672
	All (Avg.)	**0.6872**	**0.6888**	**0.6919**	**0.6872**	**0.8128**
SVM (Sigmoid)	Begin	0.6269	0.6176	0.7321	0.5341	0.7094
	Malignant Normal	0.7269 0.8385	0.6019 0.5227	0.4954 0.5149	0.7667 0.5308	0.8069 0.8525
	All (Avg.)	**0.5962**	**0.5976**	**0.6322**	**0.5962**	**0.7720**

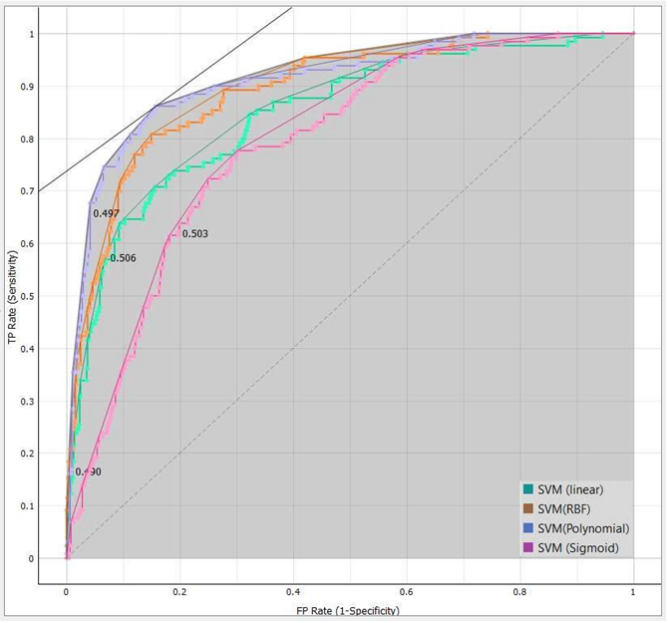

Fig 9. VGG-19 + SVM (Kernel) AUC under ROC Analysis

Figure 11 displays the performance parameters of VGG-16 + SVM for breast cancer classifications. Results show that VGG-16 transfer learning features are highly accurate for normal cancer classes, with SVM kernel models performing above 90% accuracy. The polynomial kernel SVM model classified all classes more highly than other models, while SVM + sigmoid model performance is poor compared to other kernels.

3.4 Comparative Analysis

The Inception V3 net + SVM (polynomial) model outperforms other experimental models with a CA of 0.8744 and an AUC value of 0.9444. The analysis of transfer learners' performances with SVM and kernels is detailed in Table 6.

SVM (RBF)		Predicted			Total
Class		Benign	Malignant	Normal	
Actual	Benign	338	54	48	440
	Malignant	59	146	5	210
	Normal	33	8	89	130
Total		430	208	142	780

(A) VGG-16+SVM(RBF)

SVM (Linear)		Predicted			Total
Class		Benign	Malignant	Normal	
Actual	Benign	327	64	49	440
	Malignant	65	126	19	210
	Normal	33	14	83	130
Total		425	204	151	780

(B) VGG-16+SVM(Linear)

SVM (Sigmoid)		Predicted			Total
Class		Benign	Malignant	Normal	
Actual	Benign	235	149	56	440
	Malignant	40	161	9	210
	Normal	46	15	69	130
Total		321	325	134	780

(C) VGG-16+SVM(Sigmoid)

SVM (Polynomial)		Predicted			Total
Class		Benign	Malignant	Normal	
Actual	Benign	360	46	34	440
	Malignant	50	154	6	210
	Normal	25	12	93	130
Total		435	212	133	780

(D) VGG-16+SVM(Polynomial)

Fig 10. VGG-16 + SVM Confusion matrix Analysis

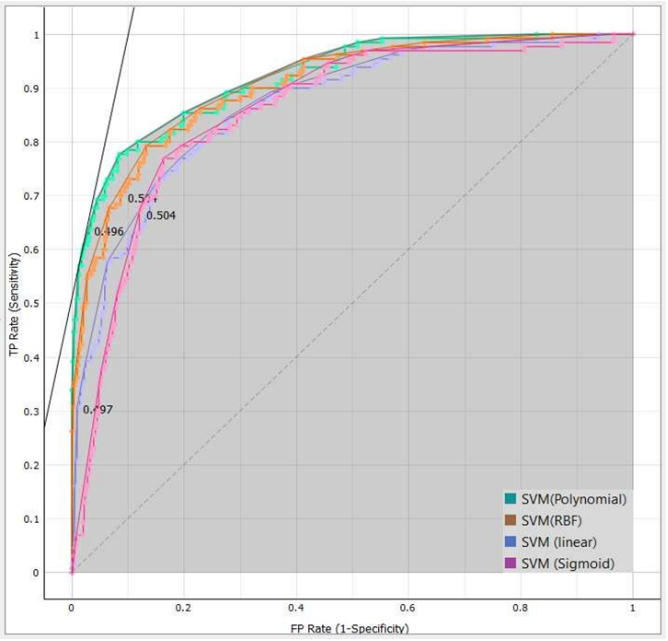

Fig 11. VGG-16 + SVM (Kernels) AUC under ROC Analysis

4 Discussion

The proposal model, Inception V3+SVM, outperformed other transfer learning models (VGG-16, VGG-19, and Inception V3) with a 10-fold cross-validation, achieving 0.8744 accuracy and 0.9444 AUC values, outperforming other hybrid models. The model's performance parameters, including CA and AUC values, were detailed in Figure 12, which shows the comparison with SVM classifiers and breast cancer imaging.

The study examines cancer data from Andhra Pradesh's zone 1 to identify patterns and risk factors. It reveals higher cancer rates among women, particularly breast cancer, and suggests links between smoking, drinking, chewing tobacco, and certain occupations [24]. Breast cancer, now surpassing lung cancer in new cases globally, necessitates increased awareness and comprehensive measures to combat this leading cancer, affecting millions of lives worldwide [25]. Vesal et al. (2018) [26] used transfer learning topologies Inception-V3 and ResNet50 networks to classify breast cancer on histology images. The Inception-V3 network had a higher testing average accuracy than the ResNet50 network. The test set accuracy of Inception-V3 was 76%. However, the study found some images in hybrid models were incorrectly classified, including malignant, benign, and

Table 5. VGG-16+SVM (Kernel) Performance Parameters Analysis

VGG-16+ SVM(Kernel)	Target Class	CA	F1	Precision	Recall	AUC
SVM (RBF)	Begin	0.7808	0.8123	0.7856	0.8409	0.8533
	Malignant	0.8526	0.7146	0.7461	0.6857	0.8746
	Normal	0.8872	0.6423	0.681	0.6077	0.8897
	All (Avg.)	**0.7603**	**0.7577**	**0.7575**	**0.7603**	**0.8625**
SVM (Polynomial)	Begin	0.7872	0.8074	0.8246	0.7909	0.8649
	Malignant Normal	0.8449 0.8987	0.7179 0.7063	0.7032 0.6835	0.7333 0.7308	0.8723 0.9071
	All (Avg.)	**0.7654**	**0.7665**	**0.7684**	**0.7654**	**0.8747**
SVM (linear)	Begin	0.6615	0.7014	0.6982	0.7045	0.708
	Malignant	0.7679	0.5371	0.5801	0.5000	0.7739
	Normal	0.8449	0.5754	0.5290	0.6308	0.8392
	All (Avg.)	**0.6372**	**0.6361**	**0.6382**	**0.6372**	**0.7639**
SVM (Sigmoid)	Begin	0.6179	0.5706	0.7795	0.4500	0.7390
	Malignant Normal	0.7026 0.8103	0.5842 0.5195	0.4684 0.4494	0.7762 0.6154	0.8070 0.7987
	All (Avg.)	**0.5654**	**0.5658**	**0.6407**	**0.5654**	**0.7611**

Table 6. TLs + SVM (Kernel) Comparative Analysis

+	Inception v3		VGG-19		VGG-16	
SVM (Kernel)	**CA**	**AUC**	**CA**	**AUC**	**CA**	**AUC**
SVM (linear)	0.8346	0.9252	0.6872	0.8128	0.6372	0.7639
SVM (Polynomial)	**0.8744**	**0.944**	**0.7782**	**0.8884**	**0.7654**	**0.8747**
SVM (RBF)	0.8487	0.9359	0.7346	0.8684	0.7603	0.8625
SVM (Sigmoid)	0.7833	0.8991	0.5962	0.772	0.5654	0.7611

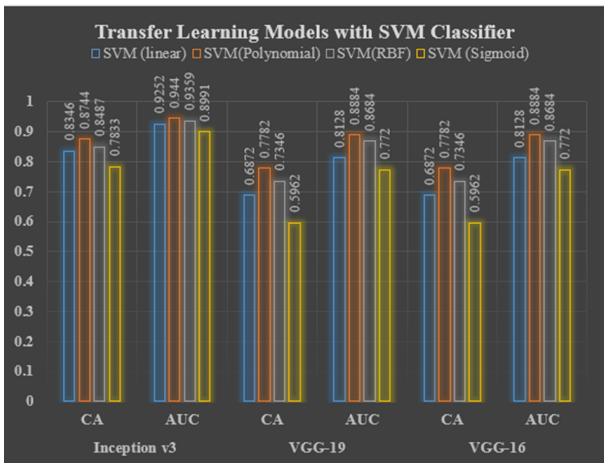

Fig 12. Comparative analysis of TL models with SVM Classifier

"normal" breast cancer. These unclassified images are shown in Figure 13. In this, all hybrid models: 11, 55, 67, 74, 121, etc. in the malignant category; 30, 62, 76, 258, 372, 425, etc. in the benign class; and 17, 113, 114, 116, etc. in the "normal" category of breast cancer.

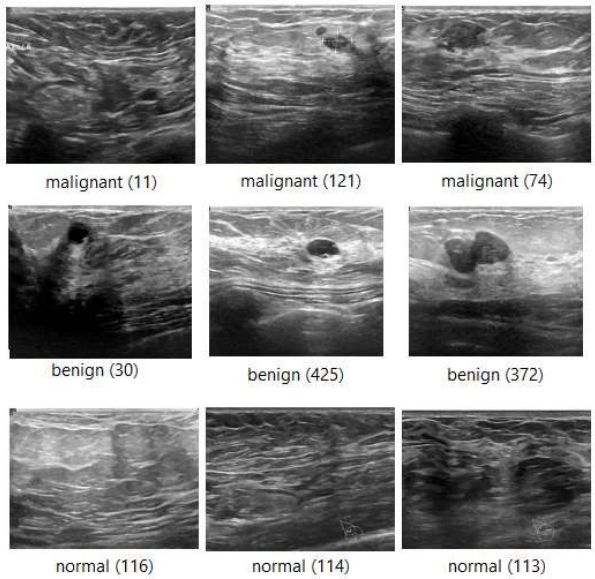

Fig 13. Incorrectly Classified UBI images of TL models with SVM Classifier

5 Conclusion

Breast cancer is a critical and deadly disease, primarily affecting women. Early detection is crucial for patient protection and survival. Transfer Deep Learning models extract features from breast cancer ultrasound images. These models are pre-trained on large datasets and then transferred to an SVM classifier model. SVM classifiers are known for handling high-dimensional data and accurately classifying it. In this research, Inception-v3, VGG-16 net, and VGG-19 net were used for feature extraction and classification with SVM. The SVM polynomial kernel performed better than other SVM kernels for all features of transfer learning. The Inception-v3+SVM model showed a high performance, with a 0.944 AUC and 87.44% classification accuracy, higher than other experimental models. The proposed system has the potential to enhance breast cancer identification accuracy, a crucial aspect for early detection and effective disease treatment. Future work aims to improve breast cancer detection by utilizing hybrid Deep Learning models, leveraging diverse architectures for enhanced accuracy. The integration of advanced features and multi-modal data will further refine diagnostic capabilities and contribute to continuous improvement.

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