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Identification of the Snail Oncomelania hupensis Lindoensis as Schistotomiasis Host Using CNN

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Abstract. *The World Health Organization reports schistosomiasis as a neglected tropical disease. In Indonesia, schistosomiasis is endemic in 3 regions of Central Sulawesi. In 2023, the prevalence rate of schistosomiasis in humans in Indonesia was 0.43%. Efforts are needed to achieve the government target of 0% prevalence in humans, snails, and mammals in 2025. Survey officers who do not recognize specific O. hupensis lindoensis snails need to ask officers who know. The identification system was made using the CNN (Convolutional Neural Network) algorithm with MobileNet architecture. With four classes and 1200 image data, the training accuracy is 93%, and the validation accuracy is 87%. The training loss function is 0.17, and the validation loss is 0.33. This research uses the Black Box testing method to test the functionality of the system with a result of 90% and Confusion Matrix testing precision with a result of 0.87. The results of this study can speed up, facilitate, and reduce the cost of snail prevalence surveys for officers and are useful for ordinary people to recognize this snail as the cause of schistosomiasis disease.*

Keywords: World Health Organization, Schistosomiasis, Endemic, O.hupensis lindoensis, CNN

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1. Introduction

The World Health Organization (WHO) released its second *road map* to address the problem of *Neglected Tropical Disease* (NTD). The new *road map* continues the 2010 *road map* that ended in 2020. The new *road map* has a period of 2021-2030 and sets targets and measures to prevent, control, eliminate, or eradicate 20 diseases in the NTD group. One of the diseases included in NTDs is *schistosomiasis*. The WHO report stated that *schistosomiasis* caused 236 million people to need treatment in 2019 and was responsible for 24,000 deaths in 2016 [1]. Muller and Tesch first discovered schistosomiasis in Indonesia in a 35-year-old male patient from Tomado village in Lindu Valley in 1973. Tomado village was later designated as a *schistosomiasis* endemic area by Brug and Tesch in the same year [2]. In Indonesia, *schistosomiasis is* endemic in 3 areas of Central Sulawesi, namely the Lindu Plateau, Napu Plateau, and Bada Plateau [3]. These three areas are included in 2 districts, namely Sigi District with five endemic villages (Anca, Tomado, Olu, Puroo, and Langko villages) and Poso District with 23 endemic villages (Banyusari Village, Sedoa, Kaduwoa, Alitupu, Tamadue, Mekarsari, Maholo, Winowanga, Dodolo, Torire, Watutau, Wuasa, Wanga, Siliwanga, Betue, Kalemango, Watumaeta, Kageroa, Tomehipi, Lengkeka, Tuare, Koloni, Leleo). [4].

Schistosomiasis in Indonesia is caused by the *Schistosoma japonicum* worm, hereafter referred to as S. japonicum [5]. This worm has two stages of development in its life cycle. The asexual development stage requires the intermediate *host* snail *Oncomelania hupensis lindoensis, hereinafter* referred to as O.hupensis lindoensis. The sexual development stage in the main host body is humans and mammals [6]. In 2019, the prevalence of *schistosomiasis* in humans in Indonesia was suppressed and dropped significantly to reach 0.1% compared to 2018, which was 0.5%. In 2020, there was no significant change from the previous year, which amounted to 0.11%. However, in 2021 and 2022, there was an increase in the prevalence rate of 0.22% and 1.44%, respectively. However, the 2023 survey showed that the prevalence rate could be reduced to 0.43% [7].

Although efforts to prevent *schistosomiasis* transmission have been made since 1974 [8], the infection still continues to occur [3][9][10]. To solve this problem, the Indonesian government, through Bappenas in 2017, issued a *schistosomiasis* elimination *road map* for 2018-2025. Then, it was strengthened by Permenkes Number 19 of 2018 with a target of 0% prevalence in humans, snails, and animals in 2025 [4]. The snail *O.hupensis lindoensis* hosts *schistosomiasis* before attacking humans and mammals. The *cercariae* phase of the *S. japonicum* worm inside the *O. hupensis lindoensis* snail at a certain time comes out looking for a new host and enters through the skin of humans or mammals as a place for further development into adult worms. *Cercariae* can only survive within 48 hours in the search for a new host. If it does not find a host, then this worm will die [11]. The position of the snail *O.hupensis lindoensis in* the *schistosomiasis* disease cycle is very important because it contains *cercariae* that can infect humans or mammals. Therefore, it is necessary to suppress or eliminate *O.hupensis lindoensis* snails. So that transmission of *schistosomiasis* to humans or mammals can be interrupted [11].

O.hupensis lindoensis snails act as *intermediate* hosts and are amphibious [12]. Therefore, they are often found on the banks of irrigation channels, drainage channels, or rivers. Several environmental conditions affect the survival of these snails, such as water temperature, water flow velocity, and vegetation cover. Other things that also affect are the type of vegetation, soil type, and water that is sufficient for the development of snails and *cercariae* in the *host-seeking* stage [13]. To find out the location of the *O.hupensis lindoensis* snail, a survey of snail locations or habitats was conducted [10][14]. In 2021, Nurwidayanti et al. [14] conducted a survey of 25 snail habitats in Anca and Tomado Villages, Lindu District, Sigi Regency. It was found that there were still snails containing *S.japonicum* cercariae.

Morphologically, the O. hupensis lindoensis snail has a shell size of 6 mm when mature, narrowed cone-shaped, smooth surface, stacked as many as 6.5 - 7.5, black, gray to brown, the size of the hole where the snail's body exits are 2.38 x 1.75 mm, and the inside of the shell (*inner lip*) is light yellow to orange yellow [5]. Currently, when conducting snail site surveys, officers use their experience to identify and distinguish *O. hupensis lindoensis* among other snails. So, officers who are first-timers or have yet to gain experience in identifying *O.hupensis lindoensis* need to ask officers who know better. This slows down the survey process. A system that can identify *O.hupensis lindoensis* among snails in schistosomiasis endemic areas can speed up the identification process and reduce survey costs. Addressing *schistosomiasis* requires cross-sectoral cooperation [1][4]. Thus, the technology sector is needed to help identify *O. hupensis lindoensis* among snails in the same habitat in *schistosomiasis* endemic areas.

Technological developments in the field of health have been widely utilized and proven to benefit humans [15][16][17][18]. Some of them are *AI chatbots* that provide health recommendations under expert supervision, sleep monitoring tools developed by *Google*, and breast cancer diagnosis through *x-ray* scan images [15]. This research aims to create a system that can identify *O.hupensis lindoensis* among other snails in the same habitat using the *Convolutional Neural Network (CNN)* algorithm. The selection of the CNN algorithm in this identification system is based on the evidence of CNN to classify or identify image data with good results. Research by Zhang et al. [16] used CNN to classify breast cancer. Artificial Neural Network as the basis of CNN is used by Utari et al. [19] to classify materials that enter the body with Ultrasonography. CNN has also been applied in brain tumor diagnosis by Wu et al. [17]. Souid et al. [18] utilized CNN with MobileNet to classify and predict lung diseases. The purpose of this research is to provide convenience to the community to recognize the *O.hupensis lindoensis snail* as the cause of *schistosomiasis*, especially for officers in conducting snail habitat surveys by utilizing the *O.hupensis lindoensis snail* identification system using CNN. This research hypothesizes that the identification system of *O.hupensis lindoensis* using CNN can help and facilitate officers in conducting snail habitat surveys so as to speed up the process, reduce survey costs, and make it easier for people in *schistosomiasis* endemic areas to recognize *O.hupensis lindoensis snails* as hosts of this disease.

2. Methods

2.1. Flowchart

System development is divided into three main parts, namely data *pre-processing*, CNN model building, and CNN model evaluation [14].

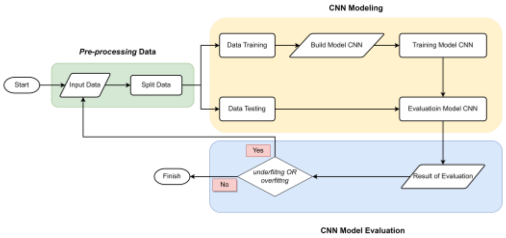


Figure 1. Flowchart

The data *pre-processing* stage begins by inputting data from the *Google Drive* folder that has been collected into the Goole Colab notebook jupyter. The data is then divided by 60% for *training data* and 40% for *validation* data. Then, augmentation is done to increase the amount of data with various variations [20]. Data that has been divided into two is included in the CNN model as model training material. The final results of model training are the accuracy rate and the loss rate or classification error. These final results can show whether the model formed is in an overfitting, underfitting, or fit condition. The ideal condition is that the model formed has a *fit* condition [20][21].

2.2. Datasets

The dataset in this study is in the form of snail image data obtained from various sources. Researchers collected data from the Central Sulawesi Provincial Health Office, Donggala LITBANGKES Center, and researchers who deal with *schistosomiasis* disease in Central Sulawesi. In addition, researchers also went to the field in Winowanga village, Lore Lindu sub-district, Poso district. The collected snails are divided into four types, namely *O.hupensis lindoensis*, *Sulawesidrobia sp*, *Thiara sp,* and *Brotia sp*. The habitats of these snails are in *schistosomiasis* endemic areas [5][22]. The snails were placed on white paper and then photographed using a *handphone* camera. Collected each type of 300 image data so that the overall dataset is 1200 images. The system created will recognize four types of snails in the dataset.

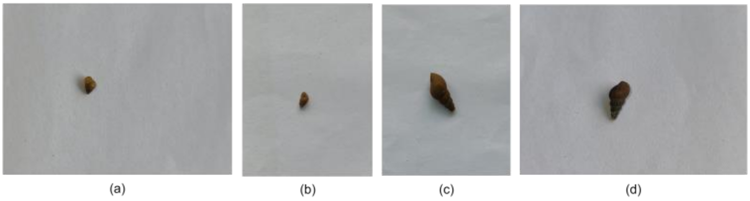


Figure 2. Images of Conch Dataset: (a) Sulawesidrobia sp (b) O. hupensis lindoensis (c) Thiara sp (d) Brotia sp

2.3. CNN

Convolutional Neural Network or CNN algorithm is a classification algorithm that is widely applied to image analysis [15][16][17][18]. CNN algorithm itself is part of *deep learning* [20]. In this study, the model formed was added to the *pre-training* layer of the *MobileNet* model. *MobileNet* is one of the development architectures of the CNN algorithm [23].

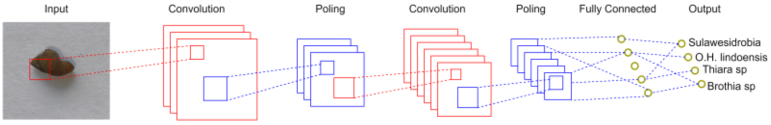


Figure 3. CNN Architectures

In general, *deep learning* has three layers, namely the *input layer*, *hidden layer*, and *output* layer. The *hidden layer* in *deep learning* aims to find the features of an object. The basic structure of the CNN hidden layer consists of *a convolutional layer*, *a pooling layer*, and a *fully connected layer* [20]. The convolutional layer is where most of the computation of the CNN architecture takes place, so it is called the core layer of the CNN. Each convolutional layer has a layer of neurons connected to a small area of the input image of a certain size called the receptive field. The size of this receptive field is expressed as a *convolutional layer* filter. The number of filters can be more than one [24]. This filter will trace the entire area of the input image and shift by a given *stride*, generally of size 1. The output of this process is the *dot product of the* filter and the receptive field of the input image [20]. Sometimes, the size of the input value and the size of the output value want to be equalized in height and width. Then, a *zero padding* can be added to the input value size [20][24]. There is a formula to determine the amount of padding, namely:

$$P = \frac{(F-1)}{2}$$

Description:
P = padding size; F = receptive field or filter size

Pooling layers are used to decrease or reduce the output size of the convolution layer. With this technique, the data becomes smaller, easier to manage, and easier to control overfitting [24]. Each result of the dot product between the filter and the receptive field will be polled. There are two types of *pooling*, namely, *max pooling* and *average pooling*. But the most commonly used is *max pooling*, taking the maximum value of the *dot product* result area [20].

$$f(x) = \max(0, x)$$

Description:
f(x) = *max pooling* result*; max* = take maximal data or 0 x = maximal data

Fully connected layers have the same form as Multi-Layer Perceptron or MLP. MLP itself is the basis of artificial neural networks. The way it works is the same as MLP, which is matrix multiplication with a bias value [20][24].

$$y = f(\sum_i x_i w_i + b)$$

Description:
y = output; f = activation function x = input; w = weights; b = bias

The output layer is the layer that produces the classification value. The classification result of the *output* layer or *output value* will be compared with the actual value or *target value of* the input data. The error distance between the *output value* and the *target value* will be calculated with a *loss function*. In this research, the *sparse categorical cross-entropy function is* used. Optimization is carried out with the optimizer function to minimize the *loss function* value while improving the CNN model. This research uses the *Adam optimizer* function.

2.4. Model created

The CNN model consists of the input layer, the pre-trained layer of the MobileNet architecture model, a trained layer, and an output layer.

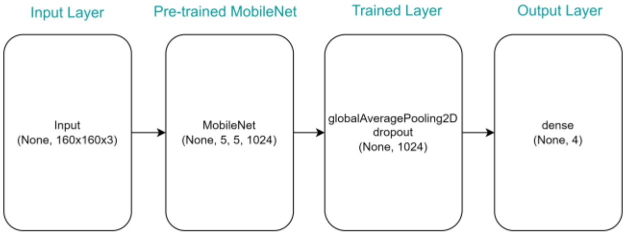


Figure 4. Layer Model Created with Output Shape of Each Layer

The input layer will receive image data with a size of (160x160x3). For this reason, each input image needs to be processed in the form of resizing the image to 160x160x3. The CNN model uses the pre-trained architecture of the MobileNet model. MobileNet itself is available in the tensorflow framework. To use the pre-trained MobileNet model, simply call the tf.keras.application. Mobile net.MobileNet function. The MobileNet pre-trained model architecture was chosen because it can provide the ability of the model to learn quickly and get good results with a small model size. Models with good results and small sizes can be used in further system development applied to mobile devices with low computational capabilities [18][23]. To adjust the model with the data used, researchers added a layer after pre-trained MobileNet. This addition is done to reduce the overfitting of the CNN model to the data. The added layer is a pooling layer, namely AveragePooling, and a dropout layer. The output layer will produce an array with a length of 4. Each value will have a range from 0.0 to 1.0. The final result is selected based on the highest value among the four output array values.

3. Results and Discussion

3.1. CNN Model Training Result

The convolutional Neural Network model is built with *the Tensorflow framework*. *Tensorflow is* run on *Google Collab,* which is an *open-source jupyter notebook* that has installed *libraries* to support the development of AI systems. The CNN architecture used is *MobileNet*, with the novelty of adjusting the dataset used and adding *global average-pooling* and *dropout* layers. The model *output* layer is 4, following the number of snail species found in *schistosomiasis* endemic areas. The 1200 datasets were divided into 60% or 720 data for training and 40% or 480 data for validation. Each group of data is augmented. The techniques performed are rescaling, random flip (horizontal and vertical), random contrast, random rotation, random brightness, random height, and random width on training data. In contrast, the validation data is only performed augmentation techniques in the form of rescaling. The augmentation process is done with a size of 64 batches.

The creation process undergoes some fine-tuning in the form of optimizer selection, input layer resizing selection, and augmentation batch size, as well as the batch size during the model training process. The suitable optimizer is the Adam optimizer. The data size for the input layer is 160x160x3, The batch size used is 64. In the process of training models on Google Colab, out-of-memory usually occurs. This is due to large data, so that the computational process is also large. To handle this problem, Google Collab was upgraded to pro and obtained a 16 GB V-100 GPU system. The CNN model trained for 100 *epochs* produced an accuracy of 93% with a validation accuracy of 87%. The *loss* value on training data is 0.16, while the *loss* value on validation data is 0.32.

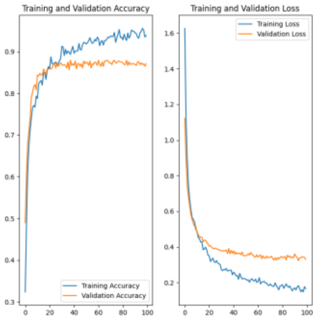


Figure 5. Visualization of CNN Model Training Results

CNN model training visualization results show an increase in Accuracy in *training* data up to the 100th *epoch*. In validation data, the Accuracy increases up to the 40th *epoch*. In visualizing the *loss* value, up to the 100th *epoch*, *training loss* continues to decrease. While *validation loss* only decreased until the 40th *epoch*.

3.2. Confusion Matrix

The data used in confusion matrix testing is validation data, namely 480 data. The confusion matrix shows the system's shortcomings in identifying the *Sulawesidrobia sp* class, which is 30 times judged as the *O.hupensis lindoensis* class. This is because the *Sulawesidrobia sp* snail has similarities with *O.hupensis lindoensis* [6]. From the confusion matrix multiclass classification, a table can be made that relates the values of True Positives (TP), False Positives (FP), and False Negative (FN) [25].

Table 1. Confusion Matrix

	Sulawesidrobia sp (1)	***O.hupensis lindoensis (2)***	***Thiara sp (3)***	***Brothia sp (4)***	**Total**
TP	*84*	*110*	*114*	*110*	*418*
FP	*31*	*16*	*1*	*14*	*62*
FN	*12*	*39*	*9*	*2*	*62*

From the table above, we can calculate Accuracy for the ability of the system to identify all data and calculate Precision on the *O.hupensis lindoensis* class because this class is the focus of research and the cause of *schistosomiasis* disease. Knowing the Precision value of the *O.hupensis lindoensis class* can provide an overview of the system identifying this class.

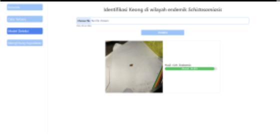
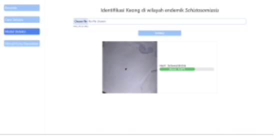
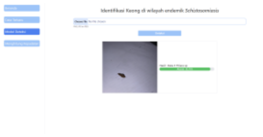
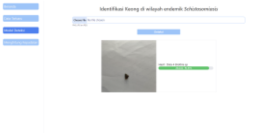
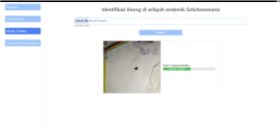
$$Accuracy = \frac{TP}{All\ data} = \frac{418}{480} = 0.87 \qquad Precision(2) = \frac{TP(2)}{TP2+FP2} = \frac{110}{110+16} = 0.87$$

Accuracy results of 0.87 or 87% were obtained, as shown in **Figure 7,** visualization of model training results. The Precision value of *O.hupensis lindoensis* was obtained as 0.87. In this study, the Precision value of the *O.hupensis lindoensis* class is more emphasized due to consideration of the system's ability to recognize O.hupensis lindoensis snails by reducing False positives. If *O.hupensis lindoensis is* identified as another snail, it can be dangerous for officers and the public.

3.3. Black Box Testing

The model that has been generated is stored in the form of a file. Then, it is loaded into a web-based system created using the Flask framework. The website can receive input in the form of images and return identification results in the form of the name of the snail class and the Accuracy of the class assessment. The system is then tested with Black Box testing.

Table 2. Black Box Testing

No.	Testing	Input	Output	Description
[1]		O.hupensis lindoensis	O.hupensis lindoensis	Valid
[2]		O.hupensis lindoensis	O.hupensis lindoensis	Valid
[3]		Sulawesidrobia sp	Sulawesidrobia sp	Valid
[4]		Thiara sp	Thiara sp	Valid
[5]		Brotia sp	Brotia sp	Valid
[6]		Brotia sp	Sulawesidrobia sp	Not Valid

Black Box testing uses six new image data that are not used in the model *training* process. Of the 6 data, 1 data was correctly identified by the system, and only one data was answered incorrectly, namely *Brotia sp* data identified as *Sulawesidrobia sp*. From this test, the system can provide 90% correctness. The prediction error of the 10th Black Box Testing data is caused by the position of taking pictures that do not show the striking shape of the snail, thus reducing the system's ability to identify. With the wrong answer, the value of confidence to assess the data is only 53%, which shows that the system needs to be more confident in the assessment given.

4. Conclusion

From the results of research on the identification of *O.hupensis lindoensis snails* among snails in *schistosomiasis* endemic areas using the MobileNet architecture CNN method, with adjustments to the addition of layer pooling and dropout and the number of data classes used, namely four classes with 1200 image data, the results obtained training accuracy of 93% and validation accuracy of 87%. The training *loss function is* 0.17, and the validation *loss is* 0.33. The ability of the system to precisely determine the class of *O. hupensis lindoensis*, which is a temporary host of schistosomiasis, is 0.87. In the black box test of 10 new data, the system can answer 9 data correctly and only one wrong. This model can be applied to help *O. hupensis lindoensis snail* habitat survey officers speed up their tasks. However, for communities in endemic areas, efforts need to be made to disseminate and introduce the system so that they can easily identify the snails that cause schistosomiasis. Although the system has achieved 93% training accuracy, it needs improvement in the form of increasing the number of datasets and data variations. This improvement is to reduce errors, as shown in Black Box testing, and increase the Precision of the *O.hupensis lindoensis* class in Confusion Matrix testing. This system is also still implemented on the website. It needs development so that this system can be applied to Mobile Devices.

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