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Prediction of Monkeypox on the Skin Lesion with the Siamese Deep Learning Model

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Abstract— **One of the viral diseases that has started to cause concern in various parts of the world is the monkeypox virus, which has emerged recently. Monkeypox is transmitted to humans from an animal infected with the virus or from another human being infected with monkeypox. Among the most basic symptoms are high fever, back and muscle aches, chills, and blisters on the skin. These blisters are sometimes confused with chickenpox and measles, resulting in incorrect diagnosis and treatment. Therefore, the need for computer-aided systems has increased and the need for more robust and reliable approaches has arisen. In this study, a deep learning model was used, and a distinction was made between monkeypox and other diseases. The study consisted of three stages. In the first stage, data were obtained and images of both chickenpox and other diseases were used. In the second stage, the Siamese deep learning model was employed, and data were classified. In the last stage, the performance of the classifier was evaluated and accuracy, precision, recall, and F1-score were calculated. At the end of the study, an accuracy score of 91.09% was obtained. This result showed that the developed deep learning-based model can be used in this field.**

Index Terms— **Artificial intelligence, Monkeypox, Siamese deep learning model**

I. INTRODUCTION

MONKEYPOX, which is seen as a possibility of a new virus outbreak has begun to be followed in detail. Infection of monkeypox virus in humans was first observed in 1970 [1]. From these years to the present, monkeypox has been regularly occurring in the African continent as sporadic reported cases. Monkeypox, which has been seen for many years in West and Central Africa and it rarely reaches different parts of the world with the contamination caused by animals exported from the region [2]. However, recently, the disease has become more widespread than in the past, and it has been diagnosed in different people from different regions [3]. Monkeypox can be transmitted to humans from an infected animal or from another person infected with monkeypox. Although the symptoms are similar to smallpox, it progresses somewhat differently [4]. The most basic symptoms of monkeypox are high fever, weakness, headache, back pain, chills, and blisters on the skin [5]. In monkeypox, rashes are first observed in the face area. It then spreads to other parts of the body. A low mortality rate is observed in monkeypox, and this value varies between 3-6% [6].

Infection from the monkeypox virus is contagious. Many situations such as being bitten by a virus-infected animal, touching the body fluids of these animals, consuming the undercooked meat of an infected animal, using its fur are among the ways of transmission of the disease. The monkeypox virus, which is transmitted to humans in this way, spreads among humans and creates a risk of turning into an epidemic. The rashes on the body of the sick individual and the fluids in these bubbles contain the disease factor. Therefore, situations such as touching the rashes of a sick person and sharing the clothes, sheets, towels, and similar items contaminated with these rashes cause the disease to be transmitted easily [7]. Paying attention to the hygiene rules that help protect against all diseases is the most important stage of protection. Since animal meat is an important route of transmission, only well-cooked meat should be consumed. Apart from this, people who spend time in nature should also be careful. Stray and wild animals, including dead animals, should not be approached. Animals that are seen in nature and do not look healthy should never be touched [8].

The disease can be confused with chickenpox and measles in some cases because of the similarity of the rashes [9, 10]. An expert interpretation is required to make a clear distinction between them. However, in the early stages of the disease, this difference cannot be fully evident and causes the diagnosis to be incorrect. Accordingly, the treatment is wrong, and this causes the patient to lose time and to be treated incorrectly. To avoid such problems, computer-aided systems are needed [11]. In this study, a computer-aided diagnostic system was created, and a decision-making mechanism was established to distinct monkeypox or other diseases (chickenpox and measles). In this direction, deep learning algorithm was used in the study and skin images of diseases were classified. The study consisted of three different stages. In the first stage, skin images of new monkeypox and other diseases were obtained. In the second stage, deep learning model was designed, and Siamese deep learning model was applied at this stage. In the final stage, the performance of the classifier was determined by accuracy, precision, recall, and F1-score evaluation metrics. The highlights of the study can be expressed as follows:

- Siamese deep learning model, which is one of the lesser-known deep learning methods, was used and monkeypox disease was predicted from skin images.

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- With this study, the differences between monkeypox and other diseases were determined by computer- aided system.
- In this study, raw skin images were evaluated without any preprocessing and classified without complicating the feature vector. In this way, both the processing load and the data load did not increase.
- It has been shown that a computer-aided system can be effective in situations that require expert interpretation.

The remainder of the study is organized as follows. In the Section II, studies in this field in the literature were examined. In the Section III, the data set and method used in the study were emphasized. Section IV showed the results of the application and the discussions. Furthermore, the advantages and disadvantages of the study were explained. In the last section, the contribution of the study to the literature was given and its impact on future studies was mentioned.

II. RELATED STUDIES

In this part of the study, studies that have predicted monkeypox disease with artificial intelligence algorithms using skin images were included. In the study [11], researchers used deep learning models to predict monkeypox. Images of three different skin diseases were used in the study. These diseases were monkeypox, chickenpox, and measles. In the study three different classifiers were employed including VGG-16, ResNet50, InceptionV3. The performances of the models were determined by the 3-fold cross-validation method and for this purpose accuracy, precision, F1-score, and recall evaluation criteria were used. At the end of the study, the highest accuracy score was obtained with the ResNet50 deep learning model, and the result was 82.96%. In study [12], the researchers predicted monkeypox disease using pre-trained deep learning models. In the study, a total of 1,754 images belonging to four different classes, including chickenpox, monkeypox, measles and normal skin images, were used. The images were then classified using thirteen different deep learning models. These models were VGG-16, VGG-19, ResNet50, ResNet101, IncepResnetV2, MobileNetV2, InceptionV3, Xception, EfficientNetB0, EfficientNetB1, EfficientNetB2, DenseNet121 and DenseNet169. The performance of the classifiers was determined by the evaluation criteria of precision, F1-score, recall, and accuracy. In the validation process, 5-fold cross-validation was applied. The lowest accuracy score was obtained with VGG-16 and the result was 82.22%. The highest accuracy score was calculated with the Xception deep learning model, and 86.51% accuracy was obtained with this model. In study [13], researchers predicted monkeypox from images using the modified VGG-16 model. In the study, two different images, monkeypox and chickenpox, were used and two different scenarios were emphasized. While a total of 90 images were used in the first scenario, the images were augmented in the second scenario and classification was performed on 1,754 images. The performance of the classifier was determined by accuracy, precision, recall and F1-score evaluation criteria. While 83% accuracy rate was obtained for the first scenario, 78% accuracy score was observed for the second scenario. In study [14], researchers predicted monkeypox disease using CNN (Convolutional Neural Networks) based features. In the study, AlexNet, GoogleNet and VGG-16 architectures were used as CNN models and separate features were obtained. Then, these features were classified with five different machine learning algorithms. In the study, NB (Naive Bayes), SVM (Support Vector Machine), KNN (K Nearest Neighbor), DT (Decision Tree) and RF (Random Forest) algorithms were used as machine learning algorithms. The performance of the classifiers was determined by the evaluation criteria of accuracy, F1-score, precision, and recall. At the end of the study, an effective classification process was carried out with transfer learning. In study [15], researchers predicted monkeypox using CNN architectures and skin images. Five classifiers were used in the study, namely VGG-16, VGG-19, ResNet50, MobileNetV2 and EfficientNetB0. The performance of the classifiers was determined by four different evaluation criteria: accuracy, F1-score, precision, and recall. In addition to these, they also used Ensemble classifiers. The highest accuracy score was obtained with Ensemble, which includes ResNet, EfficientNet and MobileNet models, and an accuracy of 98.33% was observed.

III. MATERIAL AND METHODS

A. Dataset

In this study, the publicly available data set was used, and the data were obtained from study [11]. While there are 102 images of monkeypox in the original dataset, there are 126 images of chickenpox and measles. Furthermore, there are also augmented images in the dataset. In the augmented images, there are images of 1,428 monkeypox diseases, and 1,764 images of chickenpox and measles. Augmented images were used in the study and 80% of the data was used for training and the remaining 20% for testing. Some of these images are given in Fig. 1.

Fig.1. Images of the data set. The images at the top are of monkeypox, while the images at the bottom are photos of measles and chickenpox.

B. Siamese Deep Learning Model

A Siamese Deep Learning model (SDLM) was first proposed to solve signature verification problems [17]. It is a type of neural network architecture that learns to differentiate between distinct classes by comparing new data points with existing data points. The term "Siamese" refers to the structure of the network: it contains two or more identical subnetworks with the same architecture and shared weights [16]. The SDLM decides whether the two images given as input are similar or different by training the network. SDLM determines whether the two image data are the same by matching two images given as input, according to the weight parameters. If the approximate values of the weight parameters obtained from the two images produce similar results, the images are identical. Therefore, a threshold value is used in the SDLM [18]. In SDLM, classification is performed by considering the difference between the results obtained from the two neural networks. If this difference is below the threshold value, the images are the same or similar. If it is above the threshold value, the model shows that the results are different. Since each pixel on the image has numerical values, the distance between pixels in the SDLM is usually calculated with Euclidean. The working steps of the Siamese deep learning model can be summarized as follows:

Forward Pass: First, the model processes two inputs simultaneously. Each input x_1 and x_2 is handled by two separate networks (twins of a Siamese network) that share the same weights. This is done with a set of transformation and activation functions represented by weights W. Thus, the outputs are often expressed as $f(x_1;W)$ and $f(x_2;W)$ where the function f is the feature extraction that the model has learned.

Similarity Metric: A similarity metric is then used to measure the similarity between the outputs of the two inputs. One of the most used metrics is the L1 or L2 (Euclidean) distance between two vectors. Euclidean distance is determined by the formula given in Equation 1.

$$D = |f(x_1;W) - f(x_2;W)| \qquad (1)$$

Loss Function: Finally, a loss function is calculated based on the similarity metric. Generally, it is desirable that two inputs belonging to the same class ($y = 1$) have a low distance, and two inputs belonging to different classes ($y = 0$) should have a high distance. An example of this is the Contrastive Loss function. The calculation of the Contrastive Loss function is shown in Equation 2.

$$CL(d,Y) = \frac{1}{2} * Y * d^2 + (1-Y) * \frac{1}{2} * \max(0, m-d)^2 \qquad (2)$$

In the Equation 2, d represents the distance of the outputs. While Y shows the label of the model inputs, m specifies the margin parameter. This loss function encourages to reduce the distance between instances of the same class and to increase the distance between instances of different classes.

The main reason for using SDLM in the study is that the model is effective even with a small number of images [19]. Since monkeypox is a new disease, there are not enough data yet. Existing data are either few or artificially augmented images. Therefore, the low amount of data in general lead to the use of the SDLM in this study. Furthermore, there is a semantic similarity situation in the SDLM. In this model, similar classes or concepts produce weight values close to each other [20]. Contrastive loss is generally used in Siamese networks. In this loss function, all positive images are forced to be close to each other, while all negative images are scattered a certain distance. Moreover, using the same adjustment distance for all images can be restrictive. This causes triplet loss, which requires negative images to be further away from any positive images [21]. The triplet loss function does not use a threshold value to distinguish between similar and different images. Instead, it generates various variance values for different classes. Withal, in triplet loss, positive images and negative images are close to each other. However, the contrastive loss focuses only on positive images. For these reasons, the triplet loss function was used in the study.

Triplet loss is a loss function used when training a SDLM. Triplet loss uses three instances of "triplets": an "anchor" instance, a "positive" instance (belonging to the same class), and a "negative" instance (belonging to a different class). The loss function aims to increase the distance between the anchor and negative samples, while reducing the distance between the anchor and positive samples. The formula for the triplet loss function is given in Equation 3.

$$TL(W) = \max(d(A,P) - d(A,N) + margin, 0) \qquad (3)$$

In Equation 3, $d(A,P)$ is the distance between the anchor and positive samples. The expression $d(A,N)$ represents the distance between the anchor and negative samples. The margin expression is the size of the margin, which is a hyperparameter. This controls the distance between positive and negative samples. If $(d(A,P) - d(A,N)) + margin < 0$, the loss function is set to zero. SDLM was employed in this study and the images were evaluated according to the flowchart given in Fig. 2.

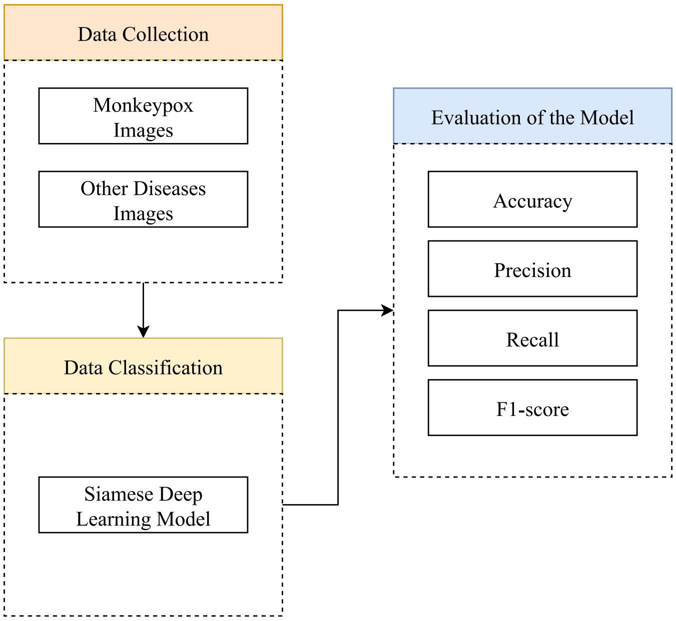

Fig. 2. Flowchart of the study

As can be seen in Fig. 2, the study consists of three stages. In the first stage (**Data Collection**), skin images of monkeypox and other diseases were obtained. Data augmentation was not performed in this study. The images in the dataset are already augmented images. Furthermore, since there are two different class labels, binary classification was made in the study. Then the images were normalized, and the pixel values were ensured to be in the same range. In the second stage (**Classification**), SDLM was designed, and images were classified. In the last stage (**Evaluation of the Model**), the performance of the classifier was determined by accuracy, precision, F1-score, and recall values.

The classification process in the study was carried out in Anaconda, Spyder environment using the Python programming language. The version of the Spyder in the study is 5.4.2. Anaconda is a popular distribution of the Python programming language. It is a platform with a rich ecosystem that includes the Python programming language as well as various data science, machine learning and deep learning tools. Libraries like Pandas, NumPy, and SciPy are used for data manipulation, mathematical calculations, and statistical analysis. Visualization libraries such as Matplotlib and Seaborn allow to visualize data. Deep learning and machine learning libraries such as Scikit-learn, TensorFlow, and PyTorch can be used for a variety of modelling and prediction tasks. The Tensorflow library was used for the classification process and the *Model, Input, Flatten, Dense* of this library were used. Additionally, the Keras library was also employed and the optimization algorithm, loss function and evaluation metrics were also imported from this library. The study was carried out on a Mac computer. The operating system of the computer is Ventura 13.2.1 and consists of 8 GB of RAM. Finally, the Mac computer has the M1 chip. The inclusion of the Apple Neural Engine in the M1 chip significantly enhances the speed and performance of machine learning and deep learning tasks on Mac devices. With its cutting-edge 16-core architecture, the Neural Engine embedded in the M1 chip from Apple empowers Mac devices to execute an impressive 11 trillion operations per second [22]. This remarkable feature results in a staggering 15-fold increase in machine learning and deep learning performance compared to previous generations. The M1 chip is specifically engineered to deliver exceptional performance in machine learning tasks. It incorporates machine learning and deep learning accelerators within the CPU and a high-performance GPU, enabling unparalleled capabilities in areas such as video analysis, voice recognition, and image processing [23]

IV. APPLICATION RESULTS AND DISCUSSION

In this study, SDLM was used and prediction of monkeypox and other diseases was carried out. The parameters of the proposed method were determined as follows:

- The first layer contains the 8 x 8 convolution layer. At the end of these layers, the ReLU (Rectified Linear Unit) activation function is used.
- LRN (Local Response Normalization) has been applied in the second layer and the pixel values in the feature map have been square normalized.
- Pooling was done in the third layer and 4 x 4 maximum pooling was employed.
- In the fourth layer, the convolution layer is used again. The size of this layer was evaluated as 6 x 6. Then the ReLU activation function was used.
- LRN was applied in the fifth layer.
- In the sixth layer, 4 x 4 maximum pooling was utilized.
- In the seventh layer, dropout was made and 15% of the data was forgotten.
- In the eighth and ninth layers, convolutional layers were formed, and the dimensions of these layers were determined as 3 x 3). ReLU was used as the activation function.
- In the tenth layer, 2 x 2 maximum pooling was employed.
- 15% of the data was forgotten by dropout in the 11th layer.
- The fully connected layer is defined in the 12th and 13th layers, and 256 and 128 neurons are defined, respectively.
- Then, the distance between the outputs of the two models was determined by Euclidean and triplet loss was used for the loss of the model.
- The training was carried out with 500 iterations. However, early stop was applied, and the training was terminated when the epoch number reached 100 sine the training accuracy reached %95 accuracy.

The form representation of the parameters of the developed model is given in Fig. 3.

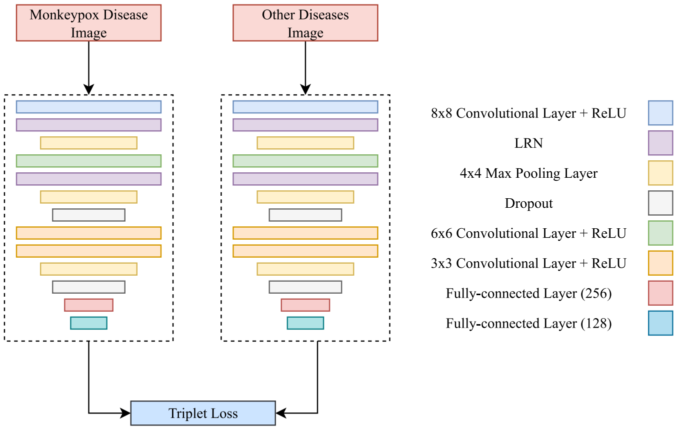

Fig.3. Parameters of the developed model

The performance of the classifier was determined by the accuracy, F1-score, precision and recall values. Classification results were given in Table 1.

TABLE I
CLASSIFICATION RESULTS

Classifier	**Accuracy**	**Precision**	**Recall**	**F1-Score**
SDLM	91.09%	89.03%	93.36%	91.14%

In line with the results obtained from Table I, an accuracy rate of 91.09% was obtained with the SDLM. Further, 89.03% precision and 93.36% recall values were observed with this deep learning model. The F1-score value was 91.14%. The data set used in the study is not a balanced data set. Accuracy score alone is not an adequate evaluation criterion in unbalanced data sets [24]. Therefore, in this study, F1-score evaluation criterion was also applied in addition to the accuracy score. The F1-score is determined by precision and recall values. The higher these values, the higher the F1-score value. The F1-score takes values between 0-1. If the value is close to 1, it indicates that the model has made a good classification. Therefore, looking at the F1-score, SDLM was successful.

The validation loss and the validation accuracy of the model were given in Fig. 4 and Fig. 5, respectively.

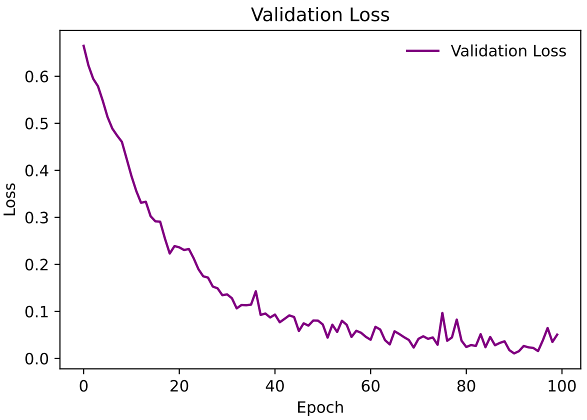

Fig.4. Validation loss of the developed SDLM

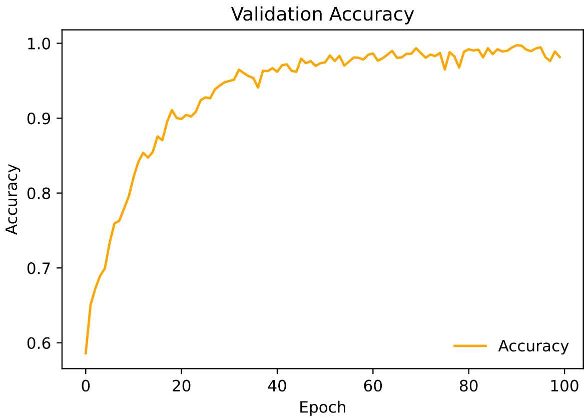

Fig.5. Validation accuracy of the developed SDLM

As seen in Fig. 4 and Fig. 5, the training was terminated when the epoch number reached 100 and the most successful validation accuracy and validation loss were obtained at this epoch value. The confusion matrix was used to show how much of the data were classified correctly and incorrectly in Figure 6.

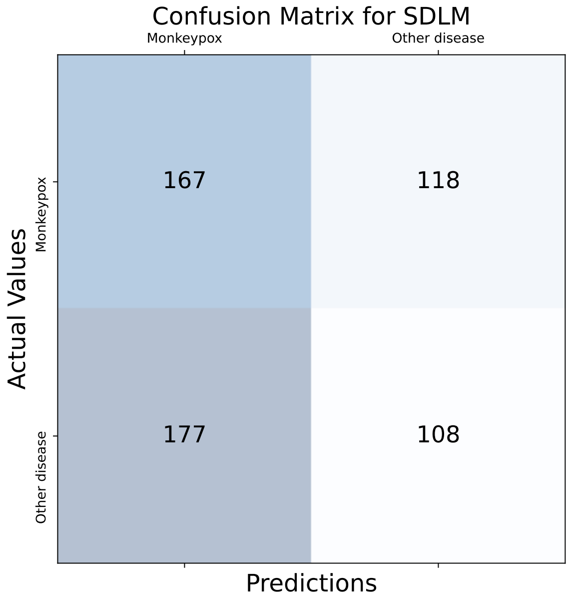

Fig. 6. Confusion matrix of the developed SDLM

The accuracy score of this study was also compared with other studies in the literature using the same dataset. The studies and their results were given in Table 2.

TABLE II
COMPARISON OF STUDIES IN THE LITERATURE (THE HIGHEST ACCURACY SCORES WERE GIVEN AND THE MOST SUCCESSFUL DEEP LEARNING MODEL WAS INCLUDED.

Ref.	Method	Accuracy	Precision	Recall	F1-Score
[11]	Ensemble	82.96%	87.00%	83.00%	84.00%
[12]	Ensemble	87.13%	85.44%	85.47%	85.40%
[13]	VGG16	78.00%	75.00%	75.00%	75.00%
[14]	Transfer learning	91.11%	93.10%	93.35%	93.15%
[15]	Ensemble	98.33%	98.33%	98.33%	98.33%
This study	**SDLM**	**91.09%**	**89.03%**	**93.36%**	**91.14%**

When the results in Table II were examined, it was observed that the SDLM was effective against some models and ineffective against others. The accuracy scores obtained in [14] and [15] were higher than this study. In the study [14], the researchers used transfer learning and obtained features with deep learning models and classified them with machine learning algorithms. This whole process takes time and increases the analysis time. Then again, obtaining features increases the size of the feature vector and causes the data to be complex. Although an accuracy score of 91.11% was obtained despite all this process, feature extraction was not used in this study and the raw data were classified only with SDLM and a result as effective as [14]. In the study [15], the most successful classification process was obtained with the Ensemble method. In that method, three deep learning models were combined (ResNet50+EfficientNetB0+MobileNetV2) and classification was made. Since three different deep learning models were used in that study, defining these models, analyzing each model with images and interpreting the results are time-consuming. However, in this study, only one model was designed, and these processes were carried out and obtained an accuracy of 91.90%. This shows how effective the method is. However, since the same data set was used in the comparison studies, there is an unbalanced data set problem in those studies. Therefore, F1-score was used in those studies and the classification of the model was evaluated. When compared according to the F1-score, the proposed method lagged behind the studies [14] and [15]. When the comparison was made according to the accuracy scores, the results of the proposed method and the study [14] were close to each other, yet when the model was evaluated according to the F1-score, it was observed that the study [14] was more effective. In study [14], transfer learning was applied and the data were not classified with raw images. In the first stage, features were obtained with deep learning models and then classification was made with machine learning algorithms. F1-score may have been more effective because of this procedure. Obtaining its properties may have caused the classification process to be more effective.Although the studies [14] and [15] are more effective than the proposed method, it has been shown that the SDLM method can be more effective than the CNN models. One of the main reasons for this is the low number of images and labels, and the Siamese deep learning model's ability to make an effective classification even with low amount of data [19]. Moreover, triplet loss was used in this study and traditional loss was abandoned. This enabled the model to be better trained despite the low data number. The advantages and disadvantages of the study can be expressed as follows:

- Siamese deep learning model was used in this study instead of traditional feature extraction methods.
- In this study, images were not subjected to any preprocessing and raw images were used directly.
- The proposed method produced high accuracy results from some of the studies performed in the literature.
- The number of data affects the performance of deep learning models. The large number of data will positively affect the performance of this model. However, despite the small number of data, a successful classification process has taken place.
- No feature extraction was performed in this study. Performing various feature extraction or transfer learning can increase the performance of this model.
- More successful methods than the Siamese deep learning model are usually ensemble methods. Similarly, by using an ensemble structure, the classification performance obtained in this study can be increased.
- While the model was being trained, an average of 17 seconds has passed for each iteration. Since the training process was completed in 100 iterations, it took $17 * 100 = 1700$ seconds, approximately 28.3 minutes in total. Although it seems long in terms of total time, the time obtained for 1 iteration is fast enough. Of course, this time varies according to the hardware and software environment used. This issue needs to be tested in more detail and on different hardware.

When the studies in the literature were examined, researchers generally used transfer learning and ensemble. In the transfer learning method, the data load increases, and the data becomes complex. Because in this approach, features are obtained by deep learning models and used for classification. This extends the analysis time. Similarly, multiple models are combined in the ensemble approach. This is a process that prolongs the classification process. In addition, it takes time to find the most suitable combination. However, the SDLM used in this study only and classified raw data. It has performed an effective classification process from most of the studies in the literature.

V. CONCLUSION

The main purpose of this study is to lay the groundwork for the development of an auxiliary model that can be used to differentiate between monkeypox and other skin diseases. For this reason, deep learning, which is used effectively in medical imaging applications, has been applied and classification of monkeypox and other skin diseases has been made. The study consisted of three stages. In the first stage, skin images of monkeypox and other diseases were obtained. In the second stage, the Siamese deep learning model was designed, and the data were classified. In the last stage, the performance of the deep learning model was evaluated. Accordingly, accuracy, precision, recall, and F1-score were used. With the proposed method, 91.09% accuracy was obtained. When compared with other studies in the literature, it was observed that the proposed method was more effective than most studies. In line with the findings obtained in the study, it has been shown that the developed model can help experts. This will facilitate the work of specialists and will provide convenience to physicians when the distinction of blisters on the skin is not made clearly.

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