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Automated Classification of Multi-Class Human Protozoan Parasites using Xception as Transfer Learning

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Abstract: Infections caused by protozoan parasites can cause serious health problems. Malaria infection is an infection with the most recorded infection cases in the world as reported by World Health Organizer (WHO) which has reported cases of Malaria infection in 2020 experienced a significant increase from the previous year. There were 241 million global cases, which previously recorded 227 million global cases. Apart from Malaria, there are still many cases caused by other protozoan parasites such as Babesia, Leishmania, Toxoplasma, Trichomonad, and Trypanosome who identified in this study. Therefore, it is necessary to use technology that can help microscopic experts to diagnose in a fast time and with optimal results. Using the Transfer Learning method with Xception architecture can produce optimal accuracy. In the research in this paper, we use four different optimizers including Adam, RMSprop, SGD, and Adadelta as comparisons with each other. Of the four optimizers, the most optimal result in this study is Adam optimizer with an accuracy of 97%. Therefore, the methodology that we use can help classify the types of protozoan parasites which can make the process faster and can reduce costs in the identification process.

Keywords: *Protozoan, Parasites, Transfer Learning, Xception Optimizer*

1. Introduction

Parasites are microorganisms that can impact health problems with a serious infection. By riding in the body tissues of other living things are used as a place to live and the main source of food to sustain life. In medicine, parasites are produced by protozoan organisms, helminths, and arthropods that can live temporarily or even permanently in the human body [1]. Disease caused by parasites can still be neglected, especially in developing countries where health access is still lacking to be able to carry out treatment and prevention [2]. The most common cases of infection caused by parasites are the case of Malaria which belongs to the group of protozoa called one-celled organisms [3].

As reported by the World Health Organization (WHO) in 2020, after the COVID-19 pandemic outbreak was reported as many as 241 million global cases of infection caused by Malaria which has the scientific name Plasmodium falciparum, previously in 2019 there were 227 million global cases of course with this experienced a significant increase. The African continent is the most cases of infection and death, especially in the Nigerian state with a total of 26.8% of infection cases. Then followed by the Democratic Republic of the Congo at 12.0% and the percentage of deaths was 31.9% from Nigeria and 13.2% from the Democratic Republic of the Congo [4]. Asides from Malaria cases, there are also cases of diseases caused by other protozoan parasites such as Babesia, Leishmania, Toxoplasma gondii, Trichomonad, Trypanosome, etc [5].

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To overcome health problems caused by protozoan parasites diseases, it is necessary to carry out an accurate analysis and diagnosis to prevent and treat these problems. Using microscopic methods remains the basis for the identification of parasitology. However, the increasing use and availability of tools in place of treatment and molecular testing in this modern era requires a faster and more accurate diagnosis and increased sensitivity in the identification of parasitic infections and using this traditional method to identify the parasites can take a lot of effort and time [6], [7].

In this modern era, it is necessary to utilize technology that can assist in diagnosing diseases caused by microorganisms, especially by protozoan parasites, quickly and accurately. In recent years, using machine learning methods has become a new way to detect infections caused by parasites automatically from microscopic images to avoid human errors in diagnosis [8]. Therefore, this study by the author will identify protozoan parasites through microscopic images using Transfer Learning with Xception architecture [9].

Transfer Learning is included in the Machine Learning scope which has been widely implemented for classification problems, especially in the aspect of Microbiology research [10]. As a conducted study by Debanshuu Banerjee et al. to classify microscopic images of dendritic morphology and non-dendritic microstructures [11]. In this study, using several architectures such as VGG16, InceptionV3 and Xception with NAG, Adagrad, RMSprop, and Adam optimizer resulted in varying accuracy. The highest accuracy is obtained by the InceptionV3 architecture with the Adam optimizer resulting in an accuracy of 86.88%. Followed by the Xception architecture with the Adam optimizer producing an accuracy of 85.94% and finally, the

VGG16 architecture with the Adam optimizer producing an accuracy of 83.13%. Therefore, in this study using Adam optimizer is superior to other optimizers.

Prudhvi Thirumalaraju et al. in the study of Human Embryo image classification based on Morphological quality using several architectures such as Inception-v3, ResNet-50, Inception-ResNet-v2, CNN multilayer, NAS-NetLarge, ResNeXt101, ResNeXt50, and Xception [12]. Xception produces the best value in distinguishing between embryo images and their morphological quality and provides good performance in shifting domain data [13].

Research on the classification of Plankton through Submersible Holographic Microscopy images conducted by Liam MacNeil et al. in their study, maximum optical image resolution is 1.5 μm which has 19 classes in the dataset [14]. Using multiple architectures VGG16, InceptionV3, ResNet50V2, and Xception. Xception architecture gets highest results from the average performance of each model in the test set with an accuracy of 90.1%, Precision of 89.8%, Recall of 90.7%, and F1-Score of 89.8%. Aya Adel et al. in their research on automatic classification of Retinal Eyes through Optical Coherence Tomography images which have four classes of retinal diseases [15]. In this study, the implementation of Transfer Learning architecture for classification process using Xception with 98% results and InceptionV3 architecture produces 93% accuracy. From the two architectures, Adam Optimizer is applied to optimize the accuracy resulting from the training process [16].

Likewise with a study conducted by Krit Sripron et al. analysis of Malaria disease with microscopic images from blood cells [17]. In the results of his research, the Xception architecture with a combination of Nadam optimizer and Mish activation function produced highest value among other architectures such as InceptionV3, ResNet50, NasNetMobile, VGG16, and AlexNet. These results obtained an accuracy of 99.28%, precision of 99.29%, recall of 99.28%, and F1 Measure of 99.28% [18].

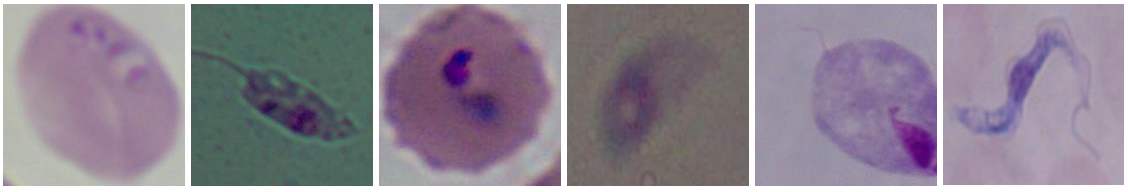
2. Methods

In this section, we will explain the experimental stages related to the types of Protozoan Parasites through the microscopic images that have been described in Table 1 with exposure of research materials and method used, then implemented into the classification stage using Transfer Learning with Xception architecture [19].

First, we will discuss the dataset used in this study. The Dataset of Protozoan Parasite was sourced from Mendeley's open-source website. The dataset provided originally consisted of 8 labels for Protozoan Parasites including Babesia, Leishmania, Plasmodium falciparum, Toxoplasma gondii, Trichomonad, Trypanosome, Red blood cell, and Leukocyte. However, we only used 6 classes from the dataset provided on the web, including Babesia, Leishmania, Plasmodium falciparum, Toxoplasma gondii, Trichomonad, and Trypanosome. Of the 6 classes, there are a total of 20.169 images. Of these, we divide the dataset by 90% Train images and 10% Test images with each class having a different number of images. Dataset label of Babesia had 1.173 images, Leishmania had 2.701 images, Plasmodium falciparum had 843 images, Toxoplasma gondii had 2.933 images, Trichomonad had 10.134 images, and Trypanosome had 2.386 images [20].

Table 1. Dataset Summary

Protozoan Parasites	Number of Images	Total Images	Total Train Images	Total Test Images
Babesia	1.173	20.169	18148	2021
Leishmania	2.701			
Plasmodium				
Toxoplasma	2.933			
Trichomonad	10.134			
Trypanosome	2.386			



(a) (b) (c) (d) (e) (f)

Fig 1. Samples of Protozoan Parasites Dataset of (a) Babesia (b) Leishmania (c) Plasmodium (d) Toxoplasma (e) Trichomonad (f) Trypanosome

Next, we will discuss the reprocessing data used in this study. Before doing the classification, we augment the dataset to increase the model's performance automatically and avoid overfitting [21]. First, we Rescale the dataset with the aim of enlarging and reducing it during the augmentation process. After that, Rotate the dataset randomly with a predetermined value. Then, set the Width Shift Range and Height Shift Range on dataset augmentation to adjust the

image position moves vertically and horizontally. And then set Shear Range on augmentation so that the machine can see the image from different perspectives like how humans see an object. After that, set Zoom Range to enlarge the image with a certain magnification value. And then, set Horizontal Flip to flip the entire row and column of image pixels horizontally. After that, set the Brightness Range for uniformity related to brightness between images in the dataset. And finally, set Fill Mode by setting 'Nearest' to complete the empty area in the image by taking the nearest pixel value [22].

Table 2. Settings for Image Augmentation

Methods	Settings
Rescale	1./255
Rotation range	40
Width shift range	0.2
Height shift range	0.2
Shear range	0.2
Zoom range.	0.2
Horizontal flip	True
Brightness range	0.2, 0.1
Fill mode	Nearest

Next will be discussed about the transfer of learning used in this study. Transfer Learning was first proposed by Pratt et al. is a reliable method for training deep CNNs [23]. This is since state-of-the-art CNN is a sophisticated model that requires more datasets to perform feature extraction and results from accurate classification and can enable faster learning process by completely resetting the last connected layer [24], [25]. Transfer Learning aims to improve performance by reusing and transferring information learned from related source domains [26]. Figure 2. represented Transfer Learning architecture. In the process, the network is pre-trained which is performed on the source domain and will be passed through the representation to the targeting domain [27].

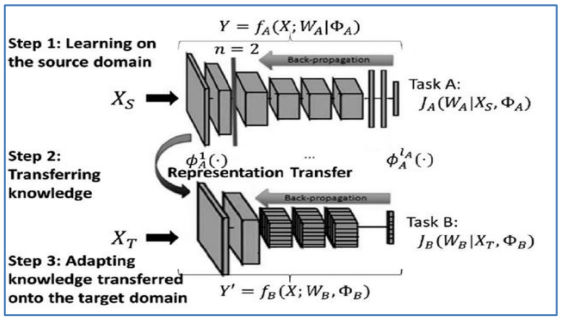


Fig 2. Transfer Learning General Architecture

Next will be discussed about the exception in this study. Xception (Extreme Inception) proposed by Francois Chollet in 2017 is the newest method of the Convolutional Neural Network (CNN) architecture for image classification. The architecture consists of a depth-separable convolution linear layer followed by a pointwise convolution with residual connections [28]. This model has 36 layers. This Xception model has 36 layers of convolution modules divided into 14 different modules. Each such layer has a linear residual connection around it by removing the initial and final layers. To retrieve cross-channel correlations in the image, the image dataset is mapped to the spatial correlation for each output channel separately. After that, a depth 1 × 1 convolution operation was performed. Correlation can be seen as a 2-dimensional mapping and then summed with a 1-dimensional mapping instead of a 3D mapping. In Xception, 2-dimensional space correlation is performed initially and then followed by 1- dimensional space correlation [24], [25].

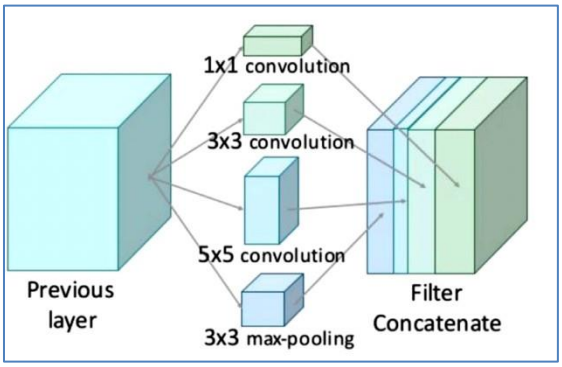


Fig 3. Xception Architecture

Next will be discussed about the experimental setup in this study. In this study, the dataset was previously collected by us and then the dataset was augmented by applying a random transformation using Keras and Tensorflow Backend. By applying several parameters aimed at ensuring data diversity, several transformations have been carried out such as Zoom and Shear with interval values between 0 to 1. Next, enter the training process using the Xception architecture. This experiment was carried out using Google Collaboratory Notebook as an online executable document with Python programming language version 3.7.12. The Protozoan Parasite dataset has 20,169 images. Prior to the augmentation process, we distributed the dataset which included 90% training and 10% testing. We uniform all image sizes in the dataset to 150x150. After that, we define settings parameters and functions for the training phase exhibited in Table 2. For optimization of the model during the training phase, we used four different optimizers for Xception architecture are Adam, RMSprop, SGD, and Adadelta as a comparison with each other [29].

Table 3. Settings Parameters and Function for Training Procedure

Training Parameters	Adam	RMSprop	SGD	Adadelta
Learning rate	0.001	0.001	0.001	0.001
Epoch	15	15	15	15
Steps per epoch	200	200	200	200
Batch size	32	32	32	32
Activation	Softmax	Softmax	Softmax	Softmax
Loss function	Categorical_crossentropy	Categorical_crossentropy	Categorical_crossentropy	Categorical_crossentropy
Metrics	Accuracy	Accuracy	Accuracy	Accuracy

By using the Xception architecture in the training process, we use ImageNet as standard training weights [17]. After carrying out the process, we present the results of the training process into performance matrix. We present four different metrics to evaluate training outcomes including:

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

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

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

$$F1\_score = 2 \times \frac{Recall \times Precission}{Recall + Precission}$$

In these formulas above, True Positive (TP) is the amount of data predicted correctly, False Positive (FP) is the amount of data predicted incorrectly, True Negative (TN) is the amount of data predicted to be wrong and the prediction is declared correct, False Negative (FN) is the amount of data from one class detected as another class [30].

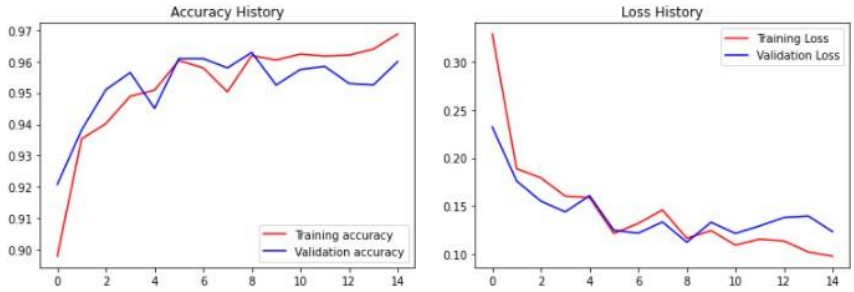
3. Result and Discussion

The results of our study of types of Protozoan Parasites classification using the Xception architecture on a convolution basis to study the representation of features from microscopic images of Protozoan Parasites. Table 3. represents the results that have been identified by applying different optimizers resulting in varying accuracy and loss.

Table 4. Trained Model Result

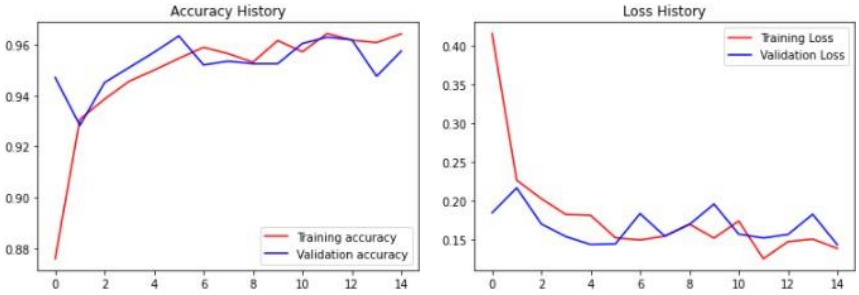
Optimizer	Train Acc	Train Loss	Test Acc	Test Loss
Adam	0.0966	0.0990	0.9688	0.1058
RMSprop	0.9646	0.1543	0.9589	0.1616
SGD	0.8932	0.3913	0.8911	0.3915
Adadelta	0.7801	0.8538	0.7897	0.8745

Table 4. presents the evaluation matrix for the Xception model with Adam, RMSprop, SGD, and Adadleta optimizer for each class of Protozoan Parasites. By using Adam Optimizer, the accuracy is 0.97. In addition, Precision, Recall, and F1-Score have been calculated for each class. With highest Precision achieved by Plasmodium class is 1.00, the highest Recall achieved by Trichomonad class is 0.99, and the F1- Score is 0.99 achieved by Trichomonad class. And then, by using RMSprop optimizer, the accuracy is 0.96. The highest precision metrics achieved by the Leishmania class is 0.98, the highest Recall metrics achieved by Trichomonad class is 1.00, and the F1-Score is 0.98 achieved by Trichomonad class. By using SGD optimizer, the accuracy is 0.89. Highest Precision achieved by the Babesia class is 0.93, the highest Recall achieved by Trichomonad class is 0.98, and the F1-Score metrics is 0.98 achieved by Trichomonad class. Last, by using Adadelta optimizer, the accuracy is 0.78. The highest Precision achieved by the Trypanosome class is 0.96, the highest Recall achieved by Trichomonad class is 0.99, and the F1-Score is 0.87 achieved by Trichomonad class. Figure 4 to Figure 6. presents plot of accuracy and loss on train and test based on different optimizer. Figure 7. presents the Confusion Matrix of this experiment.



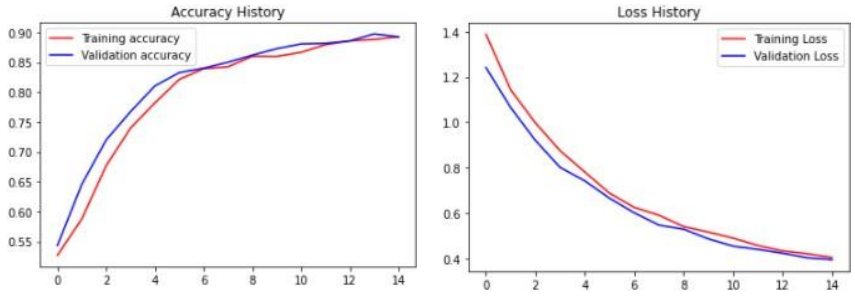
(a) (b)

Fig 4. Plot curves of (a) Training and (b) Loss Result with Adam Optimizer



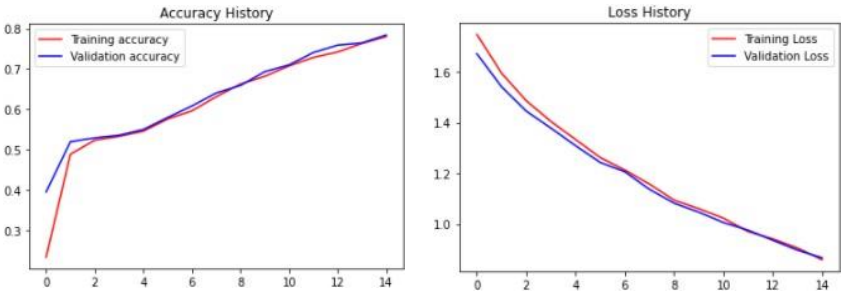
(d) (e)

Fig 5. Plot curves of (d) Training and (e) Loss Result with RMSprop Optimizer



(g) (h)

Fig 6. Plot curves of (g) Training and (h) Loss Result with SGD Optimizer



(j) (k)

Fig 7. Plot curves of (j) Training and (k) Loss with Adadelta Optimizer

Table 5. Class Performance Evaluation Matrix

Optimizer	Class	Accuracy	Time Execution	Precission	Recall	F1-Score
Adam	Babesia	0.97	3 hours 7 minutes 11 seconds	0.96	0.97	0.96
	Leishmania			0.98	0.96	0.97
	Plasmodium			1.00	0.92	0.96
	Toxoplasma			0.96	0.96	0.96
	Trichomonad			0.99	0.99	0.99
	Trypanosome			0.93	0.96	0.95
RMSprop	Babesia	0.96	3 hours 4 minutes 2 seconds	0.94	0.95	0.95
	Leishmania			0.98	0.92	0.95
	Plasmodium			0.95	0.87	0.91
	Toxoplasma			0.96	0.95	0.96
	Trichomonad			0.97	1.00	0.98
	Trypanosome			0.95	0.95	0.95
SGD	Babesia	0.89	3 hours 5 minutes 27 seconds	0.93	0.76	0.84
	Leishmania			0.87	0.85	0.86
	Plasmodium			0.87	0.73	0.79
	Toxoplasma			0.87	0.84	0.85
	Trichomonad			0.89	0.98	0.94
	Trypanosome			0.90	0.72	0.80
Adadelta	Babesia	0.78	3 hours 18 minutes 15 seconds	0.80	0.63	0.70
	Leishmania			0.69	0.60	0.64
	Plasmodium			0.84	0.32	0.46
	Toxoplasma			0.84	0.69	0.76
	Trichomonad			0.77	0.99	0.87
	Trypanosome			0.96	0.45	0.61

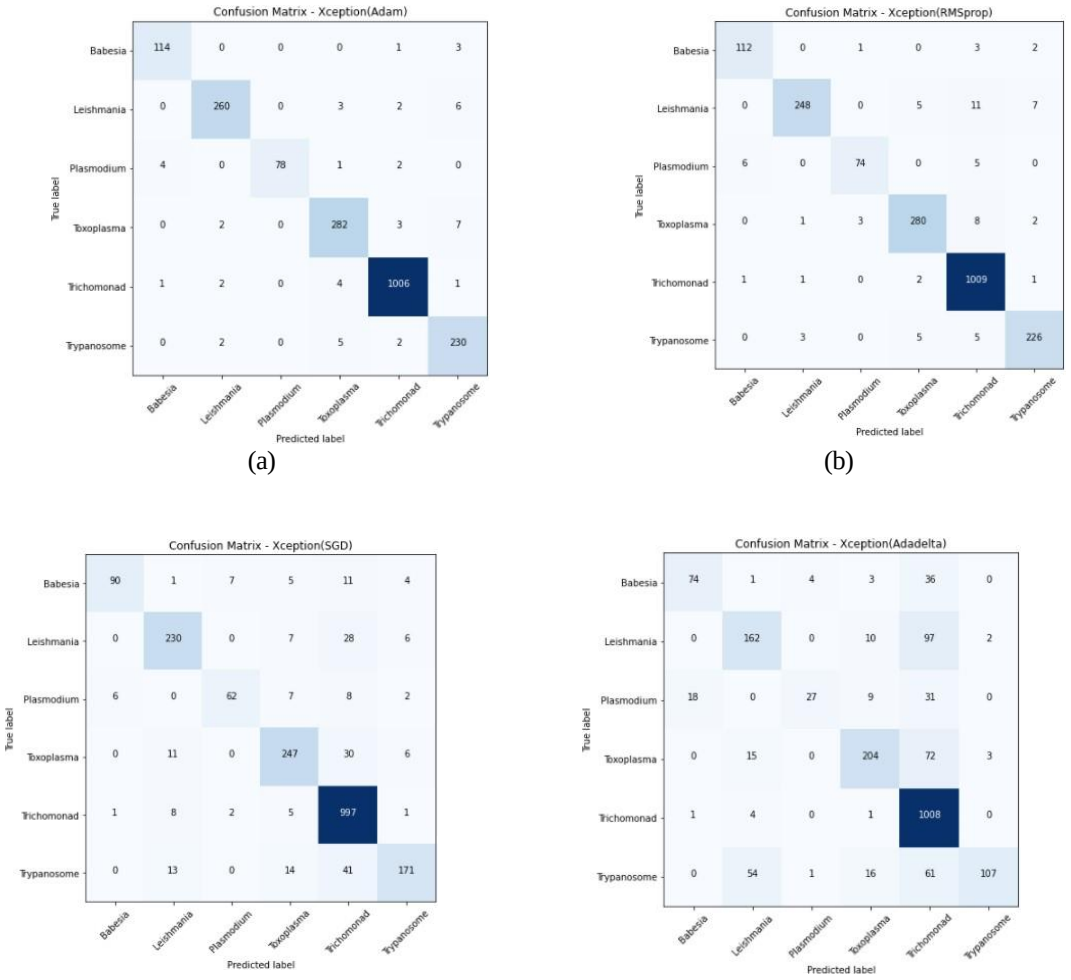


Fig 8. Confusion Matrix of (a) Adam (b) RMSprop (c) SGD, and (d) Adadelta Optimizer

4. Conclusion

In this paper, we used the Xception architecture to classify the types of Protozoan Parasites based on microscopic images identified as many as six types of Protozoan Parasites including Babesia, Leishmania, Plasmodium, Toxoplasma, Trichomonad, and Trypanosome with each having a different number of images in each type. As a result of this experiment, the greatest accuracy is obtained by Adam optimizer, which is 0.97. The fastest execution time was obtained by RMSprop optimizer for 3 hours 4 minutes 2 seconds. The highest precision value was obtained by Adam optimizer from the Plasmodium class, which was 1.00. The highest recall value was obtained by RMSprop optimizer from Trichomonad class, which was 1.00. The highest F1- Score value is obtained by Adam optimizer from Trichomonad class, which is 0.99. In other words, Adam optimizer is the best optimizer by producing highest accuracy from all aspects. However, the RMSprop optimizer is slightly superior in terms of model training execution time and produce accuracy is not much different from Adam optimizer. Therefore, by using the computational method that we use, it's hoped that it can help microscopic experts to be able to detect Protozoan Parasites quickly. And surely, we hope in future research the dataset about Protozoan Parasites is highly available to produce increased accuracy.

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Author contributions

Wikky Fawwaz Al Maki, Rifaldi Tajrial: Conceptualization, Methodology, Software, Field study, and simulating the data. **Samsul Arifin:** Data curation, Writing-Original draft preparation, Software, Validation, Field study, tidy up the theoretical basis, and the methods we use**. Suwarno:** Visualization, Investigation, Writing-Reviewing, Editing, and finalize the manuscript.

Conflicts of interest

The authors declare no conflicts of interest.

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