

DEEP LEARNING APPROACH FOR AUTOMATED SKIN CANCER DETECTION WITH COMPARATIVE ANALYSIS OF DIFFERENT BATCH SIZES IN DERMATOLOGICAL IMAGE CLASSIFICATION

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Abstract. Skin cancer is a significant public health issue, and accurate, efficient diagnostic methods are essential to reduce delays and errors associated with traditional screening, which often suffers from subjectivity and variability. This study aims to develop a reliable automated skin cancer detection system capable of improving diagnostic accuracy and reducing false negatives. We implemented an automated classification framework based on the Xception deep learning architecture. The system utilized pre-trained ImageNet weights for transfer learning, enabling effective feature extraction from dermoscopic images. Convolutional layers were used to capture discriminative features, which were combined with fully connected layers to perform binary classification of skin cancer versus not skin cancer. The proposed model achieved an overall accuracy of 99.34%, with a precision of 98.51%, recall of 98.80%, specificity of 99.52%, and an F1-score of 98.63% at a batch size of 64. These results demonstrate superior performance in early detection compared to traditional diagnostic methods. The Xception-based automated system offers a highly accurate, robust, and scalable solution for skin cancer detection. With its potential integration into dermatology clinics and telehealth platforms, the model can aid clinicians in achieving earlier and more reliable diagnoses, ultimately improving patient outcomes.

Keywords: deep learning, Xception architecture, convolutional neural networks (CNNs), ImageNet, skin cancer

PODEJŚCIE OPARTE NA GŁĘBOKIM UCZENIU DO AUTOMATYCZNEGO WYKRYWANIA RAKA SKÓRY Z ANALIZĄ PORÓWNAWCZĄ RÓŻNYCH WIELKOŚCI PARTII W KLASYFIKACJI OBRAZÓW DERMATOLOGICZNYCH

Streszczenie. Rak skóry stanowi istotny problem zdrowia publicznego, a dokładne i wydajne metody diagnostyczne są niezbędne, aby zmniejszyć opóźnienia i błędy związane z tradycyjnym badaniem przesiewowym, które często charakteryzuje się subiektywnością i zmiennością. Celem tego badania jest opracowanie niezawodnego, zautomatyzowanego systemu wykrywania raka skóry, który może poprawić dokładność diagnostyczną i zmniejszyć liczbę wyników fałszywie ujemnych. Wdrożyliśmy zautomatyzowane ramy klasyfikacji oparte na architekturze głębokiego uczenia Xception. System wykorzystał wstępnie wytrenowane wagi ImageNet do uczenia przez transfer, co umożliwiło skuteczne wydobywanie cech z obrazów dermoskopowych. Warstwy splotowe zostały użyte do wychwytywania cech dyskryminacyjnych, które następnie połączono z warstwami w pełni połączonymi, aby przeprowadzić binarną klasyfikację raka skóry versus brak raka skóry. Proponowany model osiągnął całkowitą dokładność na poziomie 99,34%, z precyzją 98,51%, czułością 98,80%, specyficznością 99,52% oraz wskaźnikiem F1 wynoszącym 98,63% przy wielkości partii 64. Wyniki te wykazują wyższą skuteczność w wykrywaniu wczesnym w porównaniu z tradycyjnymi metodami diagnostycznymi. Automatyczny system oparty na Xception oferuje wysoce dokładne, niezawodne i skalowalne rozwiązanie do wykrywania raka skóry. Dzięki potencjalnej integracji w klinikach dermatologicznych i platformach telemedycznych, model może pomagać lekarzom w uzyskiwaniu wcześniejszych i bardziej wiarygodnych diagnoz, co ostatecznie poprawia wyniki leczenia pacjentów.

Słowa kluczowe: uczenie głębokie, architektura Xception, konwolucyjne sieci neuronowe (CNN), ImageNet, rak skóry

Introduction

Skin cancer is one the commonest cancers in the world and an important global public health issue [37]. According to the latest figures on cancer worldwide, over 1.8 million individuals around the globe are diagnosed with skin cancer every year. Among these cases, Melanoma issues almost 20% and is responsible for a considerable percentage of the deaths caused by skin cancer. Melanoma is considered to be the most severe form of skin cancer with mortality rates as high as 95% at the advanced stages of the disease. However, if it is detected at an early stage, the survival rate may increase by over 90–95%, which is a very important aspect of this disease. Due to the increased number of people suffering skin cancer; especially for people living in geographic regions with the high presence of ultraviolet (UV) radiation, research efforts are increasingly focused on developing automated diagnostic methods for medical imaging and healthcare applications [37].

Traditionally, dermatologists have been using visual examination, dermoscopic imaging and biopsy to diagnose the skin cancer [1]. Asymmetry, border irregularity, colour variation, diameter and evolution rule is a frequently used guideline by clinicians to evaluate suspicious lesions in the dermoscopic photos [4, 5]. Dermoscopy magnifies the skin structures and special lighting is used to allow skin examination of the epidermis (skin layer). While biopsy is the definitive diagnostic gold standard, biopsy is time consuming, requires specialized training and is invasive. Visual assessments when done manually also suffer from the problems of subjectivity and inter-observer variability leading to false positives or negatives [7].

In the last few years, progress in computer vision, machine learning and deep learning has led to the development of automated systems for skin lesion detection and classification [19, 20]. Convolutional Neural Networks (CNNs) are very efficient for building complex features from medical images, which aids the diagnosis [9]. Among the various deep learning architectures, Xception (Extreme Inception) has received a lot of attention. It introduces depthwise separable convolutions which enhance the computational efficiency while making the classification performance high [18]. Motivated by these improvements, this research proposes an automated skin cancer detection framework with Xception deep learning architecture to classify the dermoscopic image as either benign or malignant. The major goal is accuracy in diagnosing the classification of skin lesions and minimising the subjectivity of human evaluation in clinical evaluation [11]. By providing a dependable efficient computer-aided diagnostic system, the approach hopes to assist dermatologists to make an early diagnosis and informed decision – leading to better patient outcome and healthcare delivery.

The major contributions of the proposed work are listed below:

- Implementation of an automated diagnostic system for skin cancer classification employing the Xception deep learning model.
- Comprehensive analysis of the impact of different batch sizes on model performance.
- Extensive ablation study evaluating the effects of learning rate, optimizer selection, image resolution, and dropout rate.
- Comparative evaluation with existing deep learning models for dermatological image classification.



The remainder of this paper is organized as follows. Section 2 reviews recent studies on skin cancer detection using machine learning and deep learning approaches, highlighting existing contributions and identifying research gaps. Section 3 introduces our proposed approach including the datasets chosen, the preprocessing pipeline and then implementation of the Xception architecture for classification. Section 4 describes the performance measurements that were used to test the effectiveness of our model. Section 5 presents the results validating the performance of the proposed skin lesion detection model. Section 6 analyses the shortcomings of the current research, and Section 7 provides a final conclusion that highlights the main results and defines the future research perspectives in the field of automated skin-cancer detection.

1. Related works

Ashim et al. [3] presented the approach of diagnosing the skin cancer based on the transfer learning by systematically comparing multiple deep learning architectures such as ResNet, EfficientNet, VGG16, Xception, and DenseNet with ISIC dataset as the source of the dermoscopic images. Their results showed that the ResNet architecture has the highest accuracy of 88.61%. This was followed by VGG16 (81.94%), EfficientNet (78.41%), Xception (78.44%) and DenseNet (72.37%). While the study section showed the success of transfer learning for dermoscopic image analysis, the moderate performance of some models indicates that additional refinements of the feature extraction methods and the training strategies are still required. Kirgil et al. [17] used deep learning models to classify skin cancer via dermoscopic images taken from the ISIC 2019 data set. The paper compared EfficientNet – B0 and Xception in the binary classification of different skin lesions. Results indicated that the accuracy of EfficientNet – B0 is 0.835, while the accuracy of Xception is slightly superior with an accuracy of 0.866 for benign vs malignant shall be classified.

Thepade et al. [36] analysed the use of deep convolutional neural network (DCNN) models to detect melanoma by extracting features and using them with machine-learning classifiers. The architectures that were discussed were DenseNet121, ResNet50, VGG19, and Xception; the usage of DenseNet121 with a Random Forest classifier provided a detection rate of 95.50%. In spite of better classification performance, the hybrid methodology relied on other machine-learning classifiers that increased the computational complexity and might be an obstacle to scalability in clinical environments in the future. Each of these analyses by Singh et al. [33] consisted of a comparative analysis of various deep learning algorithms, including CNN, RNN, ResNet50, and Xception, which were applied to HAM10000. Experimental results reported that CNN and RNN generated 72 and 69 classification accuracy respectively whilst ResNet50 gave 79. Xception had the largest accuracy of the models studied, and it was 93 %.

Adegun et al. [1] have created a hybrid system combining Fully Convolutional Networks (FCN) and DenseNet to extract features and classify subsequently skin lesions in 2020. The HAM10000 dataset was assessed using the model; it was created using a dataset of over 10,000 dermoscopic images of seven different dermatological disorders. Their method attained a classification diameter of 98% and a recall of 98.5%, and area under the curve (AUC) of 99%. Although its outcomes highlight the high quality of the model, the research mainly focused on multi-class classification and did not provide much discussion in terms of learning arrangement or parameter optimization. Gururaj et al. [9] presented a deep-learning-framework of detection of skin cancer using convolutional neural networks (CNNs). The dataset used was the HAM10000 data, which is used to assess two architecture structures: DenseNet169 and ResNet50. The results of the experiments showed that DenseNet169 reached the classification accuracy of 91.2%, and ResNet50 was reachable to 83%. In addition, the under-

sampling methods to overcome the class imbalance yielded an F1-score of 84%.

Imran et al. [13] used the ISIC dataset to diagnose skin cancer using ensemble learning with VGG, CapsNet, and ResNet architectures. The ensemble model trained in around 106 seconds and attained an average accuracy of 93.5%. Ramamurthy et al. [31] proposed a dual track deep learning framework of a modified DenseNet169 by combining it with Coordinate Attention Module (CoAM), and a custom convolutional neural network with Feature Pyramid Network and Global Context Network. Their model attained an accuracy of 93.2% on the HAM10000 dataset. Similarly, In 2025, Moturi et al. [25] created a convolutional neural network-based melanoma detection strategy using MobileNetV2 in conjunction with a custom CNN architecture applied to the HAM10000 dataset. The improved CNN gave an accuracy of 95% which surpassed the MobileNetV2, which gave an accuracy of 85%.

Table 1. Summary of related works

Ref.	Methodology	Dataset	Results
[3]	ResNet, EfficientNet, VGG16, Xception, DenseNet	ISIC	Accuracy: ResNet (88.61%), EfficientNet (78.41%), VGG16 (81.94%), Xception (78.44%), DenseNet (72.37%)
[17]	EfficientNet B0, Xception	ISIC	EfficientNet B0 Accuracy: 83.5%; Xception: Xception Accuracy: 86.6%
[36]	DCNN models for feature extraction in melanoma detection; use of classifiers like Random Forest	HAM10000	Detection Accuracy: 95.50% using DenseNet121 features with ensemble classifiers
[33]	CNNs, RNNs, ResNet50, Xception	HAM10000	Accuracy: CNN (72%), RNN (69%), ResNet50 (79%), Xception (93%)
[1]	Integration of Fully Convolutional Network (FCN) with Dense Net for skin lesion classification	HAM10000	Accuracy: 98%; Recall: 98.5%; AUC score: 99%
[9]	DenseNet, ResNet50	HAM10000	DenseNet169 achieved 91.2% Accuracy, outperforming ResNet50 (83%); F1-score up to 91.7%
[13]	Ensemble learning with VGG, Caps-Net, and ResNet for skin cancer detection	ISIC	Average accuracy: 93.5%; Classification training time: 106 seconds
[31]	Densenet-169 with CoAM + customized CNN	HAM10000	Accuracy: 93.2%; Recall: 91.4%; Precision: 95.3%; F1-score: 93.3%
[25]	CNN	HAM10000	Accuracy-95%
[14]	Segmentation with preprocessing and transfer learning using ResNet-50	ISIC 2016	Accuracy: 92.80%; Precision: 98.64%; Recall: 86.80%
[23]	Modified MobileNet, Modified AlexNet, and Custom CNN	ISIC	Accuracy: 84.70%; Recall: 84.78%; Precision: 84.56%; F1-score: 84.63%

Karki et al. [14] proposed a deep learning framework incorporating segmentation, preprocessing, and transfer learning using a ResNet50 backbone for the early detection of skin cancer. The method showed strong classification performance, achieving 98.64% precision, 86.80% recall, and an overall accuracy of 92.80% in identifying benign and malignant lesions. Marwa Kahia et al. [23] presented the concept of lightweight convolutional neural networks models that included a modified MobileNet with the addition of residual blocks, the AlexNet with the addition of the squeeze and excitation attention mechanism as well as a custom CNN with residual connections. Their experimental evaluation on ISIC dataset showed that the modified CNN achieved the highest performance at 84.70% accuracy, 84.56% precision, 84.78% recall and F1-score 84.63%.

Although many deep learning models have been presented for the classification of skin lesions, there are many limitations. Many studies mainly have focused on the improvements

in the model architecture without giving enough analysis of the training configurations such as batch size, learning rate and optimizer choice, etc., which play an important role in model performance and generalization. Furthermore, ensemble and multi-stage architectures tend to cause greater computational complexity making them less applicable for real-time clinical applications. In addition, differences between datasets and processing methods make comparing results between studies difficult. Consequently, a robust and computationally efficient deep learning framework is required to obtain high classification performance and to analyse the influence of training parameters on the overall effectiveness of the model. To overcome these limitations, the current work extends the analysis of the Xception architecture for automated skin cancer detection and examines the influence of varying batch sizes on the classification performance, which offers a more thorough experimental analysis. Summary of related works are shown in Table 1.

2. Materials and methods

Our proposed system employs the Xception architecture to establish a high-accuracy binary classification model for skin cancer detection. The methodology involves a number of important steps, and it begins with data collection, in which we filtered a wide range of dermoscopic images in a number of publicly available repositories. The dataset was pre-processed, through image normalization and image augmentation, to increase the quality of the dataset and variability.

2.1. Dataset

The data used in the present study was obtained in a publicly available dermoscopic image data repository on Kaggle [16] which contains annotated images of skin lesions used in skin cancer classification studies. The images were captured using dermoscopic imaging techniques [9] and labelled by dermatology experts into two categories: benign and malignant skin lesions. In total, the dataset includes 1,968 images, consisting of 1,467 benign cases and 501 malignant cases, corresponding to 74.6% and 25.4% of the dataset, respectively. This distribution represents a moderately imbalanced dataset, which is common in medical imaging applications.

To generate a model and evaluate it, we separated the dataset in an 80:20 proportion, which means that we had 1574 images to train on and 394 to validate. There were 1,173 benign and 401 malignant images in the training set and the model successfully learned distinctive features of both classes. The validation set consisted of 294 images that were benign and 100 images that were malignant and used to evaluate the performance of the trained model. Figure 1 shows the sample dermoscopic images from the dataset.

2.2. Preprocessing

Preprocessing techniques [22, 24] were applied in this study to standardize the input data and maintain consistency across the dataset. To standardize the data, pixel intensities of all input images were rescaled to the interval [0,1] using the rescale argument in the Keras ImageDataGenerator. This transformation was achieved by dividing the individual pixel value with 255, which is the highest intensity value of an 8-bit image. Normalization [30–32] improves model convergence and enhances training stability by ensuring consistent scaling of the input data. Further, all images were scaled to have the same size, which is 256×256 pixels, to ensure that they fit the neural network architecture used in this paper.

2.3. Augmentation

To strengthen the model's generalization capacity and mitigate overfitting, comprehensive data augmentation [10, 11] techniques were utilized. Random shear transformations, with a shear range of up to 40%, were employed to produce slanting effects, approximating little distortions. Table 2 shows the image augmentation strategies used for model training.

Likewise, zoom operations with a range of up to 40% were employed to simulate alterations in image scale, including modifications in viewing distance. Horizontal and vertical flips were implemented to ensure invariance to orientation, allowing the model to learn from a more varied dataset. These augmentation procedures were implemented dynamically throughout the training process, guaranteeing that each data batch sent to the model included a diverse array of modified images, thereby generating an effectively enlarged training set.



Fig. 1. Sample dermoscopic images from the dataset

Table 2. Configuration of image augmentation strategies used for model training

Augmentation Technique	Parameter/Range
Rotation	20°
Zoom	20%
Height Translation	20%
Width Translation	20%
Shear Transformation	20%
Horizontal Mirroring	Yes

2.4. Architecture of Xception

Xception is a modern convolutional neural network, that builds upon Inception architecture, except that the Inception module will be substituted with depth-wise separable convolutions. The model comprises of 36 convolutional layers, grouped into 14 modules; residual connections connect all the modules except the first and the last one [26]. It employs

ReLU activation and depth convolutions in which the individual filters are applied to each channel of input. This design is a reduction in computational cost. The results are then merged with 1×1 pointwise convolutions following the depth-wise step, to provide the model with sufficient expressiveness. The 2 initial layers are convolutional layers with depths of 64 and 128. L2 regularization occurs after the fully connected layers so as to avoid overfitting [27]. The positioning of max-pooling layers is done in a strategic manner in order to reduce space dimensions and retain important features to achieve efficiency. Lastly, Xception produces 2048 features, which describe more elaborate patterns and enhance activities like detecting skin-cancer. The architecture of Xception is shown in Figure 2.

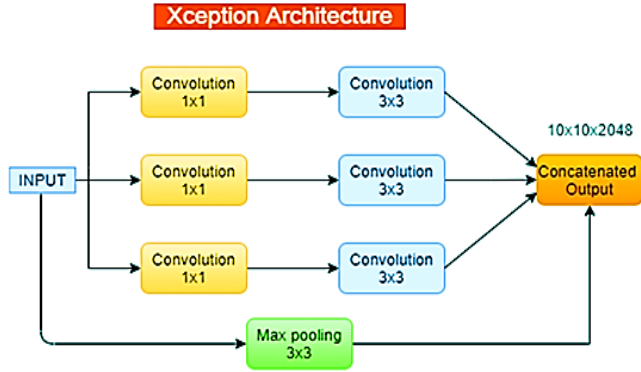


Fig. 2. Architecture of Xception [33]

2.5. Proposed methodology

The suggested methodology follows Xception model as a feature extractor and is capable of automatically detecting and classifying skin cancer. The Block diagram of proposed methodology is shown in Figure 3. The input images are scaled to $256 \times 256 \times 3$ pixel sizes to fit the requirements of the model and their values are made in the range $[0,1]$ ensuring stable training convergence.

$$I' = I/255 \quad (1)$$

The Xception model utilizes depthwise separable convolutions, which consist of two steps. First, depthwise convolution applies a single filter per input channel, defined as

$$Y_d(i, c, j) = \sum_{m=0}^{M-1} \sum_{n=0}^{N-1} X(i+m, j+n, c) K_d(m, n, c) \quad (2)$$

where $X(i, j, c)$ presents the input feature map, $K_d(m, n, c)$ is the depthwise convolution kernel, and $Y_d(i, j, c)$ is the output. Second, pointwise convolution applies a 1×1 convolution across all channels to learn cross-channel relationships:

$$Y_p(i, j, c') = \sum_{c=0}^{c-1} Y_d(i, j, c) K_p(c, c') \quad (3)$$

where $K_p(c, c')$ is the pointwise convolution filter, and $Y_p(i, j, c')$ represents the final transformed feature map. This approach significantly reduces computational complexity while retaining spatial relationships.

Following feature extraction, Global Average Pooling (GAP) is applied to reduce the feature map's spatial dimensions while retaining critical information, calculated as

$$F_c = \frac{1}{H \times W} \sum_{i=1}^H \sum_{j=1}^W X(i, c, j) \quad (4)$$

In this case, H and W are the spatial dimensions of the feature map. $X(i, j, c)$ is the values of the activation at the point (i, j) , and F_c is the formed feature vector with 2048 dimensions. This method minimizes the parameters and increases the feature strength, and the output of the GAP is then used in fully connected layers with gradually decreasing sizes ($1024 \rightarrow 512 \rightarrow 256 \rightarrow 2$). Each dense layer transforms the feature representation using

$$Z_{i+1} = W_i \sigma(Z_i + B_i) \quad (5)$$

where W_i and B_i are the weights and biases, and $\sigma(x) = \max(0, x)$ represents the ReLU activation function. To prevent overfitting, dropout regularization is applied after each dense layer, where neurons are randomly deactivated using

$$X' = X, M, M \sim \text{Bernoulli}(p) \quad (6)$$

Here, X' represents the updated activation output, and M represents a binary mask taken from a Bernoulli distribution with probability p .

At the output layer, the softmax function is used to estimate the probability distribution of the two classes, given by

$$P(y_i) = \frac{e^{z_i}}{\sum_{j=1}^C e^{z_j}} \quad (7)$$

where $P(y_i)$ is the probability of class i , Z_i is the output of the last dense layer and $C = 2$ in case of benign and malignant categories. The model is trained using binary cross-entropy loss which measures the difference between the predicted and actual labels.

$$L = -\frac{1}{N} \sum_{i=1}^N [y_i \log \hat{y}_i + (1 - y_i) \log(1 - \hat{y}_i)] \quad (8)$$

where y_i is the ground truth label, and $\hat{y}_i$ is the predicted probability.

The optimization is carried out using the Adam optimizer, which updates model parameters based on adaptive learning rates.

2.6. Experimental setup

Python was used to carry out the experiments with the assistance of the TensorFlow and Keras deep learning platforms. The training was run on the system with the processor of Intel Core i5-1135G7, the Nvidia MX450 graphic card, 16 GB RAM, and the Windows operating system. The proposed model utilized the Adam optimizer and was trained for 30 epochs with a learning rate of $1e-5$. In order to determine the impact of training set up of models, a series of batch sizes of 32, 64, 128 and 256 were systematically tested. The initialisation of model parameters was based on the default parameters of the Keras platform, and the loss functional was binary cross-entropy, which indicates the existence of two binary categories benign and malignant. In training, an augmentation of data was performed in real time through ImageDataGenerator Keras module, with transformations (rotation, shifting, zooming, and horizontal flipping). Hyperparameter configurations for model training are shown in Table 3.

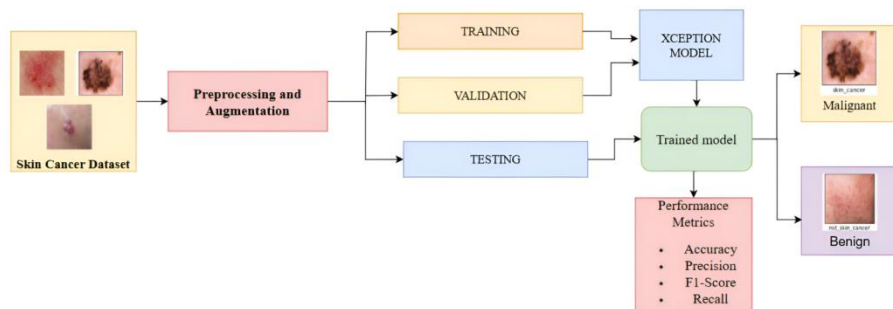


Fig. 3. Block diagram of the proposed model

Table 3. Hyperparameter configuration for model training

Parameter	Value / Description
Batch Size	32
Rotation Range	20°
Normalization	Pixel intensities scaled to [0–1] by dividing by 255
Number of Classes	2
Image Resolution	256 × 256
Learning Rate	1e-5
Epochs	30
Optimizer	Adam
Loss Function	Binary Crossentropy

3. Performance evaluation measures

To assess the performance of the proposed Xception model in classifying skin lesions as benign or malignant, we utilize several performance evaluation measures: recall (sensitivity), specificity, accuracy, and precision [16, 22].

Model performance is quantified using the accuracy metric, which reflects the proportion of correctly classified samples relative to the total number of tested observations.

$$\text{Accuracy} = \frac{C_{\text{pos}} + C_{\text{neg}}}{C_{\text{pos}} + C_{\text{neg}} + I_{\text{pos}} + I_{\text{neg}}} \quad (8)$$

Precision measures the accuracy of positive predictions generated from the predictive model, and calculates the fraction of instances predicted as malignant and that are truly malignant.

$$\text{Precision} = \frac{C_{\text{pos}}}{C_{\text{pos}} + I_{\text{pos}}} \quad (9)$$

Recall, also known as sensitivity, measures the ability of the model to recognize all positive instances (malignant lesions) of all truly positive cases.. It is calculated using the formula:

$$\text{Recall/Sensitivity} = \frac{C_{\text{pos}}}{C_{\text{pos}} + I_{\text{neg}}} \quad (10)$$

The F1-score is a harmonic mean of the precision and the recall. It gives a more balanced measure than in the cases where false positives and false negatives are equally important by giving equal importance to both measures.

$$\text{F1 - score} = \frac{2 \times C_{\text{pos}}}{2 \times C_{\text{pos}} + I_{\text{pos}} + I_{\text{neg}}} \quad (11)$$

Specificity is used to measure the ability of the model to identify negative cases correctly among all true negative cases.

$$\text{Specificity} = \frac{C_{\text{neg}}}{I_{\text{neg}} + I_{\text{pos}}} \quad (12)$$

where C_{pos} – total positive instances correctly predicted, C_{neg} – total negative instances correctly predicted, I_{pos} – negative instances mistakenly predicted as positive, I_{neg} – positive instances mistakenly predicted as negative.

4. Results and discussions

The proposed Xception based model of skin-cancer classification with dermoscopic images is tested in this section and its effectiveness is evaluated. The discussion will focus on such critical performance metrics as accuracy, precision, recall, F1-score, and specificity [29, 34]. Further, the effect of varying batch sizes (32, 64, 128, and 256) on the performance of the model to determine the best training setup is also investigated.

The experimental results indicate that batch size significantly affects classification performance. Among the tested configurations, batch size 64 achieved the best overall results with an accuracy of 99.34%, precision of 98.51%, recall of 98.80%, and specificity of 99.52.

Smaller batch sizes, such as 32, produced slightly lower precision (96.67%) due to a higher number of false positives (FP = 17), although recall remained high at 98.40%. Batch size 128 achieved competitive results with an accuracy of 98.88%, but showed a slight reduction in precision and recall compared with batch size 64. The largest batch size (256) resulted in the lowest performance, with an accuracy of 98.32%, mainly due to increased false positives (19) and false negatives (14). The confusion matrix of Xception architecture with different batch sizes is shown in Table 4.

Table 4. Confusion matrix of Xception architecture with different batch sizes

Batch size	TP	TN	FP	FN
32	493	1450	17	8
64	495	1460	7	6
128	491	1455	12	10
256	487	1448	19	14

The confusion matrix analysis further confirms that batch size 64 produces the lowest number of misclassifications, indicating improved discrimination between benign and malignant lesions.

Table 5. Comparative analysis of model performance across different batch sizes

Batch size	Precision	Recall	F1-score	Specificity	Accuracy
32	96.67	98.40	97.53	98.84	98.73
64	98.51	98.80	98.63	99.52	99.34
128	97.61	98.00	97.70	99.18	98.88
256	96.23	97.21	96.60	98.70	98.32

Table 5 gives results of a comparative evaluation of the model performance with different batch sizes. The results have shown that the batch size of 64 is the most efficient with the highest accuracy of 99.34 % and the best precision, recall, F1-score, and specificity values. These findings indicate that moderate batch sizes offer an improved compromise of convergence stability and generalization of the model. Figure 4 shows the model summary of our proposed model.

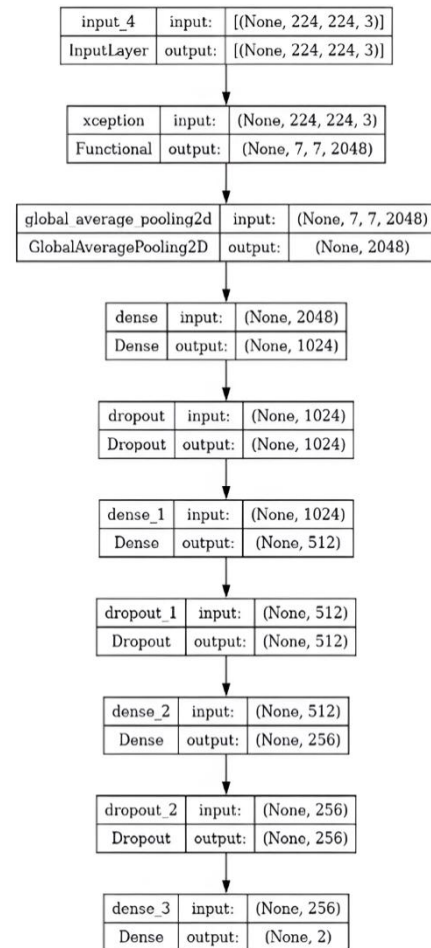


Fig. 4. Model Summary of the proposed model

Figure 5 illustrates the training and validation accuracy curves for the tested batch sizes. Batch size 64 demonstrates the most stable learning behaviour, with smooth convergence and minimal fluctuations between training and validation accuracy. In contrast, batch size 32 shows higher variability, indicating possible overfitting due to frequent weight updates. Batch size 128 converges relatively quickly but shows minor fluctuations, while batch size 256 exhibits slower convergence.

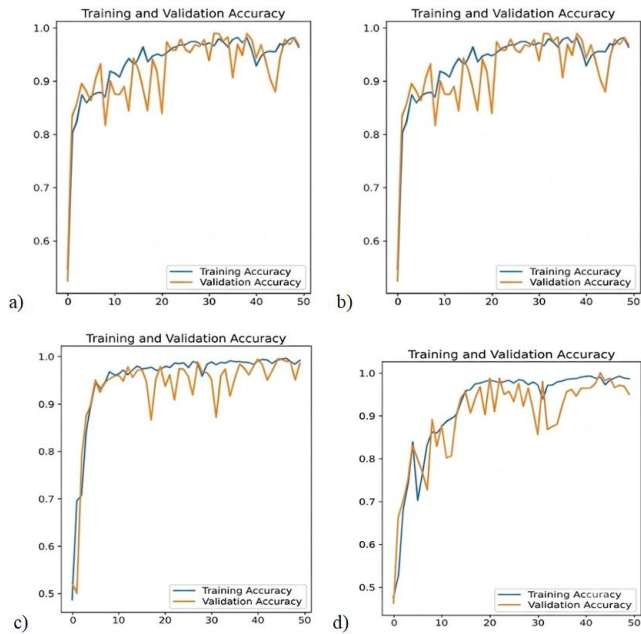


Fig. 5. Training and validation accuracy curves for skin cancer classification using different batch sizes: (a) 32, (b) 64, (c) 128, and (d) 256

Figure 6 presents the training and validation loss curves. Batch size 64 achieves the most stable loss reduction, with both curves decreasing consistently throughout training. Batch size 128 also shows smooth convergence but with slightly higher variation in validation loss. In comparison, batch size 32 exhibits larger fluctuations, while batch size 256 converges more slowly, indicating less efficient optimization during training. These observations further support the selection of batch size 64 as the most effective configuration.

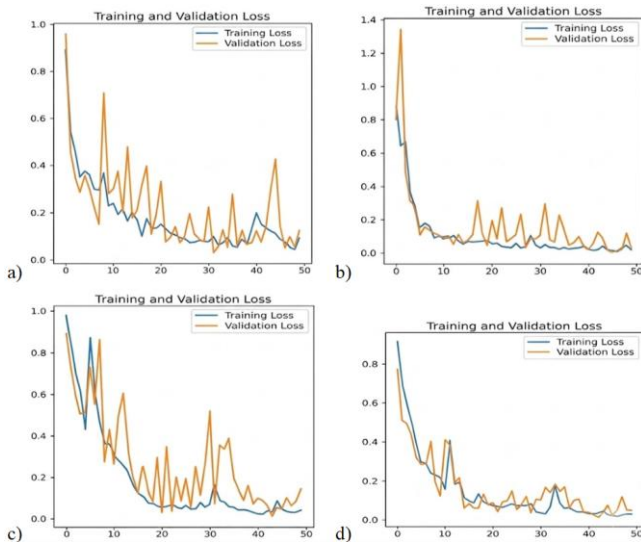


Fig. 6. Training and validation loss curves for skin cancer classification using batch sizes of (a) 32, (b) 64, (c) 128, and (d) 256

Figure 7 shows the confusion matrices for different batch sizes. The results indicate that batch size 64 achieves the highest number of correct predictions, with 1460 true negatives and 495 true positives, while maintaining the lowest number of false predictions. Batch sizes 128 and 256 exhibit slightly higher misclassification rates, which may reduce classification reliability. Overall, the confusion matrix analysis confirms that batch size 64 provides the most balanced classification performance.

The graph in Figure 8 shows ROC curves comparing 4 different batch sizes (32, 64, 128, and 256), while depicting the balance between true positive rate (TPR) and false positive rate (FPR). Batch size 64 has the highest AUC of 0.99, the second highest AUC is 0.98 for batch size 128, and the third highest AUC

of 0.97 for batch size 256, and the lowest AUC is batch size 32 with a AUC of 0.96. Overall this all indicates that the best classification performance was at batch size 64, while batch size 32 had the lowest AUC, meaning that the discrimination for convincing labelling was slightly weaker in batch size 32 in comparison to the others. Overall AUC values (based on larger values), batch sizes 64 and 128 demonstrated that they showed the most effective classification performance.

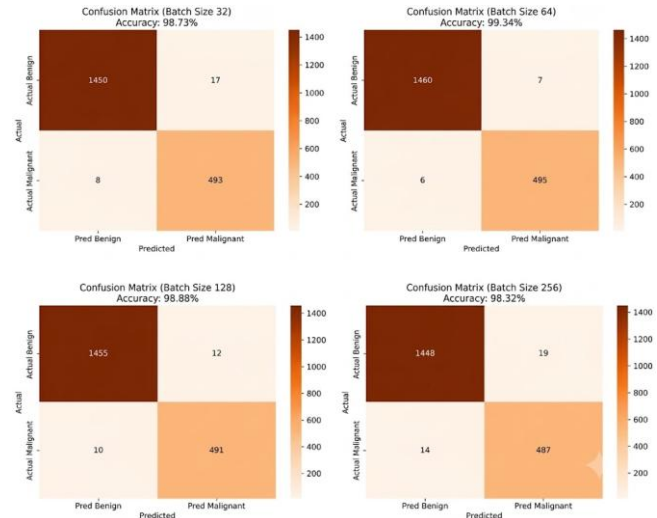


Fig. 7. Confusion matrices for skin cancer classification using different batch sizes: (a) 32, (b) 64, (c) 128, and (d) 256

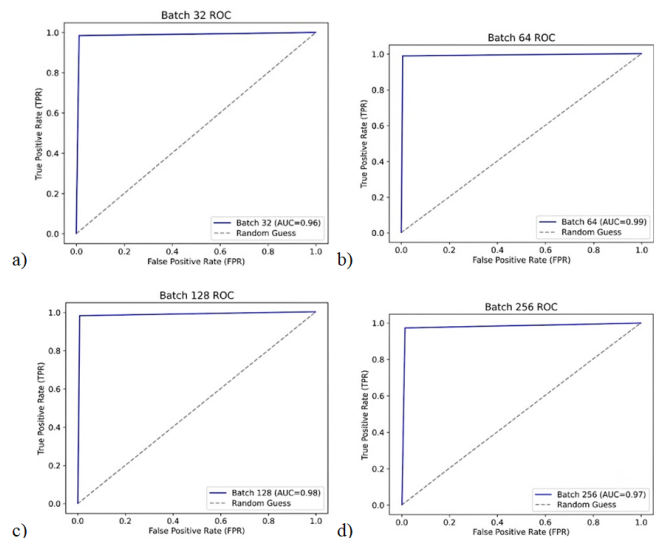


Fig. 8. ROC-AUC curves for patch-based skin cancer classification using batch sizes (a) 32, (b) 64, (c) 128, and (d) 256

4.1. Predicted results

The results obtained in the predictions prove that the proposed model of skin cancer classification can be effective in differentiating between benign and malignant lesions. In the initial sample picture, the model has made the right diagnosis (Class 0 (Not Skin Cancer)) of a benign skin structure without indicators of a malignant lesion. In the second sample picture, the model is correct in identifying a malignant lesion and classifying it as Class 1 (Skin Cancer).

The preprocessing operations such as image normalization and resizing guarantee the processing of the images with constant input to the model and help in achieving consistent prediction results. Moreover, descriptive output labels (not skin cancer and skin cancer) enhance better interpretability and enable easier comprehension of the classification findings. The Predicted results are shown in Figure 9.

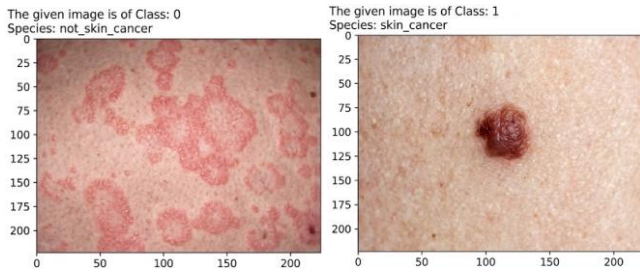


Fig. 9. Predicted results

4.2. Ablation study

This part contains a description of an ablation study that would assess the importance of major hyperparameters on the efficiency of the Xception-based skin cancer detection framework. We examine how learning rate, choice of optimizer, image resolution and the dropout rate influence the key performance measures of accuracy, precision, recall, F1-score, and specificity by varying their values. Learning rate plays a great role in conversion and classification accuracy of the model. A high learning rate (1e-3) results in unstable training, leading to lower accuracy (95.12%) due to large parameter updates. A very small learning rate (1e-6) slows down training but still achieves reasonable accuracy (98.15%). The optimal balance is achieved with 1e-5, which provides the highest accuracy (99.34%) while ensuring stable convergence and generalization which is shown in Table 6.

Optimizer selection influences the speed and stability of training shown in Table 7. SGD shows the lowest accuracy (96.45%) due to slow convergence, while RMSprop improves recall but slightly reduces precision. Adam performs the best (99.34%), balancing precision and recall effectively. AdamW shows slightly lower performance than Adam but still outperforms SGD and RMSprop.

Image resolution determines the level of detail available for feature extraction. Lower resolution (128×128) results in information loss, reducing accuracy to 95.43%. Using an input resolution of 256×256 leads to an accuracy of 99.34%, highlighting its effectiveness in maintaining important visual features without significantly increasing computational complexity. Higher resolution (512×512) does not significantly improve performance while increasing computational complexity, making 256×256 the best choice shown in Table 8.

Dropout prevents overfitting by randomly deactivating neurons during training. A lower dropout rate (0.2) results in slightly reduced accuracy (98.75%) due to overfitting. A higher dropout rate (0.5) slightly reduces accuracy (99.05%) due to excessive regularization. The optimal dropout rate is 0.4, providing the best accuracy (99.34%) while preventing overfitting shown in Table 9.

To further assess the reliability and robustness of the proposed model, several evaluation metrics were analyzed in different experimental configurations, such as accuracy, precision, recall, F1-score, specificity and AUC. The outcomes show good results in the consistent performance of the Xception architecture with different batch sizes and hyperparameters. In particular, batch size 64 always achieved the highest performance with 99.34% accuracy, 98.51% precision and recall of 98.80%, which suggests stable convergence and good generalization abilities. The little change in the model performance between two different batch sizes (98.32% ~ 99.34% accuracy) indicates that the model is reliable with different training configurations for classification. Additionally, the ablation studies of learning rate, optimizer selection, image resolution and dropout rate further validate the stability of the proposed approach. The following experiments shown that the selected configuration (learning

rate = 1e-5, Adam optimizer, image resolution = 256×256, dropout rate = 0.4) can always generate the best performance. The fact that the behaviour is the same in different experiments is an indication that the results obtained are reliable and not dependent on a particular experimental setting. The consistently high AUC values (0.96–0.99) further confirm the strong discriminative ability of the model in distinguishing benign and malignant lesions.

Table 6. Effect of learning rate on model performance

Learning rate	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)	Specificity (%)
1e-3	95.12	93.24	97.10	95.13	96.87
1e-4	97.84	96.87	98.32	97.58	98.56
1e-5 (current)	99.34	98.51	98.80	98.63	99.52
1e-6	98.15	97.10	98.12	97.61	98.24

Table 7. Effect of optimizer selection on model performance

Optimizer	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)	Specificity (%)
SGD	96.45	95.20	97.85	96.51	98.12
RMSprop	97.52	96.10	98.05	97.06	98.45
Adam (current)	99.34	98.51	98.80	98.63	99.52
AdamW	98.85	97.90	98.55	98.22	99.21

Table 8. Effect of image resolution on model performance

Resolution	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)	Specificity (%)
128×128	95.43	94.20	96.12	95.15	96.88
256×256 (current)	99.34	98.51	98.80	98.63	99.52
512×512	99.15	98.32	98.61	98.46	99.45

Table 9. Effect of dropout rate on model performance

Dropout rate	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)	Specificity (%)
0.2	98.75	97.82	98.50	98.16	99.10
0.4 (current)	99.34	98.51	98.80	98.63	99.52
0.5	99.05	98.20	98.55	98.37	99.30

4.3. Comparison with existing works

We compared the performance of our suggested scheme with other available schemes of classifying skin-cancer and discovered that it provides significant improvement in accuracy and strength which is explained in Table 10. Using the ISIC dataset, Bassel et al. implemented ResNet50, Xception, and VGG16 architectures, achieving an F1-score of 0.89. Similarly, Riya Tanna used a CNN with three layers and an SVM (RBF kernel) to perform binary classification on the ISIC dataset, with accuracies of 84.39% and 79.39%, respectively. Sabir and Mehmood [32] compared the performance of EfficientNet-B0, ResNet-18 and a simple CNN. They discovered that EfficientNet-B0 was the most successful with a 97% accuracy, a 99% sensitivity, and 93% specificity. Ghazal et al. [8] created a customized AlexNet model on a dataset of 1920 photos and achieved an accuracy of 87.1%. Ahmadi Mehr and Ameri [2] used an Inception-ResNet-v2 model combined with patient metadata to achieve 94.5% accuracy in binary classification on a large dermoscopic dataset. In comparison, the suggested Xception-based model achieved a state-of-the-art accuracy of 97% on the ISIC dataset, outperforming prior studies in terms of accuracy, sensitivity, and specificity, demonstrating its potential for effective early diagnosis of skin cancer.

Table 10. Comparative performance of existing skin cancer detection models

Reference	Methodology	Dataset	Performance
Kassem et al. (2021) [15]	GoogLeNet-based CNN	ISIC 2019	Accuracy = 94.92% Precision = 80.36% Specificity = 97% Sensitivity = 79.8%
Tanna (2021) [35]	CNN ,SVM	ISIC	Accuracy = 84.39% Accuracy = 9.39%
Hasan et al. (2021) [10]	VGG16,SVM, ResNet50, Sequential Models	Kaggle (6594 images)	VGG16: Accuracy = 93.18% SVM: Accuracy = 83.48% ResNet50: Accuracy = 84.39% Sequential: 74.24%–84.09%
Bassel et al.(2022) [6]	Resnet50/ Xception/ VGG16	ISIC	Accuracy = 90.9% F1-score = 89.00%
Ghazal et al. (2022) [8]	AlexNet	Custom Dataset	Accuracy = 87.1%
Ahmadi Mehr and Ameri (2022) [2]	Inception-ResNet-v2	ISIC	4classes- 89.3±1.1% 2classes- 94.5±0.9%
Qasim Gilani et al. (2023) [28]	Spiking VGG-13 Network	HAM10000	Accuracy = 89.57% F1-score = 90.07%
Hossain et al. (2024) [12]	Max Voting Ensemble	ISIC 2018, HAM10000	Accuracy = 93.18% AUC = 0.9320
Sabir and Mehmood (2024) [32]	ResNet-18, Basic CNN, EfficientNet-B0	ISIC	EfficientNet-B0: Accuracy = 97% Sensitivity = 99% Specificity = 93% Precision = 95% F1-score = 97% MCC = 94%
Ramamurthy et al. [31] (2024)	Densenet-169 with CoAM + customized CNN	HAM10000	Accuracy = 93.2% Recall = 91.4% Precision = 95.3% F1-score = 93.3%
Moturi et al. [25] (2024)	CNN	HAM10000	Accuracy = 95%
Marwa Kahia et al. [23] (2025)	Modified MobileNet, Modified AlexNet, and Custom CNN	ISIC	Accuracy = 84.70% Recall = 84.78% Precision = 84.56% F1-score = 84.63%
Proposed Method	Xception	Custom Dataset from Kaggle	Accuracy = 97%

5. Limitations of study

Despite the encouraging results obtained from the proposed Xception-based skin cancer detection model, there are several limitations that are to be acknowledged. First, the set of dermoscopic images used in this study consists of 1,968 images, which is rather small when compared with datasets of large-size medical images. Although data augmentation techniques were used in order to increase generalization, the amount of data that constituted the dataset may still limit its ability to acquire the entire variability of skin lesion characteristics such as those encountered in real clinical scenarios. Second, the type of classification problem in this work is binary classification (benign vs. malignant). However, the diagnosis of skin cancer in available clinical practice usually includes lesions of more than one category, such as melanoma, basal cell carcinoma, squamous cell carcinoma, etc. and other dermatological conditions. Extending the model to a multi-class classification could expand the support system to a more complete diagnosis. Third, the suggested framework was assessed with a single deep learning architecture (Xception). Lastly, patient data meaningful for study, such as age, gender, location of lesion and clinical history, were not taken into account during the experiments, which used publicly available dermoscopic images. Integrating such clinical information could further improve the diagnostic accuracy of automated systems for skin cancer detection and offer a more practical system.

Future research will aim to overcome these limitations by using larger and more diverse datasets, studying multi-class skin lesion classification, introducing clinical metadata, and studying ensemble models or models combining deep learning and other machine learning methods to potentially enhance the reliability and feasibility of automated dermatological diagnosis systems in real clinical trauma settings.

6. Conclusion and future scope

In conclusion the using of Xception architecture for the binary classification for skin cancer disease have produced an encouraging results with the result of accuracy 97%. This result emphasizes the ability of the Xception model for the effective differentiation of malignant and benign skin lesions due to the powerful feature extraction and discriminative learning. The high classification performance shows the potential of deep learning techniques to help dermatologists increase the accuracy of diagnoses and to support skin cancer early detection which can ultimately lead to better patient outcomes.

Despite the promising results there are several ways in which future research should proceed. In particular, it may be possible to improve the model's interpretability by integrating Explainable Artificial Intelligence (XAI) techniques such as Gradient-weighted class activation mapping (Grad-CAM), SHAP (Shapley Additive Explanations) and saliency maps to take, for instance, into account the regions of dermoscopic images that affect the model's predictions. Such explainability mechanisms can help build trust among clinicians, and give them better insight into how deep learning models make decisions on a diagnosis. Furthermore, incorporating Xception-based models into mobile or embedded healthcare systems could be a way to increase access to early screening for skin cancer, particularly since it could be prominent in remote or poor areas, which would lead to better and more scalable dermatological healthcare solutions.

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Code availability statement: The code supporting this is available from the corresponding author upon reasonable request.

Data availability statement: The dataset utilized in this study can be accessed publicly at the following link: <https://www.kaggle.com/code/mdismielhossenabir/binary-classification-of-skin-cancer-use-xceptio/input>

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