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# Deep Transfer Learning to Classify Mass and Calcification Pathologies from Screen Film Mammograms

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The number of breast cancer diagnoses is the largest among all cancers among women in the world. Breast cancer treatment is possible if it is diagnosed in the early stages. Mammography is a common imaging technique to detect breast cancer abnormalities. Breast cancer symptom screening is being performed by radiologists. In the last decade, deep learning was successfully applied to big image classification databases such as the ImageNet. In this study, the breast cancer pathology classification performances of the recent deep learning models were investigated by transfer learning and fine tuning. A total of 3,360 mammogram patches were used from the Digital Database for Screening Mammography (DDSM) and the Curated Breast Imaging Subset of DDSM (CBIS-DDSM) mammogram databases for deep learning model training, validating, and testing. Transfer learning and fine tuning were applied using Resnet50, Xception, NASNet, and EfficientNet-B7 network weights. The best classification performance was achieved by transfer learning from the Xception network. The computational costs of deep learning models were considered while selecting the best one. On the original CBIS-DDSM five-way test mammogram classification problem, the mean sensitivity, specificity, F1-score, and AUC were 0.7054, 0.9264, 0.7024, and 0.9317, respectively. The results show that the proposed models may be useful for the classification of breast cancer pathologies.

## 1. Introduction

Since the 1970s, researchers have been studying clinical decision support systems [1]–[3]. Breast cancer is the most frequently diagnosed cancer among women, and the incidence of the disease has been increasing in recent years [4]. If breast cancer is detected early, treatment is possible [5]. Mammography is obtained by exposing breasts to low-energy X-rays [6] in order to detect breast cancer abnormalities early [7].

The mammogram interpretation is a multistep process that is still being performed by radiologists. Mammography screening is advised for women older than 50 years [8], [9]. In Türkiye, there were 11.15 M women at this age interval in 2021, which indicates the need for the number of breast cancer screenings per year [10]. An automated highperformance mammogram screening system could

reduce the workload of radiologists and the number of unnecessary screenings and biopsies. The first computer-aided mammogram interpretation model was proposed by Ackerman and Gose in 1972 [11], wherein the researchers designed a feature extraction followed by a nearest neighbor breast lesion classification system. Automatic detection of a tumor tissue from mammography is related to texture analysis, and many different approaches have been investigated to date by new textural feature definitions and classifier models [12], such as the spherical wavelet transform [13] and geometric and textural feature extraction [14]. Computer-aided breast cancer research has also been conducted by other imaging modalities, such as microwave applications [15]. Despite these and other successful results in the literature, feature extraction-based machine learning methods can be time-consuming, particularly for medical image- or video-based

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analysis. Deep learning methods enable learning features from training data, and there are example studies in the literature related to stroke [16], carotid artery [17], [18], skin cancer [19], diabetes [20], Alzheimer's disease [21], and breast cancer [22]. Deep learning methods should be useful for the solution of problems related to other biomedical imaging modalities, so cross-disciplinary studies could possibly lead to new scientific advancements.

Regarding the applications of deep learning for breast cancer research, convolutional neural networks (CNN) were used for benign versus malignant breast mass classification [23]. In another study based on more than one million mammograms, the breast cancer screening performance of radiologists was shown to be improved when CNNbased diagnosis was used together with radiologists [24]. An end-to-end mammogram classifier based on a five-class mammogram patch classification like the one in the present study was investigated using Resnet50 and VGG16 [25]. Mass detection and classification have been performed by Momminet-V2 using multi-view mammograms [26]. The computational cost of deep learning model training is becoming a concern, and recently breast cancer mass pathology was classified by implementing pre-trained deep neural networks without transfer learning [27]. NASNet is a high performing CNN for image classification on the ImageNet [28], [29]. Recently, EfficientNets were proposed by considering the computational expense and the classification performance together [30]. Among EfficientNets, the EfficientNet-B7 is the best performing CNN model on the ImageNet.

In this study, transfer learning and fine tuning of recently proposed pre-trained deep neural networks, including Resnet50 [31], Xception [32], NASNetMobile [28], NASNetLarge [28], and EfficientNet-B7 [30] were investigated for the classification of normal, benign, and malignant

masses, and benign and malignant calcification patches. These CNN models are among the best performing ones on ImageNet and the successful implementations of these networks for the breast cancer pathology classification problem are demonstrated in the present study. The Digital Database for Screening Mammography (DDSM) and the Curated Breast Imaging Subset of DDSM (CBIS-DDSM) datasets were used for deep learning model training [33]–[35]. This study is organized as follows: Section 2 includes materials and methods that describe the mammogram dataset, preprocessing, deep learning model training, and performance evaluation. Experimental results and discussion are presented in section 3, and conclusions and suggestions are given in section 4.

## 2. Material and Method

Significant amounts of data are necessary for deep learning model training. This study was conducted using publicly available datasets.

## 2.1. Dataset and preprocessing

The CBIS-DDSM and DDSM mammograms were selected as data sources since these are large and publicly available mammogram databases. The CBIS-DDSM database includes mammogram patches with the abnormality and pathology information in the form of mass versus calcification and benign versus malignant. The mammogram patches were resampled to  $331 \times 331$  and saved as 8-bit gray level images. The normal tissue patches were randomly selected from the DDSM dataset craniocaudal (CC) views of mammogram regions which does not include any abnormalities [36], [37]. Breast cancer abnormalities have a great variety of shape, texture, and intensity, and two representative training patches from each class are given in Figure 1.



Figure 1. Two representative training patches belong to normal (a), benign mass (b), malignant mass (c), benign calcification (d), and malignant calcification (e).

Mammogram patches were classified into normal, benign mass, malignant mass, benign calcification, and malignant calcification. Patches that have a "benign without callback" annotation were considered "benign." Normal patches that do not include any breast cancer abnormalities were selected from the DDSM dataset because the CBIS-DDSM includes mammograms with abnormalities. Normal patches were extracted from the middle of the mammogram so that they do not include background pixels. Test mammograms defined in the CBIS- DDSM database were used as test data in the present study, and none of them were used for training or validating. The dataset was balanced by deleting excess files. Randomly selected 20% of the CBIS-DDSM training images were used as validation and rest of the mammograms were used for training. The percentages of the number of training, validation, and test patches were 65%, 16%, and 19%, respectively. The number of training, validation, and test patches is given in Table 1.

**Table 1.** The number of training, validating, and test patches in the dataset.

Folder	Normal	Benign	Malignant	Benign	Malignant	Total
		mass	mass	calcification	calcification	
Train	434	434	434	434	434	2170
Validation	109	109	109	109	109	545
Test	129	129	129	129	129	645
Total	672	672	672	672	672	3360

#### 2.2. Hardware configuration

Deep learning models were trained on a workstation computer that has an NVIDIA RTX 3060 GPU, double Xeon E5-2630 2.6 GHz CPU, and a 16 GB RAM.

## 2.3. Deep transfer learning and fine tuning

Deep transfer learning classification models were implemented since they are known to reduce the training time, reduce the requirements for the amount of training data, and improve the performance [25]. [38]. Data augmentation was applied to the patches by setting the width shift, height shift, zoom, and shear ranges to 0.2, rotation range to 90°, and enabling the vertical and horizontal random flips. The brightness range was not used since intensity is a feature that is used by radiologists for mass and calcification detection. Deep learning models were implemented by importing the weights of Resnet50, Xception, NASNetMobile, NASNetLarge, and EfficientNet-B7 [28] networks, which have 138 M, 23 M, 5 M, 88,9 M, and 66 M parameters, respectively. The models were named as backbone followed by TL (transfer learning). Adam optimizer was used [39]. Transfer learning and fine tuning were implemented by using the three-step approach described in Shen et al. [25]. First, all of the layers except the final layer were frozen, and the model was trained for three epochs with a 10<sup>-3</sup> learning rate. Second, 33% of layers from the end were unfrozen and the model was trained for ten epochs with a 10<sup>-4</sup> learning rate. Third, all layers were unfrozen and trained with a learning rate of  $10^{-5}$  until one of the stopping criteria was met. Early stopping criteria were: (1) the maximum number of epochs was 150, and (2) the maximum number of consecutive epochs when the loss function did not decrease was ten. (3) The minimum learning rate was  $10^{-8}$ . The transfer learning and fine tuning codes are accessible at <u>https://github.com/tiryakiv/breast-cancer-pathology-classification</u>.

## 2.4. Performance evaluation

Patch classification accuracy, sensitivity, specificity, and F-measure were defined as:

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

$$Sensitivity = \frac{TP}{TP+FN}$$
(2)

$$Specificity = \frac{TN}{TN + FP}$$
(3)

$$F - measure = \frac{2TP}{2TP + FP + FN} \tag{4}$$

where TP, TN, FP, and FN are abbreviations for true positive, true negative, false positive, and false negative, respectively. Sensitivity, specificity, and F-measure of each class were calculated. The area under the receiver operating curve (AUC) was analyzed, and a confusion matrix was constructed to evaluate the classification performance [40]. Accuracy, specificity, sensitivity, and F-measure show the classification performance, but they depend on the threshold level. Sensitivity shows the ratio of correctly selected relevant items, and specificity shows the ratio of negatively selected elements to the true negative elements. AUC shows the overall performance of the binary classifier by considering all possible thresholds. In the present study, a oneversus-rest classifier was implemented for AUC calculations.

#### 3. Results and Discussion

The classification results of normal, benign, and malignant masses, and benign and malignant calcification patches using ResNet50, Xception, NASNetMobile, NASNetLarge, and EfficientNet-B7 transfer learning methods on the validation data are shown in Table 2.

 
 Table 2. The breast cancer pathology classification results on the validation data.

on the vandation data.								
TL backbone	Accuracy	AUC	Train time					
Resnet50	0.7321	0.9392	37 min					
Xception	0.7193	0.9407	29 min					
NASNetMobile	0.6807	0.9183	47 min					
NASNetLarge	0.7376	0.9357	114 min					
EfficientNet-B7	0.7156	0.9407	259 min					

The Xception and EfficientNet-B7 TL models had the highest AUC, and the NASNetLarge TL model had the highest accuracy on the validation data. To compare the performances of all models, the confusion matrices on the validation data are given in Table 3.

**Table 3.** Breast cancer pathology classification confusion matrix on validation data. BC, MC, BM, MM, and N are abbreviations for benign calcification, malignant calcification, benign mass, malignant mass, and normal patches, respectively. TL: transfer learning. The highest *TP* for each class is given in bold.

t	BC	77	29	1	2	0		77	22	2	7	1	58	24	5	15	7
ğis	MC	14	74	0	21	0		17	68	6	18	0	4	65	10	28	2
iolo	BM	3	2	48	56	0		3	1	52	52	1	1	3	41	56	8
ad	MM	2	4	7	96	0		3	3	13	90	0	1	1	8	99	0
2	Ν	0	1	2	2	104		2	0	1	1	105	0	0	0	1	108
		BC	MC	BM	MM	Ν		BC	MC	BM	MM	Ν	BC	MC	BM	MM	Ν
		Res	net50	TL p	redict	ions		Xce	otion	TL p	redic	tions	Ν	ASN	etMo	bile T	Ľ
				-				-		-				pre	edicti	ons	
														•			
	BC	79	22	2	4	2		65	39	1	3	1					
gist	MC	22	62	4	20	1		5	85	2	16	1					
olo	BM	2	0	58	46	3		0	2	48	56	3					
adi	MM	0	0	10	99	0		2	7	14	86	0					
2	Ν	2	0	0	3	104		0	0	0	3	106					
		BC	MC	BM	MM	Ν		BC	MC	BM	MM	Ν					
			NAS	NetLa	rge TI			E	fficie	ntNet	<b>-B7</b> T	Ľ					
			pr	predictions predictions													
							-										

The confusion matrices in Table 3 showed that all models performed well in discriminating the normal patches. The highest misclassification rates were observed for the benign mass patches. *TPs* of the NASNet TL malignant mass were equal. EfficientNet-B7 TL model had the highest *TP* for malignant calcification patches. Based on overall accuracy and confusion matrices, the best breast pathology classification model was selected as NASNetLarge TL because it has the highest accuracy and the three *TPs* of the model were the highest among all of the models.

#### 3.1. Test results

The performance of the NASNetLarge TL model trained by the breast cancer pathology patches was evaluated. The AUC and accuracy on the test data were 0.9404 and 0.7318 respectively. The performance difference between the validation and test data was close. To analyze the classification errors, the NASNetLarge TL model confusion matrix on the test data is given in Table 4.

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Table 4.	Breast	cancer	pathology	classification	n confusion
		matri	x on the te	st data	

	N	0 BC	0 MC	0 BM	0 MM	129 N
Y	Ν	0	0	0	0	129
ad	MM	4	3	26	95	1
iolc	BM	6	2	88	29	4
gis	MC	35	84	0	9	1
ŗ	BC	76	33	8	10	2

The confusion matrix in Table 4 showed that the malignant calcification patch misclassification probability as benign calcification was the highest. The misclassification probability of benign calcifications as malignant calcifications and benign masses as malignant masses was high. These results showed that the model has better discrimination for abnormality types than the pathology type. The patch classification performance of mass was better than calcification. The NASNetLarge TL model's sensitivity, specificity, and F-measure for each class are listed in Table 5. The test results in Table 5 showed that the highest and lowest sensitivity were obtained on normal and benign calcification patches, respectively. Among the abnormalities, including patches, the highest specificity was obtained for malignant masses and the

 Table 5. NASNetLarge TL model classification

 performance on the test patches. The best result for each

 metric is shown in bold.

Class	Sensitivity	Specificity	F-measure
Benign calcification	0.6281	0.8989	0.6080
Malign calcification	0.6885	0.9140	0.6693
Benign mass	0.7213	0.9216	0.7012
Malign mass	0.6643	0.9323	0.6985
Normal	0.9416	1.0000	0.9699

lowest specificity was obtained for benign calcification. The multi-class receiver operating characteristic (ROC) analysis of the NASNetLarge TL model is given in Figure 2.



Figure 2. ROC analysis of a five-way breast cancer pathology classification. (One versus rest classifier)

Figure 2 showed that the mass abnormality classification performed better than the calcification abnormality classification. The performance of discriminating the malignant calcification patches was lower than benign calcification, on the other hand, the performance of discriminating the malignant mass was higher than benign mass. As expected, AUC of normal patches was better than the abnormality including patches. Computer-aided breast cancer diagnosis research involves a number of types of problems. Some studies in the literature focus on mass detection and classification [41], [42], and calcification others focus on detection and classification [43], [44]. A five-way classification of breast cancer abnormalities and the malignant behavior of tissues from mammograms were investigated in the present study. The closest work in the literature to the present one is Shen et al. [25], wherein the researchers used 2,478 CBIS-DDSM patches and achieved an accuracy of 0.99 on the test data when they applied the ResNet50 transfer learning method. The performance difference with the present study may be because of: 1) the difference in the number of patches (3,360 patches were used in the present study); 2) training, validating, and test data included DDSM normal mammograms in the present study; and 3) original CBIS-DDSM test images were used in the present study. The other study that is related to the present one is Hekal et al., where the researchers investigated the four-way classification performance of benign calcification, malignant calcification, benign mass, and malignant mass [45]. They achieved an accuracy of 0.91 using AlexNet by training with 2800 CBIS-DDSM mammograms. The relatively higher accuracy than the present study can be explained by the lower number of classes (n=4)and the performance evaluation on the validation data. The five-way classification of breast cancer pathology patches similar to the present work was investigated by Chun-ming et al. [46]. They achieved an accuracy of 0.91 using the Deep Cooperation CNN model on the CBIS-DDSM dataset. Their model performance is higher than the present study, possibly because they used a smaller test dataset (%10) and their dataset was randomly distributed. In the present study, the classification performance of state-of-theart transfer learning methods was demonstrated on the original CBIS-DDSM test dataset.

#### 4. Conclusion and Suggestions

Transfer learning and fine tuning pre-trained deep neural networks have great potential for the classification of breast cancer abnormalities and pathologies. Pre-trained deep neural networks reduce the computational cost and yield high performance when they are used for different classification domains. In this study, successful transfer learning applications have been shown using the recent deep neural networks trained with the ImageNet. By applying transfer learning and fine tuning, the useful features learned from the ImageNet database were adopted for the current breast pathology classification problem. The best classification performance has been obtained by using the NASNetLarge network, which resulted in a 0.9404 AUC and 0.7318 accuracy. The NASNetLarge network can be used for the breast cancer pathology classification at the reported performance. The proposed model may be useful for detecting breast cancer abnormalities and classifying them as malignant versus benign.

The performance ranking of CNNs on the ImageNet was not the same for the breast cancer pathology classification models. This could be due to the contextual difference between the ImageNet images and the mammograms. The sensitivity of benign mass and benign calcification showed that further performance improvement can be investigated. Novel machine learning techniques and deep ensemble models will be investigated in the future to increase the system performance. The CBIS-DDSM and other databases have lesions that sometimes have mass and calcification abnormalities overlap. The classification of such tumors with double abnormalities will be investigated in the future.

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## **Statement of Research and Publication Ethics**

The study is complied with research and publication ethics.

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