Journal of Computing Research and Innovation (JCRINN) Vol. 8 No.1 (2023) (pp32-44)
https://jcrinn.com : eISSN: 2600-8793 doi: 10.24191/jcrinn.v8i1.340

Monkeypox and Measles Detection using CNN with VGG-16 Transfer Learning

M Hafidz Ariansyah[1*], Sri Winarno[2], Ramadhan Rakhmat Sani[3]
[1,3] Information System Study Program, Dian Nuswantoro University, Indonesia
[2] Information Technology Study Program, Dian Nuswantoro University, Indonesia

Corresponding author: [*]112201906146@mhs.dinus.ac.id
Received Date: 20 January 2023
Accepted Date: 05 February 2023
Published Date: 01 March 2023

HIGHLIGHTS

- A deep learning-based approach is proposed to be applied in Monkeypox and Measles detection.
- VGG-16 transfer learning for deep learning approaches.
- Deep learning is used to develop classifier models to classify Measles, Monkeypox, and Normal skin.
- Rebuilding the CNN architecture using the VGG-16 transfer learning algorithm.

ABSTRACT

The Monkeypox virus causes the infectious illness monkeypox. This virus is spread by coming into touch with infected animals or humans. Monkeypox is very similar to Measles. The rubeola virus causes measles, a contagious infectious disease. The cause is what distinguishes Monkeypox from Measles sickness. Although they are both carried through the air and generate similar symptoms, Monkeypox and Measles are two separate forms of infectious diseases. Vaccination is the most effective way to prevent Measles, while for Monkeypox, no vaccine can be used to prevent infection. In differentiating Monkeypox and Measles disease, the researcher proposes an image classification to distinguish symptoms between Monkeypox and Measles. Researchers used the deep learning method of image classification with Convolutional Neural Network architecture and VGG-16 transfer learning to do the modeling. Transfer learning is a technique that allows a model which has been trained on a dataset to be used on a different dataset. It allowed the model to adapt knowledge from the original data for use in new data. Researchers propose this method because learning using deep learning is very useful for similar images so that the model can accurately predict new data. The result is that the VGG-16 model can achieve high accuracy with a value of 83.333% at epoch value = 15.

Keywords: *CNN, Deep Learning, Measles, Monkeypox, VGG-16*

INTRODUCTION

While the world is still dealing with the COVID-19 pandemic, public health officials are concerned about a new outbreak caused by the Monkeypox virus (Rizk et al, 2022; Yang, 2022). Monkeypox is an infectious disease caused by the Monkeypox virus. Monkeypox virus is a two-stranded DNA virus that belongs to the orthopoxviruses genus, which also contains variola, cowpox (CPX), and vaccinia viruses (Realegano et al, 2017; Gessain et al, 2022). The Monkeypox virus was first isolated from monkeys, although rope squirrels, tree squirrels, Gambian marsupial rats, and dormice are also natural hosts (Guarner et al, 2022). This virus is spread through contact with infected animals or people.

So far, two strains of the Monkeypox virus have been identified in Africa, with the first being associated with more severe disease (Durski et al, 2018; Kmiek and Kirchhoff, 2022). This virus can also be transferred through direct contact with infectious sores, scabs, bodily fluids, and sharing bedding/clothing. In smallpox-like signs and symptoms, a distinct rash precedes basic prodromal symptoms (fever, lymphadenopathy, and flu-like symptoms) (Rizk et al, 2022). Cases in the present outbreak were uncommon, with a distinct rash that began in the vaginal and perianal areas and extended to other parts of the body (Rizk et al, 2022). When prodromal or rash symptoms appear and remain until the lesions scab and fall off, the patient is considered infectious.

Monkeypox, on the other hand, displays symptoms similar to Measles. Measles is a highly contagious febrile infection that primarily affects youngsters (Di Pietrantonj et al, 2020). It spreads mostly by respiratory droplets and minute particle aerosols and can stay in the air for up to 2 hours. Exposed people who are not immune have a 90% chance of contracting Measles, and each sick person can infect 9 to 18 more people in a vulnerable population (Paules et al, 2019; Huang et al, 2022). Most Measles patients recover completely after roughly a week of sickness, which includes fever, malaise, coryza, conjunctivitis, cough, and a maculopapular rash. Measles, on the other hand, is a devastating disease; before widespread immunization, the virus killed 2 million to 3 million people globally each year (Thornton, 2019). Even today, the virus is the biggest cause of vaccine-preventable sickness and death across the world, killing over 100,000 people each year (Thornton, 2019). Measles-related immunosuppression, diarrhea, keratoconjunctivitis (which can lead to blindness), otitis media, and pneumonia are all common consequences (a primary cause of measles-related death).

Serious and frequently fatal neurologic complications, such as acute disseminated encephalomyelitis and Measles inclusion-body encephalitis, occur in around 1 in 1000 Measles infections, and the majority of those who survive these complications have long-term neurological sequelae (Paules et al, 2019; Zhu et al, 2022). Furthermore, some years after Measles virus infection, a rare neurological complication known as subacute sclerosing panencephalitis (SSPE) can develop, with a severe, progressive, and fatal outcome (Paules et al, 2019; Ramnarayan et al, 2022).

Because of the rash symptoms of Monkeypox and Measles, identification of these diseases is critical at this time. Patients can be treated efficiently with accurate detection, reducing expenses and time spent while increasing the patient's life expectancy to recover from the disease. One technology that can be used to detect rashes caused by Monkeypox and Measles is artificial intelligence. AI will recognize the rash on Monkeypox and Measles and then forecast whether it is Monkeypox or Measles. The deep learning method is used in this paper's learning technique. Deep learning is a machine learning technology that extracts features from data by using a highly sophisticated and layered (deep) artificial neural network. The neural network can be entrained with complex data to perform image recognition. Here, the researcher builds the architecture of the Convolutional Neural Network and implements transfer learning using VGG-16.

According to MA Hasan's (2021) research, image processing methods such as k-means clustering segmentation, VGG-16 feature extraction, and CNN classification can be used to identify grape leaf images. In training, the accuracy is 99.50%, while in testing, it is 97.25%. It demonstrates that this approach performs admirably in image categorization modeling. Based on the findings of Agustina R. et al. (2022), this study was able to create a system that can classify skin cancer using the CNN method and the VGG-16. Skin cancer is classified into four types under the system: melanoma, squamous cell carcinoma, dermatofibroma, and nevus pigments. The system was tested with and without pre-processing, as well as scenarios for four hyperparameters: optimizer, learning rate, epoch, and batch size. The final results with the best performance and accuracy are acquired from the test results without pre-processing using CLAHE and Gaussian filters. The image is resized to 64×64 pixels and uses the SGD optimizer hyperparameter, learning rate 0.001, epoch 50, and batch size 32. Accuracy values obtained are 99.70%, loss 0.0055, precision 0.9975, recall 0.9975, and f1-score 0.9950. The increase in system accuracy values compared to previous studies shows that the VGG-16 architecture has precise and detailed capabilities in recognizing and classifying images.

Previous research has shown that VGG-16 transfer learning is highly good at increasing the performance of deep machine learning. This information urges academics to employ transfer learning as an algorithm to develop models for diagnosing monkeypox and measles. This study intends to simplify time so that patients can save on treatment expenses since the diagnostic goes well, not just for the diagnosis of Monkeypox and Measles. Furthermore, because the model's diagnosis is right, medical professionals can provide the finest care for patients.

METHODOLOGY

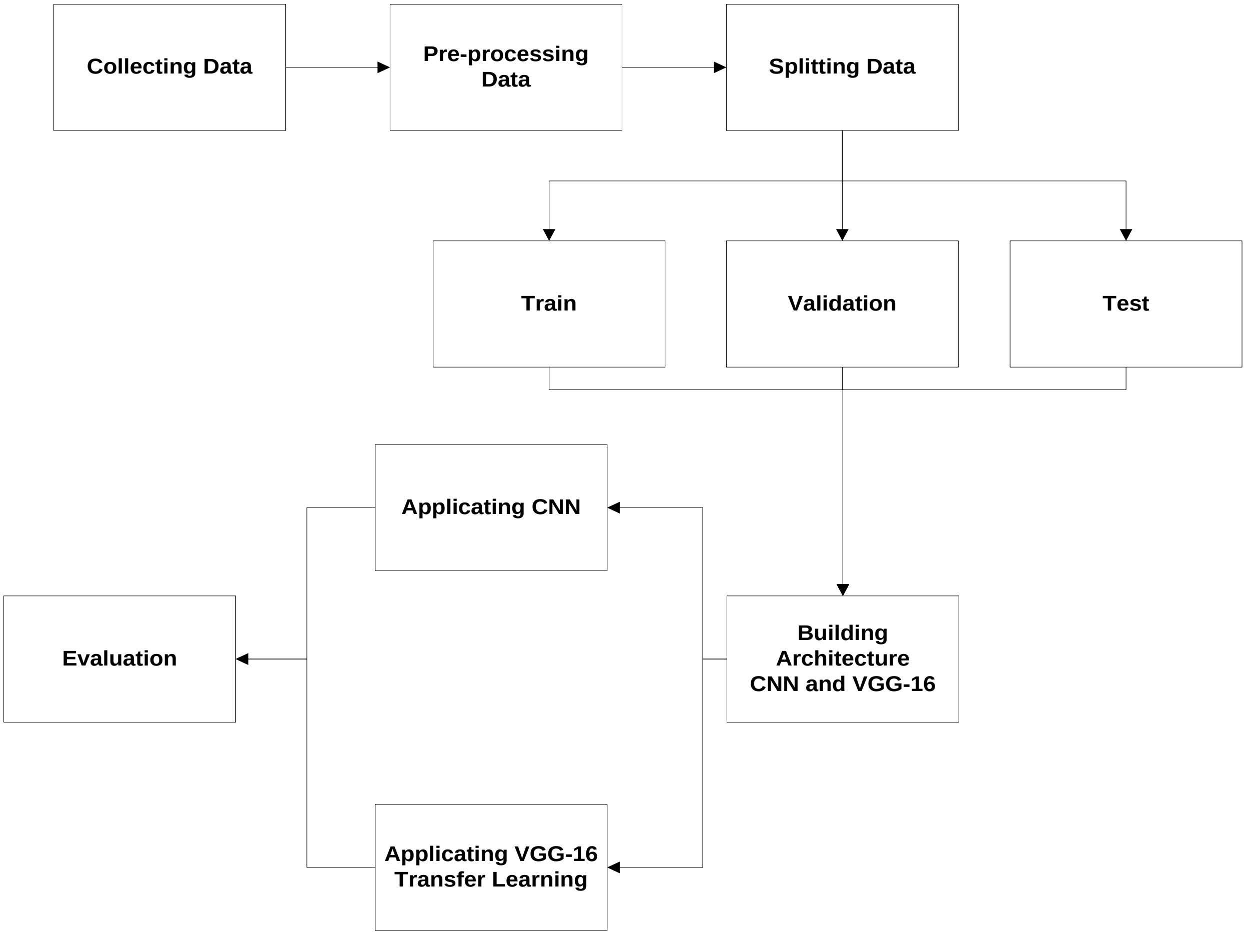

Figure 1: Research Methodology

Based on the diagram in Figure 1, the research will be divided into six steps. The first step begins with the input of skin cancer images that would enter the pre-processing steps. The pre-processing step aims to improve image quality so that it is expected to produce maximum output results. Then, the researchers split the dataset into train, validation, and test data. Then, the researchers built the architecture to train the model. Researchers trained the model using CNN and VGG-16 transfer learning. After training the model, the researcher evaluates the performance and chooses the model with the best accuracy.

Collecting Data

Researchers used deep learning algorithm on a dataset of Monkeypox, Measles, and Normal images from the Kaggle (Diponkor Bala, 2022) repository to observe the best available models. The dataset is a digital image consisting of Monkeypox, Measles, and Normal folders, which are 170 Monkeypox data, 80 Measles data, and 110 Normal data. Each image has a size of 250 x 250. Figure 2 shows an example of Monkeypox data, Figure 3 is Measles, Figure 4 is Normal, and Figure 5 shows the data distribution diagram.

Figure 2: Monkeypox Rash

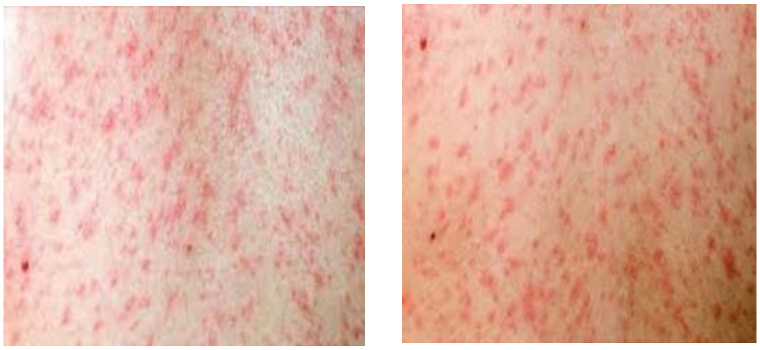

Figure 3: Measles Rash

Figure 4: Normal

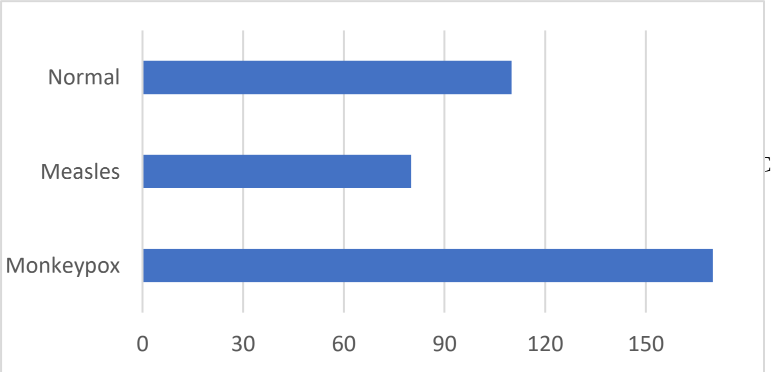

Figure 5: Data Distribution

Pre-processing Data

At the preprocessing stage, dataset augmentation is carried out using the Image Data Generator library from Tensorflow with the following parameters:
1. Rescale = 1/255
2. Random Rotation = 0.1
3. Zoom Range = 0.1

The value of each pixel in the image is scaled to 1/255. After that, the image will be randomly rotated, and then zoomed. The augmentation process will be applied to the training data. The image size is changed to 150 x 150 for each training and testing data so that the image remains clear.

Splitting Data (Train, Validation, and Test)

This split method provides more accurate results for new or untrained data. The test data is not used to train the model, so the model does not know the results of the data. It is called an out-of-sample test. The purpose of building a model is to predict data whose outcome is unknown correctly. A model is said to be good if it is accurate or performs well on out-of-sample data. A clean and ready dataset is split into training, testing, and validation data. Figure 6 shows the amount of train, test, and validation data.

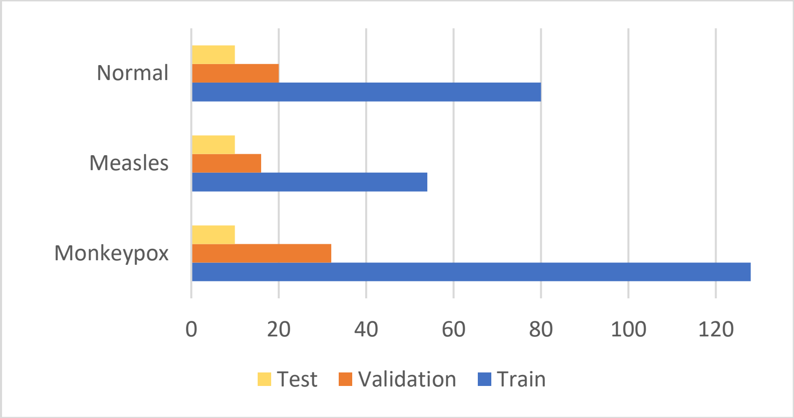

Figure 6: Splitting datasets into train, validation, and test

Convolutional Neural Network (CNN)

Convolutional Neural Network (CNN) is a form of Neural Network used to handle two-dimensional input (Fang et al, 2019; Zhang et al, 2021; Singh et al, 2021). CNN is commonly used to detect and distinguish objects in images. CNN is nearly identical to other Neural Networks. Its architecture is what makes it stand out. CNN has a method for obtaining visual features. The CNN approach is divided into two layers: feature extraction and classification (Gunawan et al, 2021). The input image is routed through the feature extraction layer, which includes the convolutional and the pooling layer. The convolution layer uses filters to be initialized with a particular value (random or using a technique), and it becomes the parameter that will be updated in the learning process. The next part is the pooling layer. The function of this pooling is to reduce the input spatially (reducing the number of parameters) with a down-sampling operation. Researchers used the max pooling method for taking the greatest value from the section. The classification layer also comprises the fully connected and softmax activation layers. Figure 7 shows the CNN Architecture.

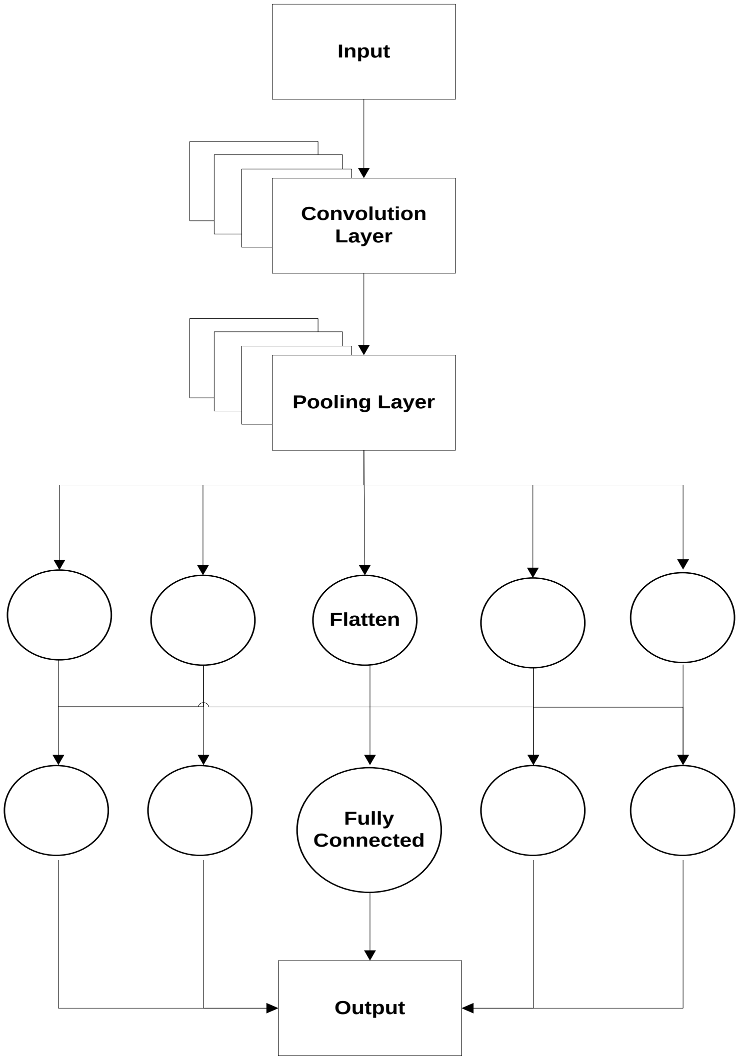

Figure 7: CNN Architecture

VGG-16 Transfer Learning

VGG-16 is a CNN model developed by Karen Simonian and Andreas Zissmann (2014). VGG-16 shows that it is a necessary combination for deep networks to perform well. The VGG-16 architecture has 16 layers which include convolutional layers and FCs. The advantage of this model is that it has a very uniform structure creating only 3x3 arcs and 2x2 layers from start to finish. The downside of VGG16 is that it is difficult to evaluate because it consumes a lot of memory, and the parameters can reach 138M. However, this weakness can be overcome with proper training.

Evaluation Matrix

This research used a confusion matrix to assess the performance of deep-learning models. In this case, the researcher uses accuracy, precision, and recall to evaluate which model is optimal for the categorization. Accuracy is defined as the difference between the exact estimate and the overall estimate (Ariansyah et al, 2023). Precision is defined as the proportion of correct absolute predictions to total positive predictions. The True Positive rate, also known as Recall, is the known fraction of true positive forecasts. The evaluation matrix is shown in Table 1 (Xu et al, 2020).

Table 1: Evaluation Matrix

	Prediction		
Actual Value	Measles	Monkeypox	Normal
Measles	Correct	Incorrect	Incorrect
Monkeypox	Incorrect	Correct	Incorrect
Normal	Incorrect	Incorrect	Correct

FINDINGS AND DISCUSSIONS

Building CNN Architecture and Applicating CNN

First, researchers will build an architecture in the form of feature extraction using a Convolutional Neural Network (CNN) and layers for classification. Then the researcher set the batch size at number 5, where each part of the layer has 5 data, and the epoch has 15 iterations (forward and backward). The total number of training at this stage reached 1,387,843, and the researcher trained all of these parameters. Table 2 shows the parameters and layers of the architecture, and Figure 8 shows the results of the architecture that has been built.

Table 2: CNN Architecture Parameters

Layer (Type)	Output Shape	Param
Sequential (input)	(None, 150, 150, 3)	0
Conv2d	(None, 150, 150, 32)	896
Max_pooling2d	(None, 75, 75, 32)	0
Conv2d_1	(None, 75, 75, 64)	18946
Max_pooling2d_1	(None, 37, 37, 64)	0
Conv2d_2	(None, 37, 37, 64)	36928
Max_pooling2d_2	(None, 18, 18, 64)	0
Dropout	(None, 18, 18, 64)	0
Flatten	(None, 20736)	0

Dense_1	(None, 64)	1327168
Dense_2	(None, 64)	4160
Dense_3	(None, 3)	195

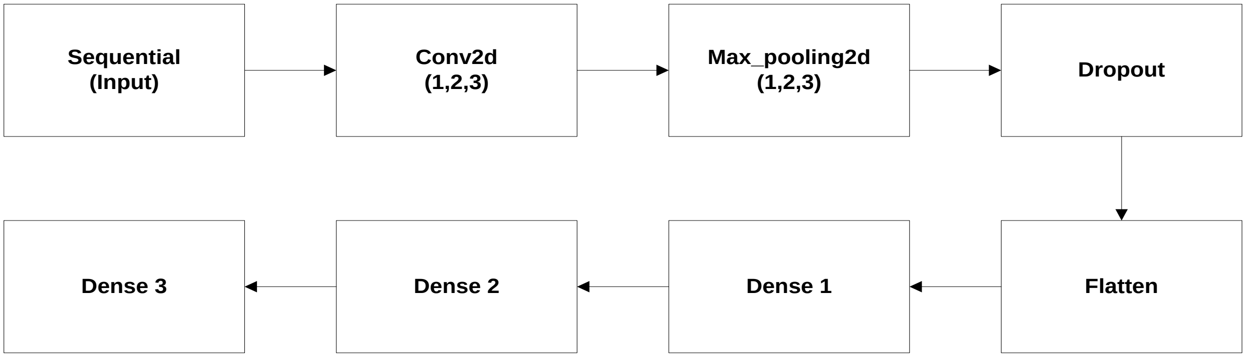

Figure 8: Proposed CNN Architecture

Building VGG-16 Architecture and Applicating VGG-16

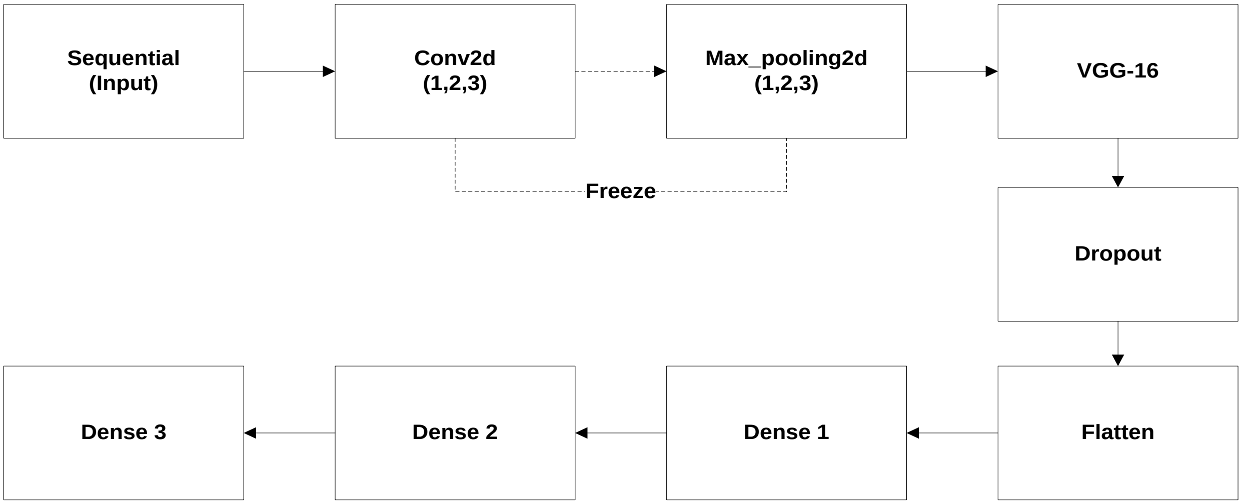

Figure 9: Proposed VGG-16 Architecture

At this stage, the researcher rebuilds the architecture using the VGG-16 model shown in Figure 9. The researchers froze the CNN layer and adds the VGG-16 model to the training process. The parameters used in this model are quite a lot, reaching 15,243,395, but the researchers set base_vgg_model.trainable = false so that the model is more efficient in the training process. Only 528,707 parameters are used in this training. Table 3 shows the parameters of VGG-16 in this study.

Table 3: VGG-16 Architecture Parameters

Layer (Type)	Output Shape	Param
Sequential (input)	(None, 150, 150, 3)	0
VGG-16	(None, 4, 4, 512)	14714688 (Non-trained)
Dropout	(None, 4, 4, 512)	0
Flatten	(None, 8192)	0
Dense_1	(None, 64)	524352
Dense_2	(None, 64)	4160
Dense_3	(None, 3)	195

Evaluation

At the evaluation stage, the researchers used the confusion matrix as an evaluator of the performance test data of the classification model. Before evaluating the test data, the researcher conducted a performance check on the accuracy of the training data and validation. Table 4 shows historical accuracy, loss, and times, in the training, and Table 5 shows validation performance for the CNN and VGG-16 models. Researchers use loss because, in deep learning, the loss is the value that the neural network tries to minimize. The neural network learns by adjusting the weights and biases in a way that reduces loss to minimize this distance.

Table 4: Evaluate Model Training Performance

Epochs	Accuracy CNN	Accuracy VGG-16	Loss CNN	Loss VGG-16	Time CNN	Time VGG-16
1	0.4735	0.5265	1.0814	0.9995	33 s	79 s
2	0.5303	0.7386	0.9927	0.6388	15 s	77 s
3	0.6212	0.7652	0.8516	0.5571	13 s	75 s
4	0.6553	0.7803	0.8255	0.5818	13 s	78 s
5	0.6477	0.7917	0.8273	0.4953	13 s	75 s
6	0.7197	0.8295	0.6780	0.4336	14 s	77 s
7	0.6780	0.8068	0.7048	0.4803	13 s	75 s
8	0.7462	0.8295	0.6517	0.4033	13 s	77 s
9	0.7273	0.8144	0.6751	0.4790	13 s	78 s
10	0.7273	0.8636	0.6491	0.3611	13 s	76 s
11	0.7614	0.8598	0.6147	0.3241	13 s	77 s
12	0.7386	0.8788	0.6256	0.3211	15 s	78 s
13	0.7500	0.8333	0.6525	0.3868	13 s	75 s
14	0.7689	0.8636	0.5860	0.3222	13 s	78 s
15	0.7689	0.9053	0.6016	0.2320	13 s	76 s

Table 5: Evaluate Model Validation Performance

Epochs	Accuracy CNN	Accuracy VGG-16	Loss CNN	Loss VGG-16
1	0.4848	0.6667	1.0418	0.8057
2	0.6515	0.6818	0.9023	0.7311
3	0.6818	0.6818	0.8357	0.7560

4	0.5909	0.7576	0.8366	0.6472
5	0.5606	0.7576	0.9020	0.6722
6	0.5303	0.6364	0.9989	0.9331
7	0.6818	0.7273	0.8023	0.5909
8	0.5909	0.7576	0.8162	0.7892
9	0.6364	0.6667	0.8046	0.9152
10	0.6515	0.8030	0.7983	0.7548
11	0.6364	0.7727	0.8864	0.6684
12	0.6364	0.8030	0.8186	0.6090
13	0.6212	0.8030	0.7878	0.5368
14	0.6667	0.7879	0.8339	0.6118
15	0.6212	0.7727	0.8466	0.5961

In the training evaluation, the VGG-16 model is superior to the CNN model. That's because the VGG-16 model has higher accuracy and lower loss. To maximize this research, researchers evaluate the test data to find the best model using the confusion matrix. Tables 6 and 7 show the evaluation of the test data using the confusion matrix on the CNN and VGG-16 models.

Table 6: CNN Confusion Matrix

Actual Values	**Measle**	**4**	**4**	**3**
	Monkeypox	0	8	2
	Normal	1	1	8
		Measle	Monkeypox	Normal
	Predicted Values			

Table 7: VGG-16 Confusion Matrix

Actual Values	**Measle**	**6**	**3**	**1**
	Monkeypox	0	10	0
	Normal	1	0	9
		Measle	Monkeypox	Normal
	Predicted Values			

For comparison purposes, from Tables 6 and 7, the researcher converted the confusion matrix into a value form for testing accuracy, precision, and recall. Figure 10 shows a comparison of the test accuracy, precision, and recall of the two models.

Figure 10: Test Performance Comparison

CONCLUSION AND RECOMMENDATIONS

From the results, the researchers concluded that the VGG-16 method was better at classifying Measles and Monkeypox disease than CNN. Even though VGG-16 provides quite a long processing time compared to CNN but VGG-16 has the best performance. It is evidenced by the high accuracy of training, low loss in the model, and high accuracy of testing reached a value of 83.33%. In addition, the precision and recall values of the VGG-16 model reached 84.21% and 83.33%. Suggestions for further research are to try the Voting Classifier algorithm on this dataset model to improve the performance of the best model from the majority vote. Researchers hope that the model can facilitate the diagnosis, treatment, and monitoring of the progress of Measles and Monkeypox diseases. The model can also assist in the planning and management of health systems, as well as in research in medicine and epidemiology.

ACKNOWLEDGMENTS

Thank you to Mr. Sri Winarno, Ph.D., and Mr. Ramadhan Rakhmat Sani, M.Kom, who have guided researchers in conducting this research so that it can run smoothly and produce the best results possible. Researchers hope that this research will help advance science in the field of AI and help in the health sector so that the process of diagnosing Monkeypox and Measles can be carried out effectively, quickly, and precisely, thereby increasing the patient's life expectancy.

CONFLICT OF INTEREST DISCLOSURE

All authors state that they have no potential conflicts of interest.

REFERENCES

Agustina, R., Magdalena, R., & Pratiwi, N. K. C. (2022). Klasifikasi Kanker Kulit menggunakan Metode Convolutional Neural Network dengan Arsitektur VGG-16. ELKOMIKA: *Jurnal Teknik Energi Elektrik, Teknik Telekomunikasi, & Teknik Elektronika*, 10(2), pp. 446. https://doi.org/10.26760/elkomika.v10i2.446.

Ariansyah, M. H., Winarno, S., & Salam, A. (2023). STB Sentiment Analysis Classification Multiclass Modeling Using Calibrated Classifier With SGDC Tuning As Basis and Sigmoid Method. International Journal of Computer and Information System (IJCIS), 4(1), pp. 1-7. https://doi.org/10.29040/ijcis.v4i1.107.

Diponkor Bala. (2022). <i>Monkeypox Skin Images Dataset (MSID)</i> [Data set]. Kaggle. https://doi.org/10.34740/KAGGLE/DSV/3971903. [Accessed in 20 December 2022].

Di Pietrantonj, C., Rivetti, A., Marchione, P., Debalini, M. G., & Demicheli, V. (2020). Vaccines for measles, mumps, rubella, and varicella in children. *Cochrane Database of Systematic Reviews*, (4). https://doi.org/10.1002/14651858.CD004407.pub4

Durski, K. N., McCollum, A. M., Nakazawa, Y., Petersen, B. W., Reynolds, M. G., Briand, S., ... & Khalakdina, A. (2018). Emergence of monkeypox in West Africa and Central Africa, 1970-2017/Emergence de l'orthopoxvirose simienne en Afrique de l'Ouest et en Afrique centrale, 1970-2017. *Weekly Epidemiological Record*, 93(11), pp. 125-133.

Fang, B., Li, Y., Zhang, H., & Chan, J. C. W. (2019). Hyperspectral images classification based on dense convolutional networks with spectral-wise attention mechanism. *Remote Sensing*, 11(2), 159. https://doi.org/10.3390/rs11020159.

Gessain, A., Nakoune, E., & Yazdanpanah, Y. (2022). Monkeypox. *New England Journal of Medicine*, 387(19), pp. 1783-1793.

Guarner, J., Del Rio, C., & Malani, P. N. (2022). Monkeypox in 2022—what clinicians need to know. *JAMA*, 328(2), pp. 139-140. https://doi.org/10.1001/jama.2022.10802.

Gunawan, R. J., Irawan, B., & Setianingsih, C. (2021). Pengenalan Ekspresi Wajah Berbasis Convolutional Neural Network Dengan Model Arsitektur Vgg16. *eProceedings of Engineering*, 8(5). https://doi.org/10.34818/eoe.v8i5.16400.

Hasan, M. A., Riyanto, Y., & Riana, D. (2021). Klasifikasi penyakit citra daun anggur menggunakan model CNN-VGG16. *Jurnal Teknologi dan Sistem Komputer*, 9(4), pp. 218-223. 10.14710/jtsiskom.2021.14013.

Huang, Y., Mu, L., & Wang, W. (2022). Monkeypox: epidemiology, pathogenesis, treatment and prevention. *Signal Transduction and Targeted Therapy*, 7(1), pp. 1-22.

Khamparia, A., Singh, A., Luhach, A. K., Pandey, B., & Pandey, D. K. (2020). Classification and identification of primitive Kharif crops using supervised deep convolutional networks. *Sustainable Computing: Informatics and Systems*, 28, p. 100340. https://doi.org/10.1016/j.suscom.2019.07.003.

Kmiec, D., & Kirchhoff, F. (2022). Monkeypox: a new threat?. *International journal of molecular sciences*, 23(14), p. 7866.

Paules, C. I., Marston, H. D., & Fauci, A. S. (2019). Measles in 2019—going backward. New England *Journal of Medicine*, 380(23), pp. 2185-2187.

Ramnarayan, P., Mitting, R., Whittaker, E., Marcolin, M., O'Regan, C., Sinha, R., ... & Rampling, T. (2022). Neonatal monkeypox virus infection. *New England Journal Medicine*, 387, pp. 1618-1620.

Rizk, J. G., Lippi, G., Henry, B. M., Forthal, D. N., & Rizk, Y. (2022). Prevention and treatment of monkeypox. *Drugs*, pp. 1-7. https://doi.org/10.1007/s40265-022-01742-y.

Realegeno, S., Puschnik, A. S., Kumar, A., Goldsmith, C., Burgado, J., Sambhara, S., ... & Satheshkumar, P. S. (2017). Monkeypox virus host factor screen using haploid cells identifies essential role of GARP complex in extracellular virus formation. *Journal of Virology*, 91(11), pp. e00011-17. https://doi.org/10.1128/jvi.00011-17.

Simonyan, K., & Zisserman, A. (2014). Very deep convolutional networks for large-scale image recognition. *arXiv*, preprint arXiv:1409.1556.

Singh, D., Kumar, V., & Kaur, M. (2021). Densely connected convolutional networks-based COVID-19 screening model. *Applied Intelligence*, 51(5), pp. 3044-3051. https://doi.org/10.1007/s10489-020-02149-6.

Thornton, J. (2019). Measles cases in Europe tripled from 2017 to 2018. *BMJ*. 364(634). https://doi.org/10.1136/bmj.l634.

Xu, J., Zhang, Y., & Miao, D. (2020). Three-way confusion matrix for classification: A measure driven view. Information sciences, 507, pp. 772-794. https://doi.org/10.1016/j.ins.2019.06.064.J.

Yang, Z. (2022). Monkeypox: a potential global threat?. *Journal of Medical Virology*. https://doi.org/10.1002/jmv.27884.

Zhang, Y. D., Satapathy, S. C., Guttery, D. S., Górriz, J. M., & Wang, S. H. (2021). Improved breast cancer classification through combining graph convolutional network and convolutional neural network. *Information Processing & Management*, 58(2), p. 102439. https://doi.org/10.1016/j.ipm.2020.102439.

Zhu, M., Ji, J., Shi, D., Lu, X., Wang, B., Wu, N., ... & Li, L. (2022). Unusual global outbreak of monkeypox: what should we do?. *Frontiers of medicine*, 16(4), pp. 507-517.