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Classification of deep features obtained from mpox images using Xception by selecting them with PCA and mRMR and using SVM



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Abstract

Mpox is a dsDNA virus that shows lesions on the skin similar to those of chickenpox, measles, and smallpox. Clinical examination is based on traditional methods such as Polymerase Chain Reaction (PCR) test kits and skin lesion testing by electron microscopy. The costly and time-consuming nature of PCR tests and the similarity of Mpox to chickenpox, measles, and smallpox make electron microscopy tests difficult for early diagnosis. In this study, we attempted to solve these challenges by using transfer learning-based convolutional neural network (CNN) models to diagnose Mpox disease. The experiments were conducted on the publicly available Mpox Close Skin Images (MCSI) dataset, which is preprocessed, homogeneous, and has a balanced distribution. DenseNet-121, DenseNet-169, DenseNet-201, Inception-V3, MobileNet, MobileNetV2, NasNetMobile, and Xception CNN models were compared, and it was analyzed that the Xception model was more successful than other models in the Mpox classification task. The 204800 deep feature maps obtained from the layer just before the fully connected layer of the Xception model were reduced to 400 by Principal component analysis (PCA). Then, the deep feature maps were filtered with the Minimum Redundancy Maximum Relevance (mRMR) algorithm and passed through the feature selection process. After feature selection, the 100 feature maps obtained after the classification process of the Support Vector Machine (SVM) algorithm yielded an accuracy of 89.70%, precision of 89.69%, sensitivity of 89.70%, F1 of 89.66%, and specificity of 96.57%. The GridCVSearch method to optimize hyper-parameters was used, and a Repeated 5-fold cross-validation technique was used in all experimental studies. As a result of these results, our approach showed that it could increase the diagnostic accuracy rate of the disease, reduce the overall misdiagnosis rate, and be a potential alternative decision support system to traditional methods such as PCR and electron microscopy.

Keywords

Deep Learning · Convolutional neural network · Mpox · Monkeypox · Transfer learning · Classification



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Introduction

“Mpox,” formerly known as “Monkeypox,” is a dsDNA virus detected in more than 110 countries. The disease is transmitted to humans by monkeys and rodents such as squirrels and rats (Campana et al., 2024). Human-to-human transmission cases were first detected in the Democratic Republic of Congo (DRC) in 1970. It was recorded as an endemic disease in the African region (Ali et al., 2024). Although mortality rates ranging between 1% and 10% are relatively low today, they are considered alarming by public health authorities (Raha et al., 2024).

This zoonotic viral infection causes headaches, fever, rash, lymph node enlargement, back pain, and muscle aches. It takes 3–17 days for symptoms to develop, which persist for 2–5 weeks. The clinical presentation of Mpox is similar to that of chickenpox, measles, and smallpox (Chakroborty, 2024). The disease is transmitted to other people through the body fluids of infected people or through close contact with each other. Among those infected, 53% of men and 47% of women have been infected (Akram et al., 2024). People with weakened immune systems, people with a history of eczema, children under one year of age, and pregnant or breastfeeding women can have severe this illness and are at higher risk of death (Campana et al., 2024).

As with any disease, early diagnosis, isolating infected persons, and providing early treatment is vital to prevent the spread of Mpox. Traditional methods for diagnosing the disease include PCR test kits and skin lesion testing by electron microscopy. PCR tests are expensive and time-consuming, and there are some difficulties in obtaining them in some countries. The rarity of Mpox cases and the resemblance of skin lesions to some cases such as chickenpox, measles, and smallpox make it difficult to diagnose early from electron microscope images (Khan et al., 2024).

Due to the lack of valid antiviral treatments for the Mpox virus, it is considered very difficult to control this disease (Thorat & Gupta, 2024). Health authorities have stated that proactive countermeasures are needed to prevent this disease, which can become a global epidemic (Campana et al., 2024). Academic studies on artificial intelligence (AI) in medical image analysis and medical diagnosis have proven the strong potential of AI in healthcare (Göl et al., 2025; Sitaula & Shahi, 2022; Şenol et al., 2024). The strong potential of AI-based systems in image analysis, pattern recognition, and classification can be used to improve outcomes in healthcare. In this context, AI-based systems can contribute significantly to the early diagnosis and differentiation of Mpox from other similar diseases.

In this study, we utilized the potential of AI to develop a new Mpox classification model.

The summary of the model proposed in the study is as follows:

- A publicly available, preprocessed dataset of 400 samples with four different homogeneous classes (mpox, chickenpox, acne, and normal) were selected for the MCSI proposed model.
- Transfer learning is adopted in the proposed model. The Xception Deep learning model performs best among the eight deep learning models in extracting the feature maps of the samples in the dataset, which consist of skin lesion images.
- The size of the feature set was compressed using the PCA algorithm to increase the model's speed and make the relationship between the attributes simpler to understand.

The minimum redundancy maximum relevance mRMR algorithm was used to select the attributes with the highest relationship between the target class and the attributes. Thus, it was analyzed that the model's

performance increased, and the runtime was significantly reduced in the classification process with the Support Vector Machine (SVM).

The rest of the paper is organized as follows. Section 2 presents the literature on CNN, one of the recently proposed artificial intelligence methods for classifying medical and Mpox images. Section 3 describes our classification model for the MCSI dataset in detail. In Section 4, we detail our experimental work and discuss the results obtained. We compare our model with other works in the literature and highlight the advantages and areas for improvement. Finally, we report the results of our study in Section 5. We provide some suggestions for the future development of the proposed research.

Related Work

In this section, the state-of-the-art Convolutional Neural Networks (CNN), one of the artificial intelligence methods used in classifying medical images and skin lesion images, will be briefly discussed. Then, the Mpox skin lesion datasets and Mpox classification techniques were analyzed.

Artificial intelligence methods have achieved successful results in many studies in the field of medical imaging and have contributed significantly to healthcare services. Toğaçar et al. (2022) modified the last layers of pre-trained AlexNet, DarkNet-19, and ResNet-18 CNN models on ultrasound-based breast cancer images with a new fully connected (FC) layer. The features from the FC layers of these networks were combined and classified into three classes using the softmax function. With their proposed approach, 97.57% overall accuracy was achieved. In his study on brain tumors, Çalışkan (2023) modified the last layers of the AlexNet, VGG-16, ResNet-50, DarkNet-19, and GoogLeNet CNN models and added a new FC layer. The features taken from the previous layers of these models were combined, and the features were obtained using the mRMR feature selection algorithm and then classified using the softmax method. The overall accuracy of the proposed model was 95.94% in the experimental studies. In a related study, Başaran and Çelik (2024) used deep features extracted from the fully connected (FC) layer of the EfficientNetB0 model and applied particle swarm optimization (PSO) and a genetic algorithm (GA) for feature selection in the skin cancer classification. The filtered features were combined and classified using support vector machines. Accordingly, the success rate of the model was 89.17%.

Mpox is a skin lesion illness that is on the rise. A limited number of publicly available datasets are used to train artificial intelligence techniques for diagnosing this disease. Ali et al. (2022) created the first available dataset, the Skin Lesion Dataset (MSLD), with 228 images collected from the internet. MSLD is a dataset with two classes: mpox cases and other cases (Varicella and Measles). The authors augmented the data to increase the sample size of the dataset. Then, they conducted experiments using pre-trained VGG-16, ResNet50, InceptionV3 models, and a 3-fold cross-validation technique for classification. ResNet50 performed the best, with an accuracy of 82.96%. In another study using the MSLD dataset, the authors (Haque et al., 2022) utilized transfer learning using the VGG19, Xception, DenseNet121, EfficientNetB3, and MobileNetV2 deep learning models and the “imagenet” weights of these models. They integrated a convolutional block attention module (CBAM) at the end of these five models. They compared these five modified deep learning models among themselves. The modified architecture, consisting of the Xception model and CBAM-Dense layers, showed superiority over the other models with a validation accuracy of 83.89%. Another dataset, mpox Skin Images Dataset (MSID) (Bala et al., 2023), consists of 4 classes and 770 images. Among these classes, mpox contains 279 images, chickenpox 107 images, measles 91 images, and normal 293 images. The images in this unbalanced dataset were collected from open-source and online sources. In their

experiments with the dataset, the authors proposed a pre-trained modified DenseNet-201 deep learning model called MonkeyNet. The proposed model achieved 98.91% and 93.19% accuracy on the augmented and original data datasets. In another study (Uysal, 2023), using the MSID dataset, the CSPDarkNet, InceptionV4, MnasNet, MobileNetV3, RepVGG, SE-ResNet, and Xception models were compared. The best-performing MnasNet and RepVGG models were combined with a long short-term memory (LSTM) encoder network to create a hybrid deep learning model. The test accuracy of this hybrid model was measured as 87.00%. Altun et al. (2023) compiled and published another dataset as an open-access resource accessible via the web. In this two-class dataset, the positive class contains only the Mpox images. In contrast, the negative class contained skin lesions of Lyme, Drug Rash, Pityriasis Rosea Rash, and ringworm diseases similar to Mpox skin lesions. There are 2056 images in this dataset, most of which are Mpox images. The authors compared MobileNetV3-small, EfficientNetV2, ResNET50, ResNET50, Vgg19, DenseNet121, and Xception deep learning models with transfer learning in their experiments with their dataset. The MobilNetV3-small model achieved the best performance with 96% accuracy. Another dataset, Data mpox (DM) (Jaradat et al., 2023), has 117 images manually collected by experts from web sources. Of these, 45 images represent cases of monkeypox, and 74 images represent other types of skin diseases (normal, scarlet fever, and roseola). The authors compared the most widely used models: ResNet50, VGG16, MobileNetV2, VGG19, and EfficientNetB3. The MobileNetV2 model using transfer learning was reported as the most successful, with an accuracy of 98.16%. Finally, the MCSI dataset (Campana et al., 2024) used in this proposed study is a balanced Mpox dataset with four classes, each with 100 homogeneous images and 400 images. Unlike other datasets, this dataset contains Mpox, chickenpox, acne, and normal classes, and the samples are homogeneously distributed. Photographs of the skin lesions were taken with smartphones at a short distance and then preprocessed. The authors compared the VGG-16, Inception, ResnetV2, NasNet Mobile, MobileNetV3 Large, and MobileNetV3 Small models in their experiments with this dataset. In the experiments using transfer learning and 10-fold stratified cross-validation techniques, MobileNetV3-small was the most successful model, with an accuracy of 93% in the binary classification task. At the same time, MobileNetV3-large was the most successful model with an accuracy of 0.882 in the multi-task.

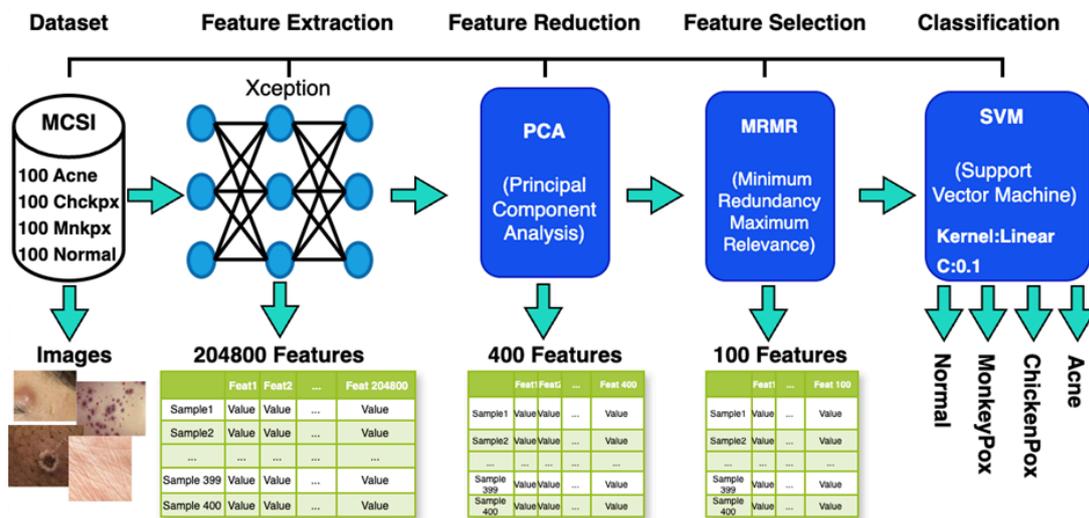
In this study, MCSI images were preferred for reasons such as being publicly available, homogeneous in terms of class distribution, and images obtained by zooming in. In addition, as a result of our literature research, the effective performance of transfer learning with existing CNNs in medical imaging led us to prefer these methods in this study. Unlike the Mpox studies in the literature, feature reduction and feature selection were added to our research. In addition, an SVM classifier, which is a different classification method than the classifiers used in Mpox studies in the literature, was used. These innovative approaches significantly contribute to the Mpox literature.

Materials and Methods

The structure of the proposed model comprises feature extraction, feature dimension reduction, feature selection, and classification steps. The structure of the model is given in [Figure 1](#).

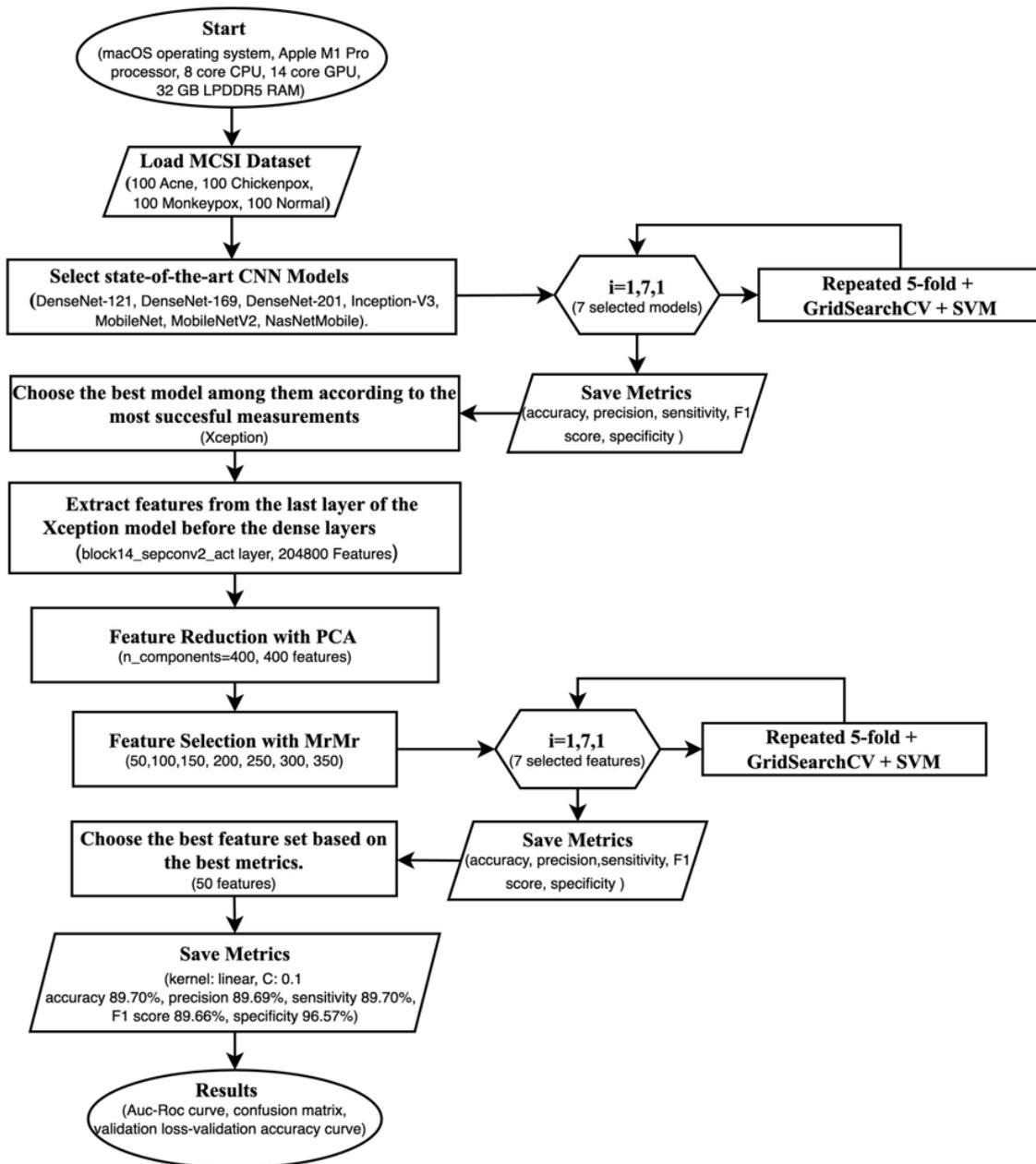
Figure 1

The general structure of the proposed architecture for the classification of the MCSI dataset



In the feature extraction phase of the model, the classification capabilities of the selected deep learning model Xception and other CNN models (DenseNet-121, DenseNet-169, DenseNet-201, Inception-V3, MobileNet, MobileNetV2, NasNetMobile) were compared. In all experiments, 5-fold cross-validation was used. At the end of the experiments, Xception was selected as the deep learning model with the most successful measurement values. A total of 204800 feature maps were obtained from the layer immediately before the fully connected layers of this model. The PCA algorithm was used to reduce the size of the feature maps extracted with the Xception model. Since the PCA algorithm cannot exceed the number of samples as the maximum number of features, the feature map was reduced to 400x400 dimensions. The minimum attribute map with the highest correlation with the target class was filtered to 400x100 dimensions with the mRMR attribute selection algorithm, which provided the maximum performance. For classification with the SVM algorithm, the most successful ones among many kernel, gamma, and margin hyperparameters were selected using the GridCVSearch technique. The model's hyperparameters C = 0.1 and the Linear kernel were obtained for the most successful classification of the filtered features. In addition, the model measurements were averaged by the repeated 5-fold cross-validation technique. The detailed working steps are given in Figure 2.

Figure 2
Proposed Workflow for MCSI Dataset Classification



Detailed descriptions of the dataset and methods used in the proposed model are given in the following sections.

Dataset

The MCSI dataset, which aims to detect different pathologies by focusing on the skin lesion, is a collection of photographs of skin lesions taken with smartphones at a short distance. The images obtained using the smartphone cameras were zoomed and cropped in the preprocessing stage. The open-access MCSI dataset was used in this study. This dataset consists of 4 classes: acne, chickenpox, monkeypox, and normal. The

MCSI dataset consists of four homogeneous classes, each containing 100 images in JPEG and PNG formats, totaling 400 images (Campana et al., 2023). Randomly selected images of the dataset are given in Figure 3.

Figure 3

Sample images from each class in the MCSI dataset



Due to the small number of samples in the dataset, the Repeated 5-fold cross-validation method was applied to the 400 mpox image data to achieve maximum testing and training. Thus, each sample will be evaluated in both the testing and training data.

K-Fold Cross Validation

Although the true value of the evaluation criterion, called the prediction error or true error, which measures the classification performance of the models used in machine learning, cannot be calculated exactly, it is estimated from the data (Rodriguez et al., 2009). Cross-validation is the most popular (Wong & Yeh, 2019) and widespread technique used for this estimation process (Fushiki, 2011). In this technique, the dataset is divided into k equal parts, $(k-1)$ parts are used for the training set, and one part is used for the test set.

In this study, the repeated k -fold technique was used to prevent overfitting due to the small size of the dataset used. In this technique, a dataset is randomly divided into five equal sub-parts, four of which are used as the training set to learn the model, and the other part is used as the test set to evaluate the model. This process is repeated 5 times in our study, and 25 folds are obtained. However, since the division is done randomly in each repetition, that is, by shuffling the samples, each sample resulting from the division is not used in the test set in equal numbers. This may create differences in the minimum deviation and class numbers resulting from the division in the confusion matrix.

Xception

Inspired by the Inception V3 model, modified “depth separable convolution” (DSC) layers are preferred instead of the inception module. The basic idea of the architecture is to separate the spatial and depth feature maps and to make strong feature maps with residual networks. Unlike other separable convolutional networks, Xception networks use first point convolution and then depth convolution. In the Xception modules of the feature maps, pointwise convolution 1×1 is used in-depth, while spatially 3×3 convolution kernels are used for each channel. The advantage of this CNN model is that it greatly reduces the number of parameters and computational costs (Chollet, 2017). To solve the problem of overfitting due to the small number of samples in the data sets we used and to shorten the training time, transfer learning was performed using Imagenet weights in our model (Lu et al., 2019).

PCA

The PCA algorithm is a versatile statistical method that reduces the size of the features by extracting the most important information in the dataset. Thus, it aims to simplify the data analysis in the dataset and make the relationship between the data simpler to understand (Greenacre et al., 2022). PCA analysis is a low-dimensional dataset representation and is one of the most widely used data compression techniques (Lasisi & Attoh-Okine, 2018). PCA allows for finding the dataset's highly correlated variables and observations and representing them in a lower dimensional subspace with minimal information loss (Kherif & Latypova, 2020).

mRMR

The mRMR method used in data mining and machine learning aims to reduce the size of high-dimensional data efficiently. For this purpose, the features that have the strongest relationship with the target class (maximum relevance) are selected, and the repetitive and similar features are filtered (Minimum Redundancy) (Peng et al., 2005). As a result, a smaller feature subset of the model provides a more effective working performance, reduces the model's running time, and increases the model's success (Başaran, 2022).

SVM

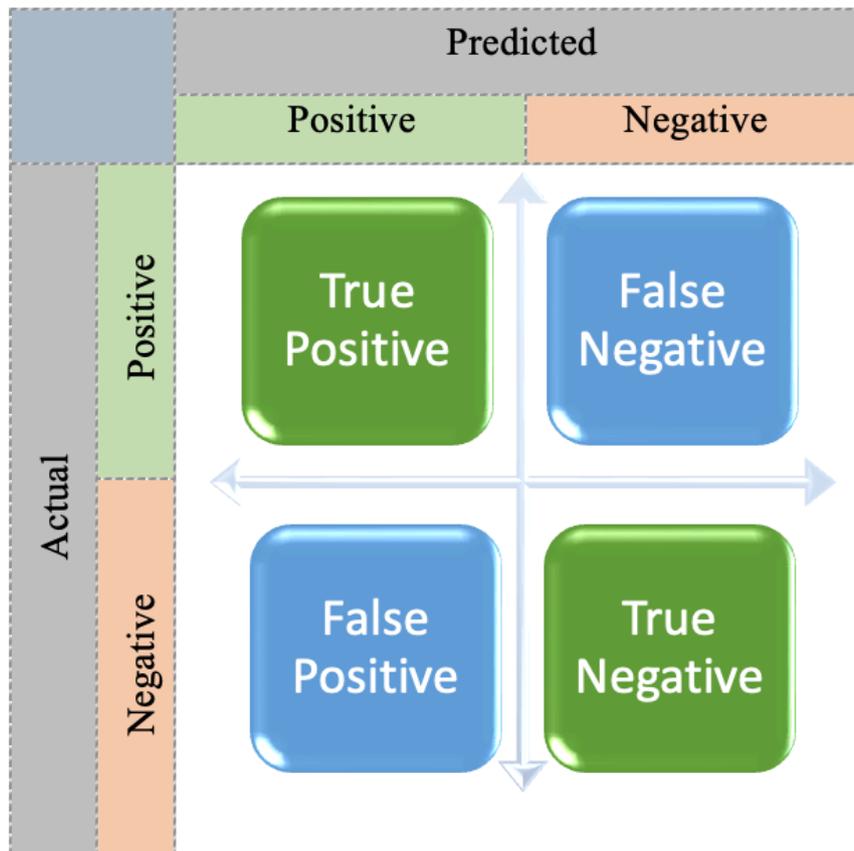
SVM is a supervised learning method that is effective in classification and regression analysis tasks. The classification process attempts to obtain the equation of the maximum margin line between classes (Bassma & Tayeb, 2018). The extreme points that determine the boundaries between classes are called support points, and the line segments that intersect these points are called support vectors.

In cases where the classes in the data set cannot be separated linearly, the cost of mapping to a higher space will be high, so the data is mirrored to the higher space, where it can be linearly separated by kernel cheating. Thus, by simulating a higher space, high cost is avoided, and the data can be divided into classes with different kernel functions (Mercier & Lennon, 2003).

Performance Metrics

The developers assess the models they develop according to their performance on the corresponding datasets. Including only the accuracy measure in this evaluation would make some questions unanswerable. The accuracy value only shows how many examples in the dataset the model predicts correctly. It does not indicate which class the prediction rate is high or low. Therefore, the confusion matrix, which calculates the prediction status of each class and provides other metrics besides accuracy, provides an effective evaluation of the model. Suppose the model's prediction is positive and the evaluation result is correct. In that case, it will be evaluated as True Positive (TP), and if the evaluation result is incorrect, it will be reviewed as False Positive (FP) in the confusion matrix. If we suppose the model's prediction is negative and the evaluation result is correct; in that case, it will be evaluated as a True Negative (TN), and if the evaluation result is incorrect, it will be reviewed as a False Positive (FP) in the confusion matrix. Using these four parameters, measures other than accuracy are obtained. The prediction performance of the positive class is considered a sensitivity measure, while the prediction performance of the negative class is a specificity measure. Precision is the measure that shows how many predicted samples in the dataset are positive. The harmonic mean of the precision and sensitivity measures is named F1. [Figure 4](#) shows a descriptive visualization of the parameters of the confusion matrix of the two-class model. Equations for the measurements obtained using the parameters obtained from the confusion matrix are given in Equations 4-8.

Figure 4
View of the confusion matrix for the two-class model



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

$$Sensitivity = \frac{TP}{TP + FN} \tag{2}$$

$$Specificity = \frac{TN}{FP + TN} \tag{3}$$

$$Precision = \frac{TP}{TP + FP} \tag{4}$$

$$F1 = \frac{2 \times Precision \times Sensitivity}{Precision + Sensitivity} \tag{5}$$

In addition, the GridSearchCV and Repeated k-fold methods of the scikit-learn library were used to find hyperparameters that will increase the proposed model's performance and evaluate the model correctly, respectively. While GridSearchCV is used to optimize the hyperparameters of a model, the k-fold technique is used to obtain the average performance of the model.

Results and Discussion

The main features targeted in the proposed model and the experimental studies are as follows: creating an original model, comparing the performance of the CNN algorithms suitable for the MCSI dataset samples,

selecting the most successful CNN algorithm to obtain the features of the Mpox samples, and evaluating and classifying the feature selection algorithms to select distinctive features and increase the performance of the model. The experimental studies used a laptop with a macOS operating system, Apple M1 Pro processor, 8-core CPU, 14-core GPU, and 32 GB LPDDR5 RAM features. The Python programming language and Sklearn, Matplotlib, OpenCV, and Tensorflow Keras libraries were used.

The publicly available MCSI is a homogeneous dataset with four classes, namely acne, monkeypox, chickenpox, and normal, with 100 samples in each class. In the proposed model, the features of the images were first extracted using the Xception CNN deep learning method. Then, the dimensions of the features extracted with the PCA method from the traditional methods were reduced by preserving the important features. Afterward, feature selection with the mRMR method and classification with different SVM kernels were performed, and the experimental test results were obtained.

To extract deep features, feature maps were taken from the 'block14_sepconv2_act' layer, the layer just before the 'avg_pool' and 'predictions' layers, the last layers of the Xception CNN model. The common hyperparameters used in all experiments for the Xception deep learning model used in the deep feature extraction are given in [Table 1](#).

Table 1
Hyperparameters of the Xception model used in all experiments

Weights	Include_Top	Input_Shape	Batch_Size	Features Layer
ImageNet	False	229× 229× 3	16	block14_sepconv2_act

Since the ImageNet weights are set as the initial weights, transfer learning is performed in the proposed model. For the Xception model, the input_shape parameter default value of 229× 229× 3 is used. The batch_size value is selected as 16, which is a divisor of 400.

In the PCA algorithm of the Python sklearn library, the n_component parameter value is set to a maximum of 400. Because according to the sklearn library, the n_components value should be between 0 and min (n_samples, n_features). When 204800 features are given to the PCA algorithm for each sample, the algorithm will return 400 features. As a result, the size of the feature map of the entire dataset will be reduced to a 400× 400 matrix.

Then, the feature selection process was performed using the mRMR algorithm for 400 reduced features of each image. In the experiments conducted for mRMR, the classification results were observed by giving values between 350 and 50 to the parameter K, which gives the number of selected features. In the MCSI classification task, the performances of different kernels, different 'C' and different 'gamma' hyperparameters used in the SVM algorithm were compared. The hyperparameters used in the SVM algorithm are presented in [Table 2](#).

Table 2
List of hyperparameters used for the SVM classifier

	C	Gamma	Kernel
Linear	0.1, 1, 10, 100, 1000	-	Linear
Non-Linear	0.1, 1, 10, 100, 1000	1, 0.1, 0.01, 0.001, 0.0001, auto	Poly, Rbf, Sigmoid



Here, the C value is the hyperparameter that controls the margin width, while the gamma value used in the nonlinear classification controls the width of the normal distribution. The kernel value is the function used in the hyperplane where the samples belonging to the dataset classes are best separated.

The most appropriate combination of SVM hyperparameters should be determined for the model's success. The GridSearchCV method was preferred to optimize the model hyperparameters. The GridSearchCV algorithm selected the "scoring," "cv," and "verbose" hyperparameters as "accuracy," "10," and "10," respectively. In addition, in the RepeatedKfold algorithm used in the cross-validation task, the 'n_splits' value was selected as '5', the 'n_repeats' value was selected as '5', and the 'random state' value was selected as '42'.

In the first experimental study for the CNN model selection, the 2D image data in the dataset were given as input to different CNN deep learning models. The hyperparameter 'include_top' which determines whether the upper layers are included in the feature extraction process from these models, was set to False.

This means that we obtain feature maps without including fully connected layers or, in other words, the upper layers in the process. Then, these feature maps are classified with different kernels of the SVM classification algorithm. The measurements of the performance of the models as a result of the classification task are given in [Table 3](#).

Table 3

CNN models compared for feature extraction from the MSCI dataset

Model	feature	kernel	C	gamma	Acc.	Pre.	Sen.	F1	Spe.
DenseNet121	50176	sigmoid	10	auto	0.8175	0.8203	0.8175	0.8142	0.9392
DenseNet169	81536	sigmoid	10	auto	0.862	0.8617	0.862	0.8598	0.954
DenseNet201	94080	sigmoid	10	auto	0.8355	0.8339	0.8355	0.8342	0.9452
Xception	204800	rf	10	auto	0.8645	0.8661	0.8645	0.8643	0.9548
InceptionV3	131072	rf	10	auto	0.814	0.8218	0.814	0.8147	0.938
MobileNet	50176	linear	0.1	-	0.847	0.8475	0.847	0.8464	0.949
MobilNetV2	62720	linear	0.1	-	0.843	0.8403	0.843	0.8403	0.9477
NasNetMobile	51744	rf	10	auto	0.842	0.8449	0.842	0.8418	0.9473

It was observed that the most successful deep learning model in classifying the examples in the MSCI dataset was Xception. Accordingly, the highest results were obtained in the {kernel: RBF, C: 10, gamma: auto} hyperparameters with 204800 features taken from the Xception model. According to the results, the most successful measurement was observed with an accuracy of 86.45%, precision of 86.61%, sensitivity of 86.45%, F1 score of 86.43%, and specificity of 95.48%.

The next experiment used the PCA algorithm to reduce the feature size without losing important information in the 204800 features. It was observed after the experiments that important features were preserved after the feature reduction with PCA. The classification results with SVM after the reduction of the features obtained from the Xception model with PCA are given in [Table 4](#).

Table 4

SVM classification results of feature reduction with PCA

Model	feature	kernel	C	gamma	Acc.	Pre.	Sen.	F1	Spe.
Xception	25	rf	100	0.0001	0.864	0.8627	0.864	0.8626	0.9547
Xception	50	rf	1	0.0001	0.8695	0.8694	0.8695	0.869	0.9565

Model	feature	kernel	C	gamma	Acc.	Pre.	Sen.	F1	Spe.
Xception	100	sigmoid	1	0.0001	0.863	0.8659	0.863	0.8632	0.9543
Xception	150	sigmoid	1	0.0001	0.8545	0.8593	0.8545	0.8549	0.9515
Xception	200	sigmoid	1	0.0001	0.8475	0.853	0.8475	0.8481	0.9492
Xception	250	sigmoid	1	0.0001	0.846	0.8511	0.846	0.8464	0.9487
Xception	300	linear	0.1	-	0.8505	0.8564	0.8505	0.8509	0.9502
Xception	350	linear	0.1	-	0.8525	0.858	0.8525	0.8532	0.9508
Xception	400	linear	0.1	-	0.851	0.8554	0.851	0.8513	0.9503

The experimental study concluded that despite a large reduction in data size, negligible decreases or small increases were detected in the model classification performance. The most successful performance was achieved when the parameter 'n_component,' which is the number of components to be stored that gives the reduced number of features, was set to 50. The hyperparameters of the SVM algorithm were obtained using the GridCVSearch technique as {kernel: rf, C: 1, gamma: 0.0001}. Accordingly, an accuracy of 86.95%, precision of 86.94%, sensitivity of 86.95%, F1 score of 86.9%, and specificity of 95.65% measurements were obtained.

In the next experiment, the mRMR feature selection algorithm was used to select the features with the strongest relationship with the target class and filter out repetitive similar features. The experimental results show that the feature selection process significantly contributes to the model's performance. After filtering the 50 features obtained because of reduction with PCA with the mRMR algorithm, the classification results with SVM are given in Table 5.

Table 5

Classification results of the reduced 50 features with SVM after filtering with the mRMR algorithm

Model	feature	kernel	C	gamma	Acc.	Pre.	Sen.	F1	Spe.
Xception	45	rf	1	0.0001	0.878	0.8771	0.878	0.8773	0.9593
Xception	40	rf	1	0.0001	0.88	0.8794	0.88	0.8792	0.96
Xception	35	poly	1	0.0001	0.8845	0.8839	0.8845	0.8834	0.9615
Xception	30	rf	10	0.0001	0.8805	0.8798	0.8805	0.8797	0.9602
Xception	25	rf	100	0.0001	0.878	0.8784	0.878	0.8773	0.9593
Xception	20	rf	1	0.0001	0.871	0.8723	0.871	0.8707	0.957

According to the SVM hyperparameters {kernel: poly, C: 1, gamma: 0.0001} that give the most successful classification performance, accuracy 88.45%, precision 88.39%, sensitivity 88.45%, F1 score 88.34%, specificity 96.15% measurements were achieved. The results revealed that there was an increase in the performance of the model.

In the last experiment conducted for the model, instead of 50 features reduced with PCA, the effect of filtering the maximum feature obtained from PCA with mRMR on the model's performance was investigated. It was determined that the model's classification performance was further increased by filtering the maximum value obtained from the PCA algorithm, which is 400 features, with the mRMR algorithm according to the dataset. The results of filtering the 400 features obtained because of reduction with PCA with the mRMR algorithm and then classifying them with SVM are presented in Table 6.

Table 6

Classification results of the reduced 400 features with SVM after filtering with the mRMR algorithm

Model	feature	kernel	C	gamma	Acc.	Pre.	Sen.	F1	Spe.
Xception	350	linear	0.1	-	0.852	0.8554	0.852	0.852	0.9507
Xception	300	linear	0.1	-	0.8665	0.8705	0.8665	0.8667	0.9555
Xception	250	linear	0.1	-	0.869	0.874	0.869	0.8696	0.9563
Xception	200	linear	0.1	-	0.8735	0.8761	0.8735	0.8734	0.9578
Xception	150	linear	0.1	-	0.8925	0.8936	0.8925	0.8922	0.9642
Xception	100	linear	0.1	-	0.8970	0.8969	0.8970	0.8966	0.9657
Xception	50	rf	1	0.0001	0.888	0.888	0.888	0.8877	0.9627

Accordingly, according to the SVM hyperparameters {kernel: linear, C: 0,1} that provide the most successful classification performance, accuracy 89.70%, precision 89.69%, sensitivity 89.70%, F1 score 89.66%, specificity 96.57% values were reached. The obtained results provide the most successful classification performance among the experiments. According to the results of this experiment, it was seen that reducing the maximum number of features with PCA affected the feature selection process with mRMR more positively and, as a result, increased the classification performance of the model. In addition, the standard deviation value of the model was measured as 0.0367, 95% confidence interval (0.8743, 0.9047) and t-statistics as 53.0042. The confusion matrix of the last experimental study and the AUC-ROC graph visually showing the ratio between accurate and incorrect predictions are given in Figures 5 and 6, respectively. The results comparing the model proposed in this study with other models are shown in Table 7.

Figure 5

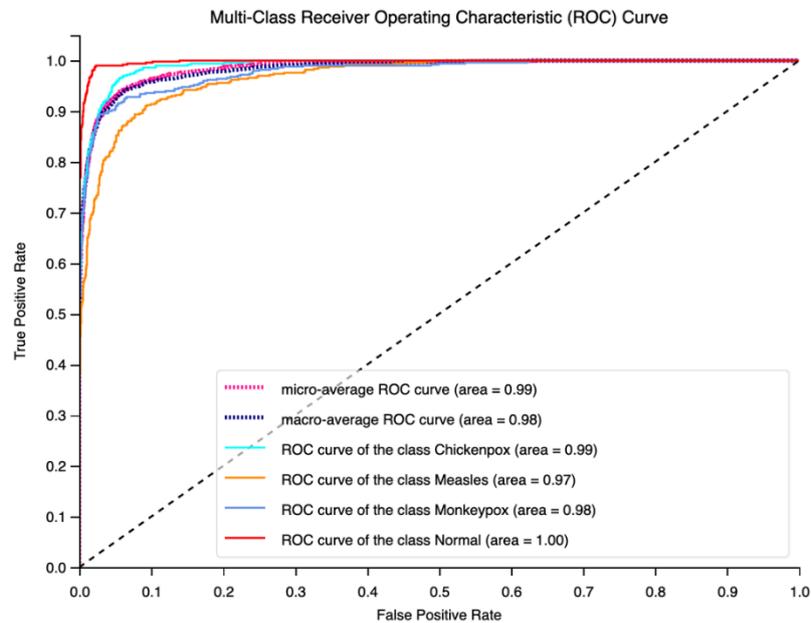
Confusion matrix of the proposed model

Acne	90	4	6	0
Cpox	7	82	8	3
Mpox	1	7	90	2
Normal	0	1	1	97
	Acne	Cpox	Mpox	Normal

Figure 6

ROC curve of the proposed model



**Table 7**

Results of comparing the model with other models

Method	Dataset	Accuracy	Class
MobilNetV3-small and transfer learning (Campana et al., 2024)	MCSI	0.928	2
ResNet50 and transfer learning (Ali et al., 2022)	MSLD	0.8296	2
XceptionCBAM-Dense (Haque et al., 2022)	MSLD	0.8389	2
CNN + LSTM (Uysal, 2023)	MSID	0.87	4
DenseNet-201 and transfer learning (Bala et al., 2023)	MSID	0.9319	4
Proposed	MCSI	0.897	4

The MSLD and MSID datasets are lesion images collected from different sources. They were created by collecting images from web scraping methods (news portals, websites, and publicly available case reports) and processing them. Therefore, the photos do not provide complete data about the environments from which they were obtained and the real dimensions of the original images. Because the resolutions for each image will vary depending on the platform from which they were collected, they may not provide a healthy result for evaluation. The pictures of both the MSLD and MSID datasets were obtained to include the entire body or multiple limbs. This means that we do not know exactly what the model learned from the data during the training phase. In all other studies, the methods did not use feature selection methods to increase the classification performance. The classification success of the model was affected.

Among the CNN models used to extract deep feature maps of images belonging to the MCSI dataset, the most successful performance was given by the Xception deep learning model, as shown in Table 3. Despite this success, the number of features taken from an image is 204800, which is much more than that of other models. This affects the running time and performance of the model. As a disadvantage, the computation time may increase for large feature sets. Therefore, the size of the feature set was reduced using the PCA algorithm before applying the mRMR feature selection algorithm. When the mRMR algorithm is used without applying the PCA algorithm, the time complexity will be very high for large feature sets (Hu

et al., 2010). PCA has greatly reduced the mRMR algorithm's running time and contributed to the model's performance, albeit slightly. Here, the disadvantage of the PCA algorithm is that important information may be lost while reducing the feature set. In addition, since the number of features in the feature selection algorithm is selected manually, models such as RFECV can be used instead, in which the algorithm performs the feature selection process automatically. In addition, there is still no publicly available, reliable Mpox dataset containing sufficient samples, which is also seen as an important problem for researchers (Bala et al., 2023).

Conclusion

This study presents a new model that can distinguish mpox images from other skin lesion images. The dataset used consists of four classes. These classes are acne, chickenpox, monkeypox, and normal image data. The classification accuracy of our proposed model concerning the number of classes was competitive with that of previous studies. The most innovative and distinguishing features of the proposed model are as follows:

- The PCA algorithm reduces the size of the feature set, which increases the model's speed and simplifies the relationships between features.
- The mRMR algorithm was used to select the attributes with the highest correlation between the target class and the attributes. This process significantly reduced the classification time and improved the classification performance.

In this study, the classification success obtained using the SVM classifier was 89.7%. Future studies will analyze the performance of different CNN and vision transform models. We also plan to develop a preprocessing process using the grad glass technique. In the future, better results can be obtained using transformer-based models and different feature selection methods. The models used in the Mpox recognition task can be used as an application in a mobile device, saving on high-cost devices.



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