Transfer learning: classifying balanced and imbalanced fungus images using inceptionV3

Muhamad Rodhi Supriyadi, Muhammad Reza Alfin, Aulia Haritsuddin Karisma, Bayu Rizky Maulana, Josua Geovani Pinem
Research Center for Artificial Intelligence and Cyber Security, BRIN, South Tangerang, Indonesia

Article Info

Article history:

Received Oct 10, 2023
Revised Feb 1, 2024
Accepted Feb 15, 2024

Keywords:

Balanced dataset
Fungus
Image classification
Imbalanced dataset
InceptionV3
Transfer learning

ABSTRACT

Identifying the genus of fungi is known to facilitate the discovery of new medicinal compounds. Currently, the isolation and identification process is predominantly conducted in the laboratory using molecular samples. However, mastering this process requires specific skills, making it a challenging task. Apart from that, the rapid and highly accurate identification of fungus microbes remains a persistent challenge. Here, we employ a deep learning technique to classify fungus images for both balanced and imbalanced datasets. This research used transfer learning to classify fungus from the genera Aspergillus, Cladosporium, and Fusarium using InceptionV3 model. Two experiments were run using the balanced dataset and the imbalanced dataset, respectively. Thorough experiments were conducted and model effectiveness was evaluated with standard metrics such as accuracy, precision, recall, and F1 score. Using the trendline of deviation knew the optimum result of the epoch in each experimental model. The evaluation results show that both experiments have good accuracy, precision, recall, and F1 score. A range of epochs in the accuracy and loss trendline curve can be found through the experiment with the balanced, even though the imbalanced dataset experiment could not. However, the validation results are still quite accurate even close to the balanced dataset accuracy.

Corresponding Author:

Muhamad Rodhi Supriyadi
Artificial Intelligence and Cyber Security Research Center, National Research and Innovation Agency (BRIN)
St. Puspiptek, South Tangerang, Indonesia
Email: muha242@brin.go.id

1. INTRODUCTION

Fungus is one of many microorganisms with high biodiversity characteristics that play a crucial role in varying aspects of human life. Its various benefits include diverse sectors ranging from medicinal, and pharmaceutical, to the food industry. For instance, the Aspergillus genus is known to be useful in fabricating natural products in the form of bioactive compounds [1] and becomes one of the main sources of microbial organic acid production in the global context, namely citric acid [2]. Next, there are also other equally important fungus genera, such as Cladosporium. This indoor and outdoor living genus is known to have versatile potentiality because it can produce compounds such as anticancer, antimicrobial, and antiviral agents [3]. Lastly, the food industry has made extensive use of Fusarium genera as one of the primary sources of mycoprotein-rich foods [4]. Therefore, it is essential to perform a fast, accurate, and energy-efficient visual identification task to differentiate among these specific fungi.

Despite the wide range of benefits of fungi for human needs, the process of rapid and accurate identification of fungus genera remains a challenge to date. Conventionally, the identification of fungus genera can be based on morphological identification of macroscopic and microscopic characteristics [5]. In addition, there is also another method on the molecular level based on rDNA sequence data from the Internal Transcribed Spacer (ITS) region which results in higher accuracy up to the fungus species identification [6]. While the conventional approach is commonly used, it exhibits significant drawbacks, including the prerequisites for specialized skills in the manual classification of fungus images. Furthermore, the manual classification of fungus images is time-consuming, spanning multiple days to complete particularly when dealing with microbes in large numbers. The process of identifying microbes based on morphology, which involves microscopic observation which is simple and fast. Yet, the high variability in the morphological characteristics of microbes can increases the difficulty of the identification process, necessitating the involvement of seasoned experts with specialized knowledge about various fungal forms. For the reasons stated above a novel and reliable approach are needed to identify fungus based on their morphological characteristics. Rather than replacing the entire process of microbial identification, the primary goal of our experiment ought to be aiding microbiologists in the future discovery of new species of microfungus.

Until now, researchers have put their effort into improving the performance of fungus classification. A widely employed strategy for overcoming this challenge involves using artificial intelligence technology. The artificial intelligence approach has been proven to provide benefits in terms of time efficiency, and cost-effectiveness, and does not require specialized training skills, making it intuitively accessible even to non-experts. Several artificial intelligence techniques are known for their capability in assisting the process of identifying microorganisms so that they can assist in the recognition of object images of microorganisms. In previous studies, feature extraction of fungus-based images has been carried out through classical machine learning methods [7] and deep learning methods [8], [9].

Wu *et al*. [7] used the Adaptive Robust Binary Pattern (ARBP) method to detect hyphae in fungal keratitis images. With an accuracy of 99.74%, it could accurately differentiate aberrant corneal pictures from normal corneal images. Using data augmentation and picture fusion, Liu *et al.* [9] described that the AlexNet framework provides a perfect trade-off between the diagnostic performance and the computational complexity, with a diagnostic accuracy of 99.95%. The aforementioned studies were mostly done on a visual classification task utilizing traditional machine learning methods resulting in decent testing accuracy results. Some of the previous works only conducted on a single fungi species which exhibits a comparatively lower variance value in contrast to the multi-class classification task. Whereas, in this study, a classification procedure has been done on three class fungi genera.

In this paper, we implemented one of the deep learning techniques namely InceptionV3 architecture because it produces greater performance on image classification tasks and better use of processing resources [10]. To improve the studies, this study also analyzed the epochs used during the training and validation phases of the model with two types of data: balanced and imbalanced. This was done to determine the computational efficiency and convergence behavior, enabling us to optimize the training process. As a result, the performance of the two model based on different data types was assessed based on their epoch analysis. Thus, this study proposes a novel method that utilizes deep learning to assist in the morphological identification of microfungi. Additionally, it includes a performance analysis to evaluate the epochs used for training the model, aiming to improve the model's time and computational efficiency.

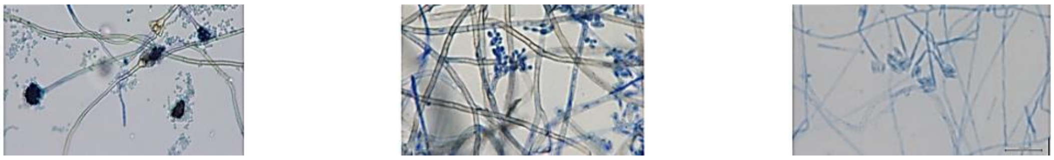
2. METHOD

One of the cutting-edge and well-liked technologies for classification is deep learning, a technology that sets trends and can provide creative solutions for future projects [11], [12]. It is capable of categorization using pictures or videos. It is a type of machine learning that uses neural networks. It contains numerous hidden layers with the capacity to automatically pick up on data representations or properties [13]. Deep learning's benefit is its capacity for learning transfer [14], [15]. Transfer learning is reusing a model that has already been trained for a new job that often has a smaller and limited dataset [16], [17] or it seeks to adapt previously learned knowledge to new knowledge by using current models [18]. Transfer learning's primary goal is to improve target learners' performances by utilizing information from related but unrelated source domains.

The pre-trained model has learned to extract pertinent spatial characteristics or representations from the input data after being trained on a sizable dataset. These learned features then be used as an initial point for a new model that is trained on a smaller and limited dataset. This strategy can improve the new target model's accuracy and effectiveness since it focuses on learning the specifics of the new task without requiring the model to be trained from scratch [19]. In this study, the InceptionV3 network is the model of choice for Transfer Learning. The pre-trained model, which was previously trained using the ImageNet dataset, is provided by the Keras framework.

2.1. Data preparation

To complete this research, data must be collected using three different methods: interviews, observation, and literature review. The information utilized is a set of three genera's worth of fungal microscopic image data from the Research Organization for Life Sciences and Environment, BRIN. A sample of the dataset's microscopic photos of fungi is shown in Figures 1(a)-(c).



(a) (b) (c)

Figure 1. A fungal microscope image from the dataset: (a) Aspergillus, (b) Cladosporium, and (c) Fusarium

The image data used consists of balanced data and imbalanced data. The total of balanced fungus images is 510 images and each genus has 170 data. While the total of imbalance fungus images is 732 images. Aspergillus has 372 images, Cladosporium has 180 images, and Fusarium has 180 images. Additionally, the images are enlarged to 300x300 pixels, improved with the following settings: rescale 1/255, the rotation range 30, and validation split 0.1, then the dataset is separated into two categories: training data and testing data, which are shown in Tables 1 and 2, respectively.

Table 1. First dataset (balanced dataset)

Genus	Training Data	Testing Data	Total Data
Aspergillus	150	20	170
Cladosporium	150	20	170
Fusarium	150	20	170

Table 2. Second dataset (imbalanced dataset)

Genus	Training Data	Testing Data	Total Data
Aspergillus	352	20	372
Cladosporium	170	20	190
Fusarium	166	20	186

2.2. Modeling

This study will be built using InceptionV3. It is a deep neural network architecture commonly used for image analysis and object detection tasks that was originally developed by Google in 2015 as a module for GoogLeNet [20], [21]. It is the third variant of the original Inception Convolutional Neural Network that was first proposed in 2014. This model comprises 48 layers of deep networks, but it divides huge convolution into a smaller grid and uses multiple-size filters along with it [22]. This Architecture was built to improve the accuracy and computational efficiency of image classification tasks, specifically in large-scale visual recognition challenges. The ImageNet Large Scale Visual Recognition Challenge (ILSVRC) dataset, which includes 1.2 million photos from 1,000 distinct item categories, achieved state-of-the-art performance in 2015. In terms of the error rate of the image classification task, InceptionV3 achieved a top-5 error rate of 3.46%, which was more excellent than the previous BN-Inception state-of-the-art architecture of 4.9% accuracy. An architectural illustration of InceptionV3 can be seen in Figure 2. InceptionV3 was trained in the study with the sequential model and has some parameters. Parameters of the sequential model used during training can be seen in Table 3.

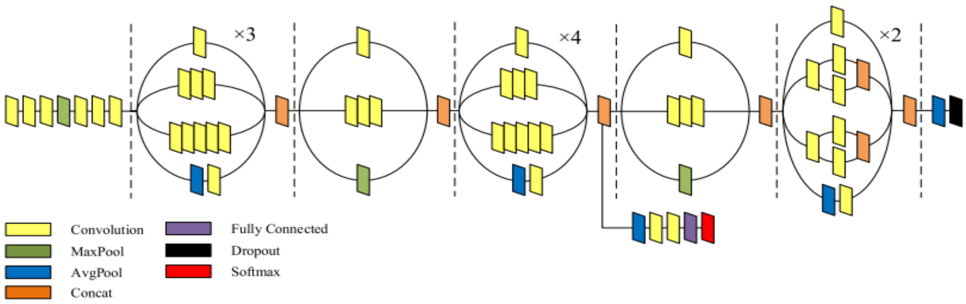


Figure 2. Illustration of InceptionV3 architecture [23]

Table 3. Parameters of the sequential model training

Parameters	Type/Value
Optimizer	Adam
Epoch	150
Batch size	32
Activations	Softmax
Dropout	0.15

2.3. Evaluation

The evaluation stage requires the classification model performance and the trendline of deviation method for data analysis. The trendline of deviation method is used for data analysis to give the range optimum epoch position. While, the model's performance should be evaluated in terms of accuracy, precision, recall, and F1 score. These metrics, which include true positive (TP), true negative (TN), false positive (FP), and false negative (FN), are created using information from the confusion matrix based on (1)–(4) [24]. TP stands for the number of true positive predictions, TN for true negative predictions, FP for false positive predictions, and FN for false negative predictions [25], [26].

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

$$Precision\ = \frac{TP}{TP+FP} \tag{2}$$

$$Recall\ = \frac{TP}{TP+FN} \tag{3}$$

$$F1\ Score\ = 2 \text{ x } \frac{recall\ x\ precision}{call\ +precision} \tag{4}$$

3. RESULTS AND DISCUSSION

The result of each training process is the model to be used during testing. Each model is then used in the testing stage to see each performance. Testing is done using each of the 20 images for each genus class. Based on the confusion matrix generated in testing using the first model. The first model is generated by the training process using balanced data, namely 150 training images for each class. There is no tendency for data to enter certain classes to be greater than in other classes. The performance of the first model shows that the highest precision is obtained by the Cladosporium and Fusarium class, which is 0.85, meaning that Cladosporium and Fusarium get the highest level of accuracy in making identification, while Aspergillus gets a Precision value of 0.80 which is the lowest value compared to other classes, which means that Aspergillus gets the lowest level of accuracy in making identification correctly.

Aspergillus got the highest recall value, which was 1, meaning that the success rate of the model in re-finding the Aspergillus class was high compared to other classes, such as the Cladosporium class, which only got a recall value of 0.74. Tables 4 and 5 show the confusion matrix and the results of the first experiment, respectively.

Table 4. The confusion matrix of 1st experiment

Class	Aspergillus	Cladosporium	Fusarium
Aspergillus	16	3	1
Cladosporium	0	17	3
Fusarium	0	3	17

Table 5. The performance of 1st experiment

Class	Precision	Recall	Accuracy	F1 Score
Aspergillus	0.80	1	0.80	0.89
Cladosporium	0.85	0.74	0.85	0.79
Fusarium	0.85	0.81	0.85	0.83

Furthermore, training is carried out using the second model. The second model is generated by the training process using imbalanced data for each class. Data testing each uses 20 images per class. The resulting confusion matrix shows that the Aspergillus class obtained the highest precision with a value of 0.95, while the class with the lowest precision was obtained by Cladosporium and Fusarium, which was 0.80. The Aspergillus class obtained the highest recall value, with a value of 0.95, while the Cladosporium class obtained the lowest recall, with a value of 0.76. Tables 6 and 7 show the confusion matrix and the results of the second experiment, respectively.

Table 6. The confusion matrix of 2nd experiment

Class	Aspergillus	Cladosporium	Fusarium
Aspergillus	19	1	0
Cladosporium	1	16	3
Fusarium	0	4	16

Table 7. The performance of 2nd experiment

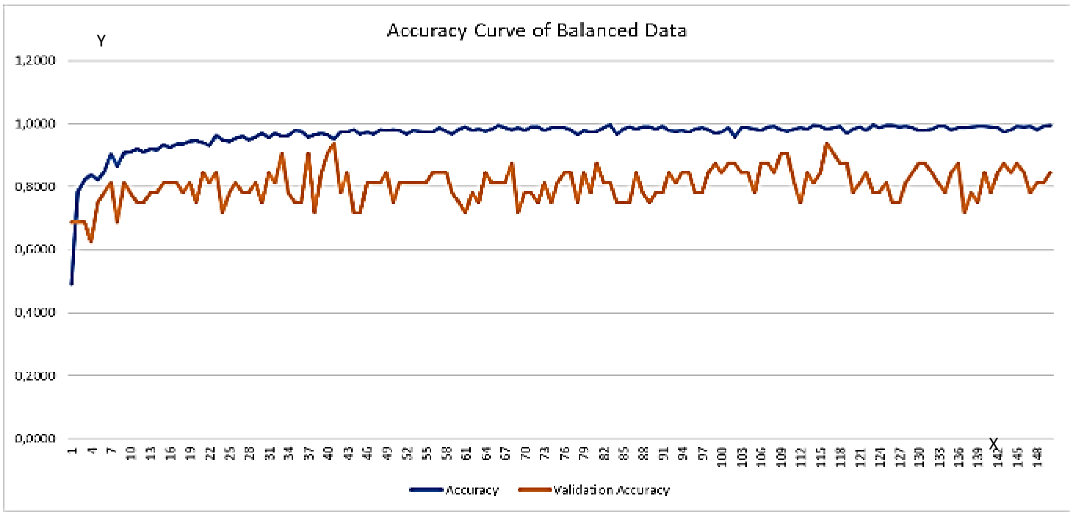
Class	Precision	Recall	Accuracy	F1 Score
Aspergillus	0.95	0.95	0.95	0.95
Cladosporium	0.80	0.76	0.80	0.78
Fusarium	0.80	0.84	0.80	0.82

The evaluation metrics results for the two experiments are shown in Table 8. It shows that the balanced dataset has precision, recall, accuracy, and F1 score of 0.83, 0.85, 0.83, and 0.84 respectively. While the imbalanced dataset has precision, recall, accuracy, and F1 score of 0.85 respectively.

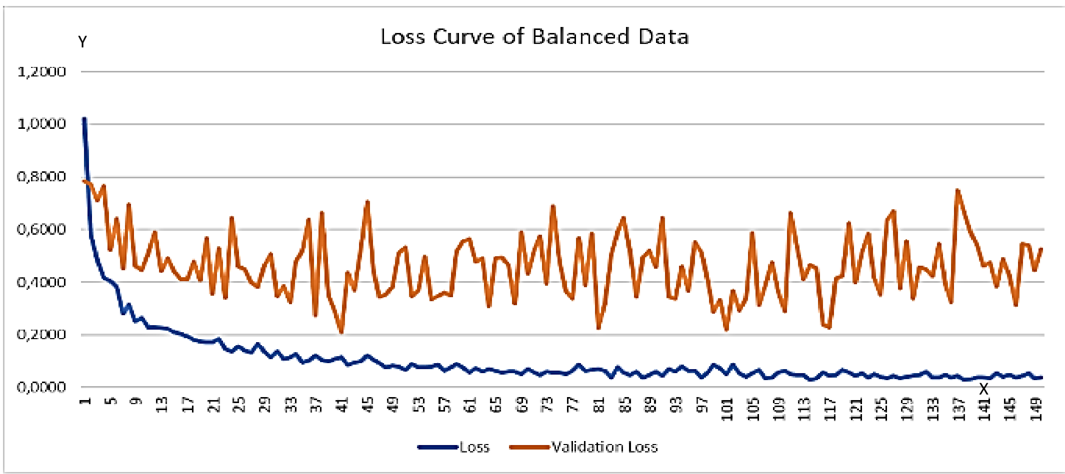
Table 8. Evaluation metrics for the fungus classifier's trained InceptionV3 model

InceptionV3Model with	Precision	Recall	Accuracy	F1 Score
Balanced Data	0.83	0.85	0.83	0.84
Imbalanced Data	0.85	0.85	0.85	0.85

However, we do not know whether the epoch used is sufficient or not. And then, we analyzed the accuracy and loss curves for each model. Figure 3 shows the curves of balanced data with accuracy in Figure 3(a) and loss in Figure 3(b). While Figure 4 shows the curves of imbalanced data with accuracy in Figure 4(a) and loss in Figure 4(b).

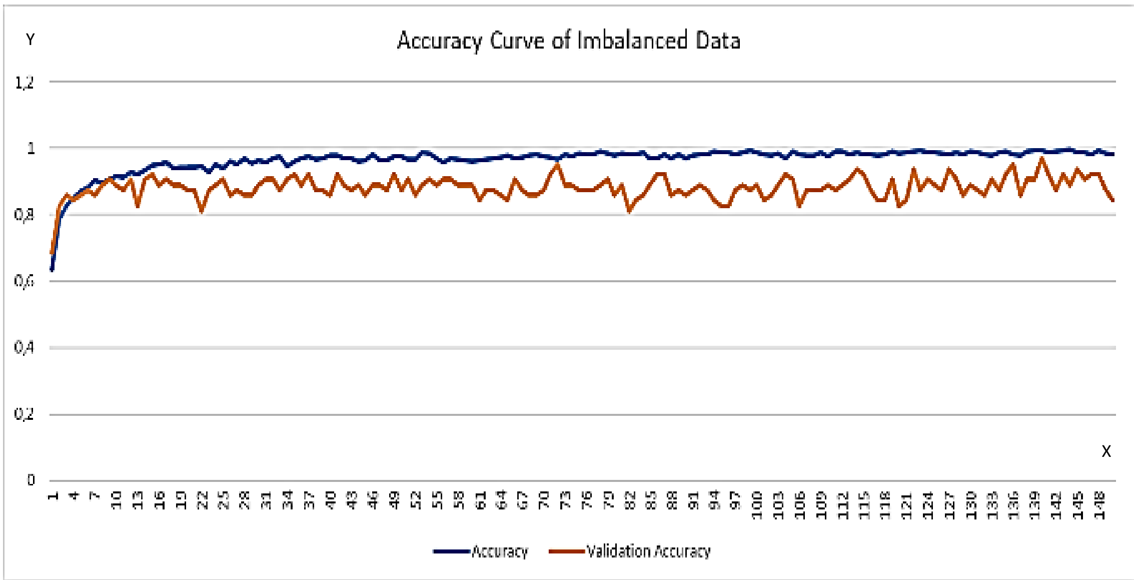


(a)

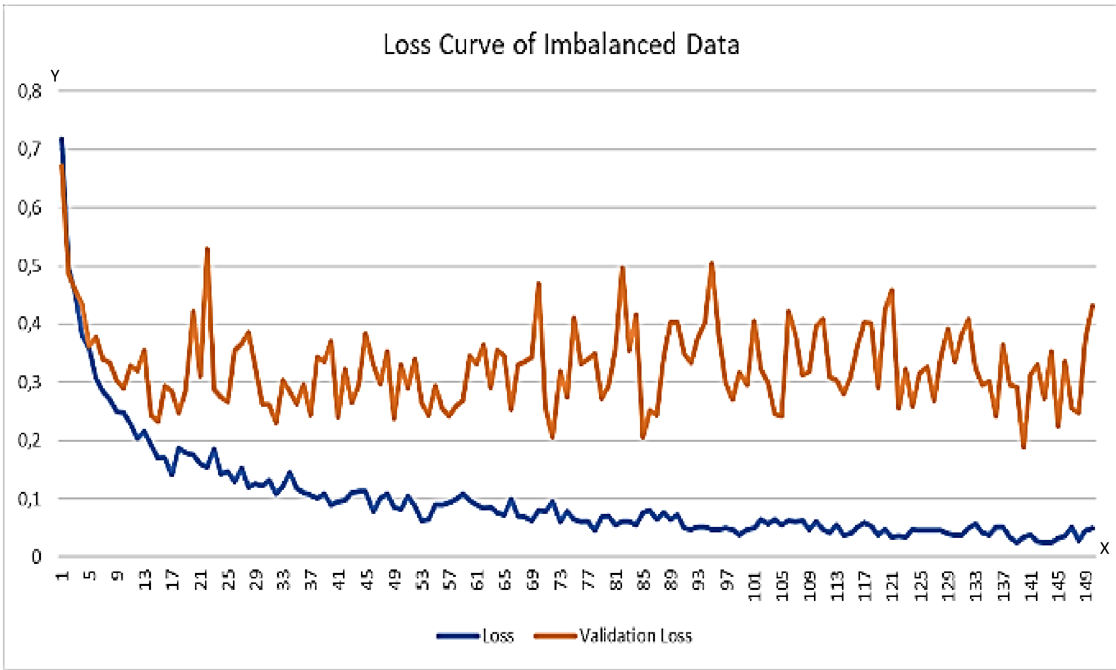


(b)

Figure 3. Accuracy (a) and loss (b) curve of balanced data



(a)

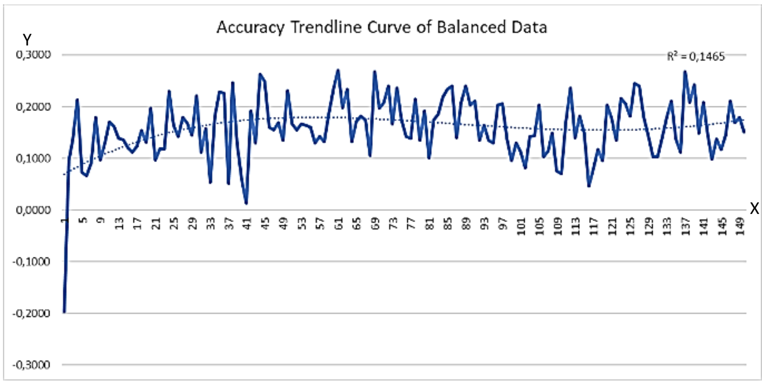


(b)

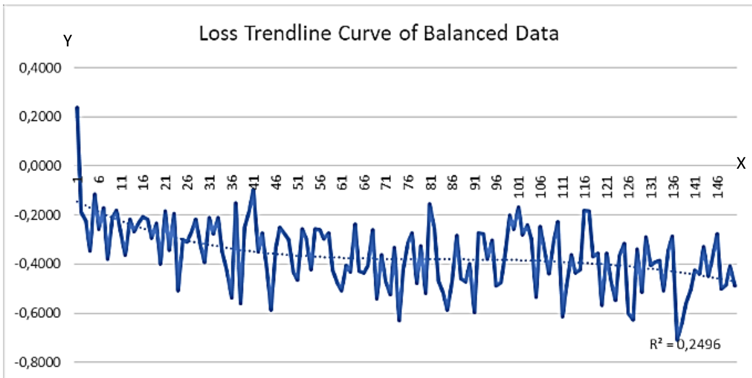
Figure 4. Accuracy (a) and loss (b) curve of imbalanced data

Both models produce curves that tend to be similar. There is a gap between performance during training and validation. The training process was carried out until epoch 150 and then, was carried to the accuracy and loss deviation between training and validation. Furthermore, we made the trendline of accuracy and loss deviation. From the trendline, the value of R^2 is obtained to determine the optimum epoch range for each model. Figure 5 shows the trendline curve of balanced data with an accuracy trendline in Figure 5(a) and a loss trendline in Figure 5(b). While Figure 6 shows the trendline curve of imbalanced data with an accuracy trendline in Figure 6(a) and a loss trendline in Figure 6(b).

The trendline of deviation succeeded in deciding the optimum epoch range for each model. It shows that in the balanced dataset, there is a range of epochs between 106 epochs for the loss trendline curve to 113 epochs for the accuracy trendline curve which gives the optimum results. While accuracy and loss trendline of imbalanced data did not have the end of the curve, so it could not find a range of epochs.

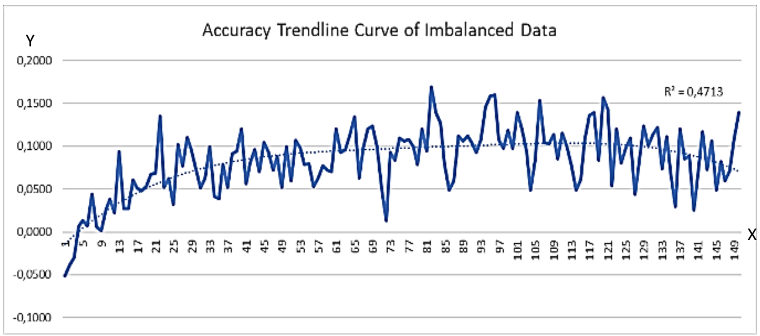


(a)

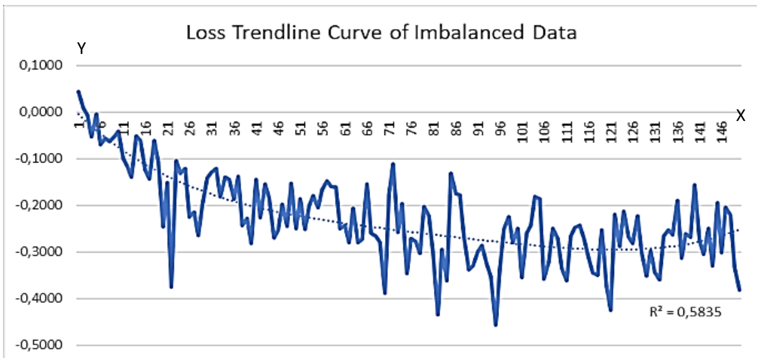


(b)

Figure 5. Accuracy (a) and loss (b) trendline curve of balanced data



(a)



(b)

Figure 6. Accuracy (a) and loss (b) trendline curve of imbalanced data

4. CONCLUSION

A deep learning InceptionV3-based fungus classification model was created in this research. The deep learning method is considered more efficient than using the classic machine learning method. This study established a model for fungus classification of the Aspergillus, Cladosporium, and Fusarium genera. Two models were produced: a model with imbalanced data and a model with balanced data. The results obtained are the balanced dataset has precision, recall, accuracy, and F1 score of 0.83, 0.85, 0.83, and 0.84 respectively. It is capable to find a range of epochs between 106 epochs for the loss trendline curve to 113 epochs for the accuracy trendline curve which gives the optimum results. While the imbalanced dataset has precision, recall, accuracy, and F1 score values of 0.85 respectively. It could not find an epoch range in the accuracy and loss trendline curve, but the validation results are still quite accurate even close to balanced data accuracy. In future studies, added new genus and expand dataset using InceptionV3 architecture for fungus classification. Then, try other deep learning architectures with the same datasets in this paper such as ResNet-50, VGG-16, and DenseNet-201.

ACKNOWLEDGEMENTS

We appreciate the help of the Research Organization for Life Sciences and Environment teams of National Research and Innovation Agency as data collectors, namely Ariza Yandwiputra Besari, Danang Waluyo, Avi Nurul Oktaviani, and Dyah Noor Hidayati. Further, we appreciate the help of the Research Group for Computer Vision teams of BRIN as part of the pre-processing dataset (Raden Putri Ayu Pramesti, Mukti Wibowo, Gilang Mantara Putra, and Umi Chasanah) and technical support (Dewi Habsari Budiarti, Jemie Muliadi, and Anto Satriyo Nugroho).

REFERENCES

[1] J. L. Li, X. Jiang, X. Liu, C. He, Y. Di, S. Lu, H. Huang, B. Linc, D. Wangd, and B. Fan, "Antibacterial Anthraquinone Dimers from Marine-Derived Fungus Aspergillus sp.," *Fitoterapia,* vol. 133, pp. 1-4, 2019, doi: 10.1016/j.fitote.2018.11.015.

[2] B. C. Behera, "Citric Acid from Aspergillus Niger: A Comprehensive Overview," *Critical Reviews in Microbiology,* vol. 6, no. 46, p. 27–49, 2020, doi: 10.1080/1040841X.2020.1828815.

[3] G. A. Mohamed and S. R. M. Ibrahim, "The Untapped Potential of Marine Associated Cladosporium Species: An Overview on Secondary Metabolites, Biotechnological Relevance, and Biological Activities," *Marine Drugs,* vol. 19, p. 645, 2021, doi: 10.3390/md19110645.

[4] E. J. Derbyshire and K. T. Ayoob, "Mycoprotein Nutritional and Health Properties," *Nutrition Today,* vol. 54, pp. 7-15, 2019, doi: 10.1097/NT.0000000000000316.

[5] J. I. Pitt and A. D. Hocking, Fungi and Food Spoilage. 3rd ed., New York: Springe, 2009.

[6] C. L. Schoch, K. A. Seifert, S. Huhndorf, V. Robert, J. L. Spouge, C. A. Levesque, W. Chen, E. Bolchacova, K. Voigt, and P. W. Crous, "Nuclear Ribosomal Internal Transcribed Spacer (ITS) Region as A Universal DNA Barcode Marker for Fungi," *Proc. Natl. Acad. Sci,* vol. 109, p. 6241–6246, 2012, doi: 10.1073/pnas.1117018109.

[7] X. Wu, Q. Qiu, Z. Liu, Y. Zhao, B. Zhang, Y. Zhang, X. Wu, and J. Ren, "Hyphae Detection in Fungal Keratitis Images with An Adaptive Robust Binary Pattern," *IEEE,* vol. 6, p. 13449–13460, 2018, doi: 10.1109/ACCESS.2018.2808941.

[8] H. Ma, J. Yang, X. Chen, X. Jiang, Y. Su, S. Qiao, and G. Zhong, "Deep Convolutional Neural Network: A Novel Approach for The Detection of Aspergillus Fungi via Stereomicroscope," *Journal Microbiol,* vol. 59, p. 563–572, 2021, doi: 10.1007/s12275-021-1013-z.

[9] Z. Liu, Y. Cao, Y. Li, X. Xiao, Q. Qiu, M. Yang, Y. Zhao, and L. Cui, "Automatic Diagnosis of Fungal Keratitis Using Data Augmentation and Image Fusion with The Deep Convolutional Neural Network," *Comput. Methods Programs Biomed,* vol. 187, 2020, doi: 10.1016/j.cmpb.2019.105019.

[10] J. Liu, M. Wang, L. Bao, X. Li, J. Sun, and Y. Ming, "Classification and Recognition of Turtle Images Based on Convolutional Neural Network," *IOP Conf. Series: Materials Science and Engineering,* vol. 782, 2020, doi:10.1088/1757-899X/782/5/052044.

[11] S. H. Ing, A. A. Abdullah, M. Y. Mashor, Z. A. Mohammed-Hussein, Z. Mohamed, and W. C. Anf, "Exploration of Hybrid Deep Learning Algorithms for Covid-19 MRNA Vaccine Degradation Prediction System," *International Journal of Advances in Intelligent Informatics,* vol. 8, no. 3, p. 404, 2022, doi: 10.26555/ijain.v8i3.950.

[12] F. J. P. Montalbo and A. A. Hernandez, "Classifying barako coffee leaf diseases using deep convolutional models," *International Journal of Advances in Intelligent Informatics*, vol. 6, no. 2, pp. 197–209, 2020, doi: 10.26555/ijain.v6i2.495.

[13] T. Badriyah, D. B. Santoso, I. Syarif, and D. R. Syarif, "Improving Stroke Diagnosis Accuracy Using Hyperparameter Optimized Deep Learning," *International Journal of Advances in Intelligent Informatics,* vol. 5, no.3, pp. 256-272, 2019, doi: 10.26555/ijain.v5i3.427.

[14] R. Faurina, A. Wijanarko, A. F. Heryuanti, S. I. Ishak, and I. Agustian, "Comparative Study of Ensemble Deep Learning Models to Determine The Classification of Turtle Species," *Computer Science and Information Technologies,* vol. 4, pp. 24-32, 2023, doi: 10.11591/csit.v4i1.p24-32.

[15] B. P. Gyires-Tóth, M. Osváth, D. Papp, and G. Szucs, "Deep learning for plant classification and content-based image retrieval," *Cybernetics and Information Technologies,* vol. 19, no. 1, pp. 88–100, 2019, doi: 10.2478/CAIT-2019-0005.

[16] X. Li, Y. Grandvalet, F. Davoine, J. Cheng, Y. Cui, H. Zhang, S. Belongie, Y. H. Tsai, and M. H. Yang, "Transfer Learning in Computer Vision Tasks: Remember Where You Come From," *Image Vis. Comput.,* vol. 93, 2020, doi:

10.1016/j.imavis.2019.103853..

[17] J. S. Murugaiyan, M. Palaniappan, T. Durairaj, and V. Muthukumar, "Fish Species Recognition Using Transfer Learning Techniques," *International Journal of Advances in Intelligent Informatics*, vol. 7, no. 2, p. 188, 2021, doi: 10.26555/ijain.v7i2.610.

[18] S. Y. Prasetyo, G. Z. Nabilah, Z. N. Izdihar, and S. M. Isa, "Pneumonia Detection on X-Ray Imaging Using Softmax Output in Multilevel Meta Ensemble Algorithm of Deep Convolutional Neural Network Transfer Learning Models," *International Journal of Advances in Intelligent Informatics,* vol. 9, no. 2, pp. 319-330, 2023, doi: 10.26555/ijain.v9i2.884.

[19] F. Zhuang, Z. Qi, K. Duan, D. Xi, Y. Zhu, H. Zhu, H. Xiong, and Q. He, "A Comprehensive Survey on Transfer Learning," *Proceedings of the IEEE*, vol. 109, no. 1, p. 43–76, 2020, doi: 10.1109/JPROC.2020.3004555.

[20] T. Yampaka, S. Vongganansup, and P. Labcharoenwongs, "Feature Selection Using Regression Mutual Information Deep Convolution Neuron Networks For COVID-19 X-Ray Image Classification," *International Journal of Advances in Intelligent Informatics,* vol. 8, no. 2, pp. 199-209, 2022, doi: 10.26555/ijain.v8i2.809.

[21] C. Szegedy, V. Vanhoucke, S. Ioffe, J. Shlens, and Z. Wojna, "Rethinking The Inception Architecture for Computer Vision," *In Proc. IEEE Computer Society Conference on Computer Vision and Pattern Recognition*, pp. 2818–2826, 2016, doi: 10.1109/CVPR.2016.308.

[22] M. K. Rusia and D. K. Singh, "A Color-Texture-Based Deep Neural Network Technique to Detect Face Spoofing Attacks," *Cybernetics and Information Technologies Journal, vol. 22, no. 3,* vol. 22, no. 3, p. 127–145, 2022, doi: 10.2478/cait-2022-0032.

[23] N. Dong, L. Zhao, C. H. Wu, and J. F. Chang, "Inception V3-Based Cervical Cell Classification Combined with Artificially Extracted Features," *Applied Soft Computing Journal*, vol. 93, pp. 1568-4946, 2020, doi: 10.1016/j.asoc.2020.106311.

[24] Y. Ferdinand and W. F. A. Maki, "Broccoli Leaf Diseases Classification Using Support Vector Machine with Particle Swarm Optimization Based on Feature Selection," *International Journal of Advances in Intelligent Informatics,* vol. 8, no. 3, pp. 337-348, 2022, doi: 10.26555/ijain.v8i3.951.

[25] Ž. Vujović, "Classification Model Evaluation Metrics," *International Journal of Advanced Computer Science and Applications,* vol. 12, p. 599–606, 2021, doi: 10.14569/IJACSA.2021.0120670.

[26] Y. J. Kee, M. N. Shah Zainudin, M. I. Idris, R. H. Ramlee, and M. R. Kamarudin, "Activity recognition on subject independent using machine learning," *Cybernetics and Information Technologies*, vol. 20, no. 3, pp. 64-74, 2020, doi: 10.2478/cait-2020-0028.

BIOGRAPHIES OF AUTHORS

Muhamad Rodhi Supriyadi received the S.Kom. degree in informatics from the department of informatics at the University of Bengkulu, Indonesia, in 2018. Currently, he is working in National Research and Innovation Agency for Artificial Intelligence and Cyber Security Research Center. And He is a Master of Philosophy student, Computer Science in Faculty of Computing, Universiti Teknologi Malaysia. His research interests include image processing, deep learning, computer vision, and artificial intelligence. He can be contacted at email: muha242@brin.go.id.

Muhammad Reza Alfin holds a Bachelor of Engineering (B.Eng) degree in Mechanical Engineering from the University of Indonesia. He is currently working at Research Center for Artificial Intelligence and Cyber Security, part of the National Research and Innovation Agency. His research interests encompass Machine Learning, Deep Learning, and Computer Vision. Email: muha163@brin.go.id.

Aulia Haritsuddin Karisma Muhammad Subekti Graduated from Bachelor Degree in Electrical Engineering Universitas Gadjah Mada. Currently working at Artificial Intelligence and Cyber Security, Indonesia National Research and Innovation Agency (BRIN). Research focuses are in Computer Vision, Deep Learning, and Natural Language Processing. Email: auli008@brin.go.id.

Bayu Rizky Maulana is currently working in National Research and Innovation Agency for Artificial Intelligence and Cyber Security Research Center. He completed his bachelor of Information System from Binus University. Her main research interests focus on Computer vision, Data Mining and Information System. Email: bayu019@brin.go.id.

Josua Geovani Pinem is a full time research engineer at National Research and Innovation Agency Republic of Indonesia. He received his B.Eng in Computer Engineering from University of Indonesia in 2017. His research is concentrated in area of computer vision, knowledge graph and applied deep learning with focus on algorithm optimization. He can be contacted at email: josu001@brin.go.id.