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DETECTION OF MONKEYPOX DISEASE FROM SKIN LESION IMAGES USING MOBILENETV2 ARCHITECTURE

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Abstract. Monkeypox has recently become an endemic disease that threatens the whole world. The most distinctive feature of this disease is occurring skin lesions. However, in other types of diseases such as chickenpox, measles, and smallpox skin lesions can also be seen. The main aim of this study was to quickly detect monkeypox disease from others through deep learning approaches based on skin images. In this study, MobileNetv2 was used to determine in images whether it was monkeypox or non-monkeypox. To find splitting methods and optimization methods, a comprehensive analysis was performed. The splitting methods included training and testing (70:30 and 80:20) and 10 fold cross validation. The optimization methods as adaptive moment estimation (adam), root mean square propagation (rmsprop), and stochastic gradient descent momentum (sgdm) were used. Then, MobileNetv2 was tasked as a deep feature extractor and features were obtained from the global pooling layer. The Chi-Square feature selection method was used to reduce feature dimensions. Finally, selected features were classified using the Support Vector Machine (SVM) with different kernel functions. In this study, 10 fold cross validation and adam were seen as the best splitting and optimization methods, respectively, with an accuracy of 98.59%. Then, significant features were selected via the Chi-Square method and while classifying 500 features with SVM, an accuracy of 99.69% was observed.

1. Introduction

Monkeypox virus, a zoonotic orthopox DNA virus related to the virus that reasons smallpox, was first observed in humans in 1970 in the Democratic Republic of Congo (namely Zaire) [1, 2]. Sporadic outbreaks of infection have been declared in Africa, typically resulting from contact with wildlife reservoirs (especially rodents) [2, 3]. Such epidemics and travel-related events outside Africa have had

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restricted secondary spread, and thus human-to-human infection has been assumed ineffective [2, 4–7]. Although the monkeypox virus has been prevalent for years in zones where it was conventionally an endemic disease, the search for monkeypox has been disregarded and non-financed [2]. As of early May 2022, more than 3000 monkeypox virus infections have been noticed in more than 50 countries through five zones, canalizing the World Health Organization to declare monkeypox a developing medium public health fear threat on June 23, 2022 [2, 8]. Anxieties about the appearance of various infections in the coronavirus pandemic have been rising daily. The monkeypox disease was also feared by the people. To diagnose monkeypox early and take the necessary precautions, deep learning algorithms could be preferred by speeding up the process. For this purpose, one of the deep learning algorithms was used to detect monkeypox disease. Nowadays, deep learning algorithms have been widely used, particularly in image classification [9–15]. When images were classified, generally convolutional neural network (CNN) was utilized as a classifier. However, it has been considered that creating a novel CNN was difficult. Therefore, pre-trained architectures were determined as facilitators of this problem. In this study, MobileNetv2 which was a pre-trained architecture was preferred because of faster and more effective to recognize monkeypox disease. For determining the disease, the dataset was utilized from the publicly available website. This dataset contained monkeypox skin images and non-monkeypox skin images. Not only MobileNetv2 was used as a classifier but also performed as a deep feature extractor from these images. First, it was utilized as a classifier in different ways and then, it was performed as a feature extractor and merged with the Chi-Square feature selection method and Support Vector Machine (SVM) algorithm to provide confidence in the structure. Therefore, created this structure was called the hybrid algorithm. The pipeline of this study was displayed in Figure 1. The main contributions of this study are as follows:

- Used MobileNetv2 to detect monkeypox disease from skin images.
- Different splitting methods as training and testing (70:30 and 80:20) and 10 fold cross validation were carried out.
- Diverse optimization methods: adam, rmsprop and sgdm were also investigated in terms of classification success.
- Found the best splitting method as 10 fold cross validation and the best optimization method as adam based on performance metrics: accuracy, specificity, sensitivity, precision, G-Mean, F1-score, and AUC (Area Under Curve).
- Extracted 1280 features for each image from global average pooling of MobileNetv2 to improve monkeypox detection.
- Reduced these features to 250, 500, and 1000 by using the Chi-Square method and decisioned to the number of the minimum features was 500 according to results.

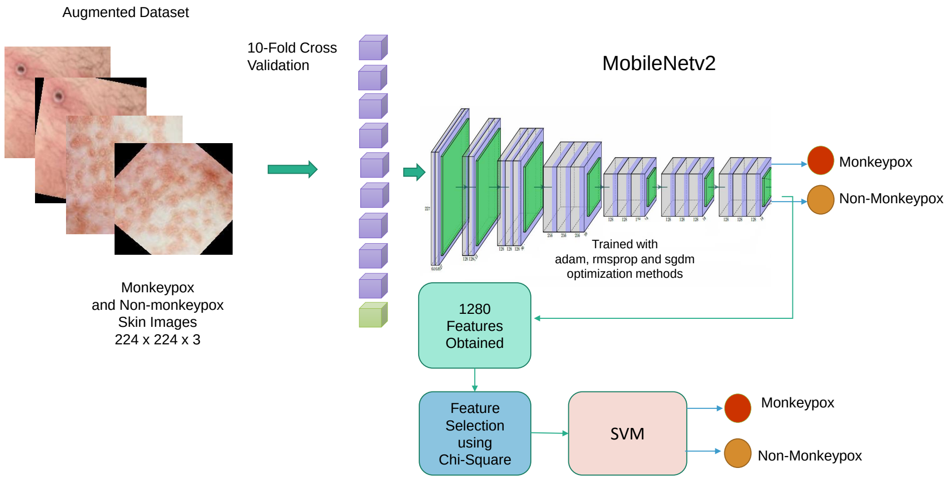


Figure 1. The pipeline of the study.

- Classified the reduced features based on SVM with linear, gaussian, and polynomial kernel functions to detect as monkeypox or non-monkeypox in the final of the study.
- Obtained the top results with the hybrid algorithm.

The rest of the study is organized as follows: In Section 1, the literature review was expressed. Then, utilized methods were stated in Section 2. In Section 3; the dataset, performance metrics, Receiver operating characteristic (ROC) curve, cross validation, hyperparameter selection, and experimental results were clarified. Then, the advantages and disadvantages of this study were discussed in Section 4. Finally, the study has been finalized the study in Section 5.

1.1. **Literature Review.**

In this study, when the monkeypox image classification studies were searched, not much more studies were seen. Though monkeypox disease emerged in 1970 [16], deep learning based studies have been newly raised. Sahin et al. [16] used a monkeypox image dataset to detect monkeypox via mobile device. They performed some pre-trained architectures: ResNet18, GoogleNet, Efficientb0, NasnetMobile, ShuffleNet, MobileNetv2. At the end of their study, the best performance was obtained based on MobileNetv2 with an accuracy of 91.11%. Ali et al. [17] utilized a monkeypox image dataset for binary classification using pre-trained architectures: VGG-16, ResNet50, and InceptionV3 with 3 fold cross validation. Final of the study, ResNet50 obtained the highest accuracy at 82.96%. Ahsan et al. [18] created two studies for recognizing monkeypox virus from images.

First one was which detecting monkeypox from original collected images, another was which detecting monkeypox from augmented images. Both studies were analyzed through deep learning based algorithms. They also benefited from one of the pre-trained architectures, VGG-16. Eventually, they obtained an accuracy of 97% and 88% for original images and augmented images to classify, respectively. Alakus and Baykara [19] researched to find monkeypox disease from DNA sequences via a deep learning approach. This is because monkeypox disease has different DNA sequences from warts and sometimes warts and monkeypox are not differentiable from each other. Therefore, they obtained DNA sequences of both warts and monkeypox and mapped them. Then, the mapped sequences were classified to detect monkeypox via bidirectional long/short term memory (BiLSTM) algorithm. In final, their study acquired an average accuracy of 96.08%. Sitaula and Shahi [20] used monkeypox image dataset to determine the disease via deep learning algorithm. Firstly, they performed two different visualization methods: Gradient weighted Class Activation Mapping (Grand-CAM) and Local Interpretable Model-Agnostic Explanations (LIME). Next, Xception architecture was used for classifying monkeypox dataset and it obtained an accuracy of 86.51%. Akin et al. [21] employed 12 different pre-trained architectures to classify the monkeypox image dataset into normal and monkeypox classes. At the end of the comparison, MobileNetv2 hit to top with an accuracy of 98.25%. Abdelhamid et al. [22] classified monkeypox image dataset based on transfer learning method with created hybrid deep learning algorithm. The algorithm first realized deep feature extraction via GoogleNet and then, it selected significant features through the Al-Biruni earth radius optimization algorithm. Finally, their proposed hybrid algorithm reached an accuracy of 98.8%.

2. Methods

2.1. **Convolutional Neural Network.** Convolutional Neural Network (CNN) has been one of the deep learning algorithms to analyze data generally used for images [23]. This name has come from the mathematical linear operation between matrices called convolution [24].It has been inspired by the structure of the animal visual cortex [23, 25, 26] and also created to automatically learn spatial hierarchies of features, from low to high level forms. CNN has had a complex mathematical structure because of including black-box [27]. The CNN processes an image in different layers and separates all its properties. The most generally applied layers have been: convolution layer, activation layer, pooling layer (maximum, average, or global), flattening layer, fully connected layer expressed as [28–30].

2.2. **MobileNetv2: Classification architecture and Deep Feature Extractor.** MobileNetv2 [31, 32] has used lightweight depth wise convolutions to filter features. It has two main blocks and contained the initial fully convolutional layer with 32 filters. Then, 19 residual bottleneck layers have been traced. In fact, it was put forward for mobile devices. MobileNetv2 is known as pre-trained architecture. In general, a CNN is created very hard and consumed time. Therefore, this situation was considered and this architecture was effectively used as a classifier and deep feature extractor. MobileNetv2 utilized in this study possesses some advantages: speedy performance, few parameters, needs little memory, etc. In addition, it can be employed in mobile applications, as well [12]. When a pre-trained architecture or other CNN architectures were applied, Stochastic gradient descent momentum (sgdm) [33] had been preferred as an optimization method [10, 12, 34]. However, the presented study, not only used sgdm but also employed Adaptive moment estimation (adam) [35] and Root Mean Square Propagation (rmsprop) [36]. In this study, 1280 features of each monkeypox image were obtained from the global average pooling layer called global-average while it was applied as a deep feature extractor. Next, obtained features were selected via Chi-Square (χ^2) method.

2.3. **Feature Selection through Chi-Square(χ^2)Method.** The Chi-Square has been a preferable statistical method to generate a rank about the effectively of a cell in a knowledge table. Sometimes, it has been expressed as the Pearson Chi-Square test or the Chi-Square test [12]. The rank is determined by using the difference between the expected value and the actual value of a cell in a Chi-Square test [12,37,38]. The Chi-Square value is computed as follows in Equation(1) [37,38]:

$$\chi^2 = \sum_{i=1}^{R} \sum_{j=1}^{C} \frac{(f_{ij} - e_{ij})^2}{e_{ij}} \tag{1}$$

where f_{ij} : actual value, e_{ij} : expected value, R : row, C : column, $i = 1, 2, ..., R$, $j = 1, 2, ..., C$, and χ^2: calculated Chi-Square value are represented. In first, the expected value is calculated for each cell. Then, it is calculated squared of the actual value and the expected value difference and divided by the expected value for each cell. After that, calculated these values are summed up. To obtain p-value, this sum is utilized in the probability density function(pdf) [12]. Before this stage is initiated, the degree of freedom should be found as follows in Equation (2):

$$\nu = (R - 1)(C - 1) \tag{2}$$

The pdf is calculated as follows in Equation (3) [39]:

$$f\left(x, \nu\right) = \frac{1}{2^{\frac{\nu}{2}} \Gamma\left(\frac{\nu}{2}\right)} x^{\frac{\nu}{2} - 1} e^{-\frac{\nu}{2}}, x > 0 \tag{3}$$

The p-value is also seen as follows in Equation (4) [12]:

$$p - value = \int_{\chi^2}^{\infty} f\left(x, \nu\right) dx \tag{4}$$

p-value is widely found through Chi-Square tables instead of calculating in many implementations since integrating this equation is not an easy way [12]. When applied to feature selection, the table for which the Chi-Square value should be computed is composed of set feature records against classes [12]. Therefore, this value was computed and features were sorted via their relation with class. Then, the highest related 250, 500, and 1000 features were investigated. At the end of the part, the dimension of the features was effectively reduced through Chi-Square method.

2.4. **Support Vector Machine (SVM).** In general, a classical learning approach is constructed to minimize errors in the training dataset based on empirical theory [40]. However, a Support Vector Machine (SVM) is built for the minimization of structural risk based on the statistical learning theory. Additionally, it can be explained with mathematical equations [41]. For this reason, it can be preferred in healthcare analysis. SVM possesses the potential to tackle very large feature spaces. This is because the training of SVM is realized so that the dimension of classified vectors does not have as different an effect on the performance of SVM as it possesses on the performance of the conventional classifier [40]. Therefore, it is observed to be mainly effective in big classification problems [40]. In this study, SVM was efficiently employed as a classifier after selecting features from monkeypox images with Gaussian, Linear, and Polynomial kernel functions.

3. Results

3.1. **Monkeypox Dataset.** In this study, Monkeypox skin image dataset was used for binary classification (monkeypox and non-monkeypox) and obtained from Kaggle website [42]. The non-monkeypox images consisted of both chickenpox and others, and it could be expressed that non-monkeypox images were similar to monkeypox. In fact, the dataset included original images: 102 monkeypox, and 126 non-monkeypox. However, if the original dataset was used for classification, it would be overfitting because of including fewer images. Therefore, the augmented dataset was performed to overcome overfitting. The augmented dataset contained 1428 monkeypox and 1764 non-monkeypox images. In total, 3192 images were employed to detect monkeypox disease. Besides, each image dimension was 224 x 224 and in RGB (Red, Green, Blue) format, and thus the dimension was 224 x 224 x 3. Two different splitting methods were applied in this study: training testing and cross validation. The ratio: 70:30, 80:20 training and testing were performed. In addition, a 10 fold cross validation was carried out.

3.2. **Performance metrics.** In this study, classifier performance was evaluated with accuracy, sensitivity, specificity, precision, F1-Score, and Geometric mean (G-Mean) and detailed in Table 1 [43–45].
where TP :True Positive, FP : False Positive, TN : True Negative, and FN : False Negative were shown.

TABLE 1. Formulas of performance metrics.

Performance Metric	Formulas
Accuracy	$\frac{TP+TN}{TP+TN+FP+FN}$
F1-Score	$\frac{2\times TP}{2\times TP+FP+FN}$
G-Mean	$\sqrt{Sensitivity \times Specificity}$
Precision	$\frac{TP}{TP+FP}$
Sensitivity	$\frac{TP}{TP+FN}$
Specificity	$\frac{TN}{TN+FP}$

3.3. **Receiver operating characteristic (ROC) curve.** While any classifier performance was calculated, the receiver operating characteristic (ROC) curve was widely carried out in a classification issue. Here, the false positive rate and true positive rate are respectively displayed as the ROC curve's x-axis and y-axis. Generally, the area under the curve (AUC) is also computed to identify whether a particular condition exists considering test data. When found the AUC value is approximately 1, the classifier has perfect performance [44, 46]. In this study, the AUC value was calculated to evaluate classification performance, and also ROC curve was demonstrated.

3.4. **Cross Validation.** To obtain trusted results from processes that contain black boxes like deep learning, cross validation has been widely preferred as a splitting method to avoid overfitting [47–49]. This method randomly splits the dataset with specified fold number (k) and thinks that one of the subconvolutions has been trained as a test set and leftovers [9, 50]. This operation is repeated up to k folds and tested in the pipeline [51]. In this study, k was determined as 10 for confident classification results.

3.5. **Hyper-parameters Selection.** In this study, hyperparameters were used to achieve better performance in classifying monkeypox images. Parameters identified were that adam, sgdm, rmsprop were performed as optimization methods, the learning rate was 0.0001 as a constant, the maximum epoch was 5, and the minibatch size was 8. All hyperparameters were determined by trial and error.

3.6. **Experimental Results.** In this study, the classification of the monkeypox skin image dataset effectively benefitted from a deep learning algorithm. This deep learning algorithm was MobileNetv2 pre-trained architecture which accepted images with 224x224 dimensions. The architecture was adapted with a transfer learning method to detect monkeypox disease from images both classifier and deep feature extractor. This is because deep learning algorithms can be carried out feature extraction from images without expert opinion, efficiently. First, the monkeypox image dataset was classified using different splitting (70:30, 80:20 training-testing, 10 fold cross validation) and optimization methods (adam, sgdm, rmsprop) where the best splitting and optimization method was found. Although the results obtained in this section were very good, the goal was to achieve excellent results in the detection of monkeypox disease. Thereafter, one of the feature selection methods: Chi-Square was used to reduce the dimension of features obtained from the MobileNetv2 global average pooling layer. More related 250,500, and 1000 features were chosen via Chi-Square method. Eventually, selected features were classified with SVM. Therefore, novel hybrid algorithm was designed via MobileNetv2, Chi-Square, and SVM. The results were acquired in MATLAB 2021b through intel core i7 7500U CPU, NVIDIA GeForce GTX 950M,16 GB RAM, and 64-bit operating system. All performance results are seen in Table 2 and Table 3.

Table 2. Mobilenetv2 performance metrics to classify Monkeypox images by different optimization methods and splitting methods.

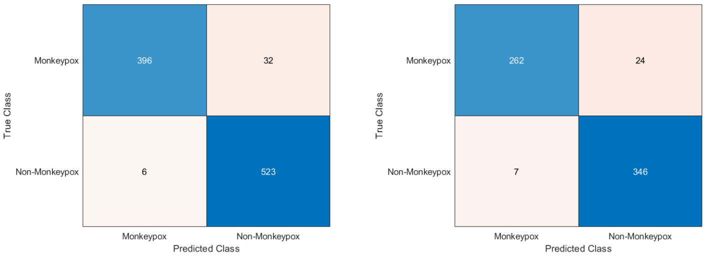
Splitting Method	**Optimization Method**	**Sensitivity**	**Specificity**	**Precision**	**F1-Score**	**G-Mean**	**Accuracy**	**AUC**
70:30 Train-test	adam	0.9252	0.9887	0.9851	0.9542	0.9564	0.9603	0.9933
	rmsprop	0.9369	0.9773	0.9709	0.9536	0.9569	0.9592	0.9900
	sgdm	0.8341	0.9679	0.9545	0.8903	0.8985	0.9080	0.9780
80:20 Train-test	adam	0.9371	0.9433	0.9306	0.9338	0.9402	0.9405	0.9866
	rmsprop	0.9161	0.9802	0.9740	0.9441	0.9476	0.9515	0.9930
	sgdm	0.8986	0.9292	0.9113	0.9049	0.9138	0.9155	0.9806
10 Fold Cross Validation	adam	**0.9811**	**0.9898**	**0.9873**	**0.9842**	**0.9854**	**0.9859**	**0.9985**
	rmsprop	0.9692	0.9881	0.9851	0.9771	0.9786	0.9796	0.9979
	sgdm	0.8704	0.9654	0.9532	0.9100	0.9167	0.9229	0.9747

*Bold values were shown as the highest metrics in this part.

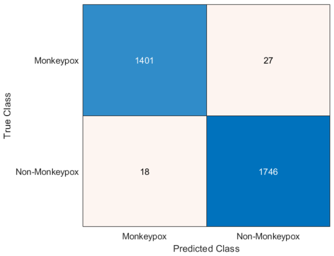
According to Table 2, in the examined 70:30 splitting method, the best ones had an accuracy of 96.03%, an AUC of 0.9933, an F1 score of 0.9542, a precision of 98.51% and a specificity of 98.87% obtained “adam” optimization method. A sensitivity of 92.52% and G-Mean of 95.64% were achieved to classify the monkeypox image dataset in this experiment.

Furthermore, Table 2 showed that the highest had an accuracy of 95.15%, an AUC of 0.9930, a G-Mean of 94.76%, an F1 score of 0.9476, a precision of 97.4%, and a specificity of 98.02% by using 80:20 splitting method and “rmsprop” optimization method. In this experiment, a sensitivity of 93.71% was achieved to classify monkeypox image datasets. When training and test splitting methods were interpreted, it was found that the 70:30 was more successful than another.

When Table 2 was investigated in regards 10 fold cross validation, the top had an accuracy of 98.59%, an AUC of 0.9985, a G-Mean of 98.54%, an F1-Score of



(A) 70:20 (B) 80:20



(C) 10 fold cross validation

FIGURE 2. Confusion matrices of MobileNetv2 by using diverse splitting methods.

0.9842, a precision of 98.73%, a specificity of 98.98% and a sensitivity of 98.11%. This experiment demonstrated that all performance metrics hit to top based on 10 fold cross validation and "adam" optimization method and hence, it could be expressed that cross validation was the best splitting method and adam was the best optimization method to classify the monkeypox image dataset. The confusion matrix and ROC Curve belonging to the 10 fold cross validation and "adam" optimization method were shown in Figure 2(C) and Figure 3. In addition, Figure 2(A) and (B) displayed confusion matrices of other splitting methods.

Although the results of this experiment were remarkably good, the aim was to further enhance these results in the recognition of monkeypox disease. Then, MobileNetv2 was used as a feature extractor from images and 1280 features for each image were obtained from its global average pooling layer. Then, these features were diminished to association 250, 500, and 1000 features using Chi-Square feature selection method. The rank of the 1280 features based on Chi-Square was demonstrated in Figure 4. After all, SVM was utilized to classify these features with different kernel functions in this part. Therefore, MobileNetv2- Chi Square-

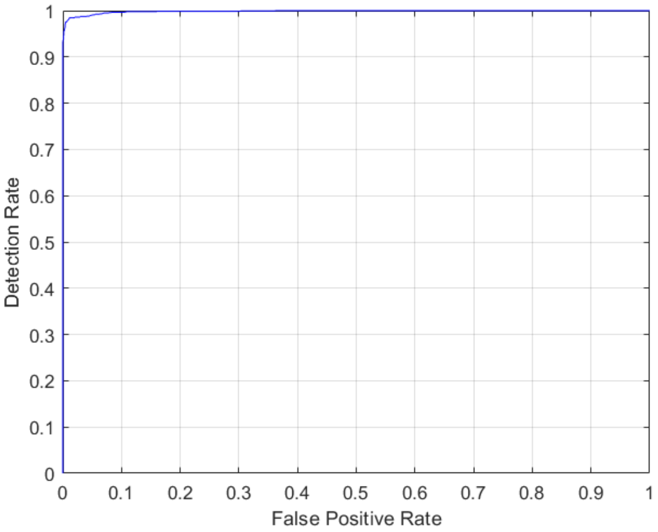


FIGURE 3. ROC curve of MobileNetv2.

SVM structure was named as Hybrid Algorithm. Experimental results were displayed in Table 3.

When Table 3 was examined in terms of both the number of features and different kernel functions, it was seen that the highest success was obtained with the number of 500 features and the polynomial kernel function. The performance metrics were as follows: an accuracy of 99.69%, an AUC of 0.9999, a G-Mean of 99.69%, an F1-Score of 0.9965, a precision of 100%, a specificity of 100% and a sensitivity of 99.30%.

Other interesting results shown in Table 3 for the number of 250 and 1000 features as follows: The first, linear and gaussian kernel functions gave the same performance metrics for both features. The second, although the polynomial kernel function displayed the maximum level for the number of 500 features, it was the opposite in others. This situation may be due to random selection.

Moreover, the results in Table 3 were increased in all experiments. For selected 250 features, when linear and gaussian kernel functions were used, the results had an accuracy of 98.96%, an AUC of 0.9986, a G-Mean of 98.9%, an F1-Score of 0.9883, a precision of 99.29%, a specificity of 99.43% and a sensitivity of 98.36%. While the polynomial kernel function was performed, the results had an accuracy of 98.33%, an AUC of 0.9984, a G-Mean of 98.33%, an F1-Score of 0.9814, a precision of 97.91%, a specificity of 98.30% and a sensitivity of 98.36%.

For selected 500 features, when linear and gaussian kernel functions were applied,

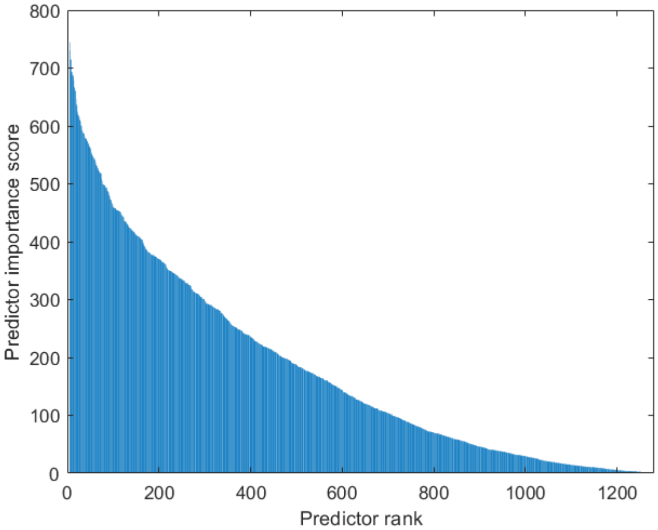
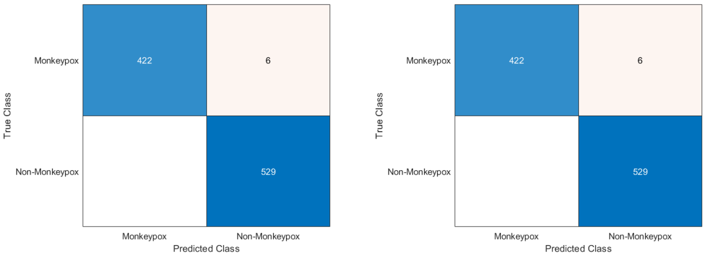


Figure 4. The ranks of features by importance rating using the Chi-Square method.

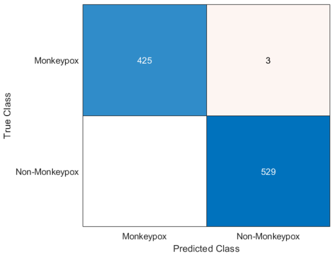
Table 3. Performance of the Hybrid Algorithm using the Chi-Square Feature Selection Method.

Number of Features	**Kernel Function**	**Sensitivity**	**Specificity**	**Precision**	**F1-Score**	**G-Mean**	**Accuracy**	**AUC**
250	gaussian	0.9836	0.9943	0.9929	0.9883	0.9890	0.9896	0.9986
	linear	0.9836	0.9943	0.9929	0.9883	0.9890	0.9896	0.9986
	polynomial	0.9836	0.9830	0.9791	0.9814	0.9833	0.9833	0.9984
500	gaussian	0.9860	1.0000	1.0000	0.9929	0.9930	0.9937	1.0000
	linear	0.9860	1.0000	1.0000	0.9929	0.9930	0.9937	1.0000
	polynomial	0.9930	1.0000	1.0000	0.9965	0.9969	0.9969	0.9999
1000	gaussian	0.9930	0.9943	0.9930	0.9930	0.9937	0.9937	0.9989
	linear	0.9930	0.9943	0.9930	0.9930	0.9937	0.9937	0.9989
	polynomial	0.9907	0.9735	0.9680	0.9792	0.9821	0.9812	0.9967

the results had an accuracy of 99.37%, an AUC of 1.000, a G-Mean of 99.30%, an F1-Score of 0.9929, a precision of 100%, a specificity of 100% and a sensitivity of 98.60%. When 1000 features were specified, the results had an accuracy of 99.37%, an AUC of 0.9989, a G-Mean of 99.37%, an F1-Score of 0.9930, a precision of 99.30%, a specificity of 99.43% and a sensitivity of 99.30% by using linear and gaussian kernel functions. While the polynomial kernel function was performed, the results had an accuracy of 98.12%, an AUC of 0.9967, a G-Mean of 98.21%, an F1-Score of 0.9792, a precision of 96.80%, a specificity of 97.35% and a sensitivity of



(A) Gaussian (B) Linear



(C) Polynomial

FIGURE 5. Confusion matrices of hybrid algorithms using different kernel functions.

99.07%. Therefore, it could be stated that minimum 500 features should be selected to detect monkeypox disease via this hybrid algorithm. The confusion matrices for different kernel functions were exhibited in Figure 5. ROC Curve of the hybrid algorithm was shown in Figure 6 by utilizing 500 features and polynomial kernel function.

4. DISCUSSION

In this part of the study, some advantages and disadvantages were submitted. As a first step, the advantages of the study were presented as follows: (i) To detect monkeypox disease from skin images, MobileNetv2 was employed with different perspectives. (ii) The comprehensive comparisons were done in regard to splitting methods and optimization methods. Two training-testing set splitting ratios were investigated 70:30 and 80:20. Besides, cross validation was also examined and the k value was taken as 10 in this study. In addition to adam, rmsprop and sgdm were also evaluated as optimization methods and their effectiveness in the classification was shown. (iii) The best splitting method as 10 fold cross validation and the best

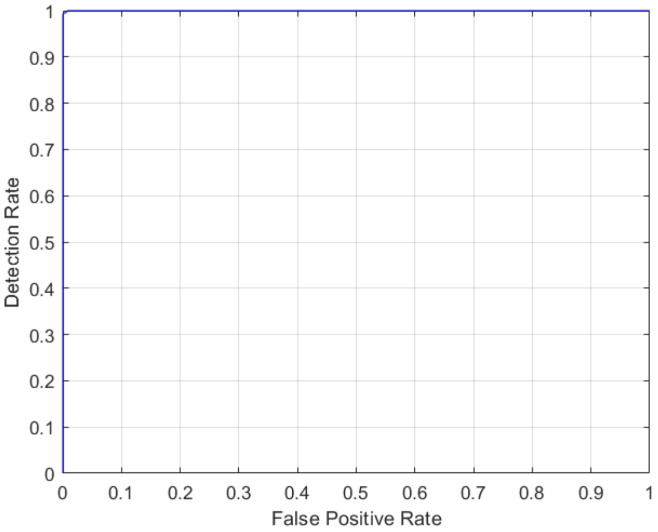


FIGURE 6. ROC Curve of hybrid algorithm.

optimization method as adam were determined with accuracy, specificity, sensitivity, precision, G-Mean, F1-score, and AUC. So far, Mobilenetv2 was assigned as the classifier. (iv) To improve monkeypox detection, MobileNetv2 was used to automatically extract features from the global pooling layer. (v) The Chi-Square method was carried out as feature selection and so, the dimension of the features was reduced using it. (vi) Finally, SVM was utilized with diverse kernel functions to classify as monkeypox or non-monkeypox based on these reduced features. Next, the disadvantage of the study was mentioned in that limited classes were investigated, which could be seen effectiveness of the study.

5. CONCLUSION

Concerns about the emergence of various diseases related to the coronavirus pandemic have been increasing day by day. Monkeypox was one of them. By diagnosing monkeypox early and taking the necessary precautions, it could be prevented from becoming a pandemic. To accelerate solving of this issue, the deep learning algorithm would be a savior. Through this impulse, monkeypox disease was aimed at detection using a deep learning algorithm: MobileNetv2 pre-trained architecture with transfer learning method. This architecture was used both a classifier and a deep feature extractor. First, it was performed as a classifier and investigated with comprehensive perspectives in terms of splitting (70:30 and 80:20 training-testing, and 10 fold cross validation) and optimization methods (Adam, rmsprop, and sgdm).

When viewing 70:30 splitting method, the best accuracy of 96.03%, an AUC of 0.9933 were achieved using adam optimization method to classify monkeypox image dataset in this experiment. When examining the 80:20 splitting method, the highest accuracy of 95.15%, and an AUC of 0.9930 were obtained by utilizing rmsprop optimization method to detect the monkeypox image dataset in this experiment. Note that, when using adam optimization method, the results were close to the highest one. At the end of this splitting method, it might be seen that 70:30 was better than another. When investigating 10 fold cross validation, it was hit to the top accuracy of 98.59%, and an AUC of 0.9985 using "adam" optimization method. As a result, cross validation and adam were the best splitting method and optimization method, respectively to determine monkeypox disease from image dataset. Next, it was performed a deep feature extractor from images and 1280 features were obtained from the global average pooling layer of MobileNetv2. To select significant features, Chi-Square method was utilized and 250, 500, and 1000 features were chosen by using it. Finally, selected features were classified via SVM classifier by using diverse kernel functions.

While selecting 250 features and using the SVM, results of linear and gaussian kernel functions were obtained the same: an accuracy of 98.96% and an AUC of 0.9986. However, polynomial kernel function result was lower than the others. While identifying 500 features, it was seen an accuracy of 99.37%, and an AUC of 1 for linear and gaussian kernel functions. An interesting result was shown with polynomial kernel function in this experiment. It was observed an accuracy of 99.69% and an AUC of 0.9999. Finally, the results of linear and gaussian kernel functions while choosing 1000 features, it was achieved an accuracy of 99.37% and an AUC of 0.9989. As well as polynomial kernel function result was the lowest. Therefore, it could be remarked that a minimum of 500 features should be chosen in order to diagnose monkeypox disease using this hybrid algorithm.

As a result, the performance was significantly increased and confidence in the study was enhanced by the hybrid algorithm created. In this study, the highest performance was obtained to diagnose monkeypox from skin images with an accuracy of 99.69% by MobileNetv2- Chi Square-SVM. Finally, it could be said that our designed pipeline had a perfect performance. In future works, it has been aimed to determine monkeypox disease better with new structures to be created.

Author Contribution Statements Ozaltin O. analyzed the dataset and wrote this study. Yeniay O. supervised and approved final manuscript.

Declaration of Competing Interests The authors declared that they have no competing interests.

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