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A Breakthrough in Viral Pneumonia Detection: Unveiling Insights with ResNet-152

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Abstract

Viral pneumonia is one of the most serious health issues. The key problem in providing early detection and rapid mitigation through the use of chest X-ray imaging has become the ability to identify accurately. The ResNet-152 convolutional neural network approach will be used in this study to predict viral pneumonia. The input dataset was obtained from Kaggle.com. The accuracy findings from this investigation obtained a substantial value, namely 0.99, indicating that the model used performed admirably. The model used can efficiently distinguish between the viral pneumonia dataset and other datasets. It is intended that the findings of this study will be used to inform early decisions in related medical sectors.

Keywords: *viral pneumonia, prediction, ResNet-152.*

1. Introduction

If a breathing disorder such as viral pneumonia (Pagliano et al., 2021), is not treated promptly, it might have significant implications. Young children and adults with underlying disorders or a weakened immune system are more vulnerable (Galván et al., 2015). If the diagnosis is true, this condition can be effectively treated (Gu et al., 2020). The use of artificial intelligence in the recent decade has yielded great results, particularly in image detection in the health sector (Aini et al., 2023; Hastomo, Widi Karno, Adhitio Satyo Bayangkari Kalbuana, Nawang Nisfiani, Ervina ETP, 2021; W. Hastomo, 2020; Widi Hastomo et al., 2021, 2022; Karno et al., 2023). The ResNet-152 convolution neural network implementation has been extensively explored in the medical field, with one application being the classification of pneumonia viruses (Widi Hastomo, 2021b, 2021a; Widi Hastomo & Bayangkari, 2021; Karno, A. S. B., Hastomo, W., Efendi, Y., & Irawati, 2021). ResNet-152's deep network is capable of detecting complicated features in chest x-ray images.

Various challenging chest x-ray images and characteristic patterns of viral pneumonia can be classified and identified by ResNet-152 (Kundu et al., 2021). Symptoms of viral pneumonia infection in images and uninfected images can be differentiated and studied on a large number of training input datasets (Wang et al., 2021). The high level of accuracy and precision in the ResNet-152 algorithm can contribute to the field of rapid mitigation (Ananda Kumar et al., 2022).

Research conducted by (Kundu et al., 2021) used the DenseNet-12, GoogLeNet, and ResNet-18 models using the chest X-ray image dataset, with the best accuracy results reaching 98.81%. Previous research by (Hasanah et al., 2023) used the ResNet-50, ResNet-101, and ResNet-152 algorithms with a dataset of 21,885 radiological images, with an optimal F1-score of 94%. Research conducted by (Abubeker & Baskar, 2023) used the B2-Net method with an accuracy of 97.69%. Research conducted by (Naronglerdrit et al., 2021) used ResNet, MobileNet, and DenseNet after transfer learning methods, with the best accuracy reaching 100% with ResNet-50.

2. Method

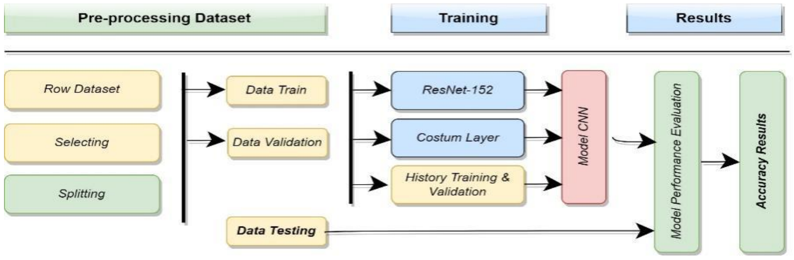
The study flow using the ResNet-152 method to detect viral pneumonia in chest x-ray images is as follows (Ayan et al., 2022):

1. Data Preprocessing

   The input dataset for this study comes from kaggle.com (Muhammad Chowdhury; & Khandakar, 2021), which has been tested by Chowdhury et al. (Chowdhury et al., 2020). Performance optimization of deep learning models is very important when processing chest x-ray images, especially in the ResNet-152 model.
2. ResNet-152 Model

   ResNet-152 is a layer with a depth of 152 layers. A model with a network of deep layers and quite complicated. Medical image patterns can be recognized with this procedure.
3. Model Training and Validation

   Model pelatihan pada dataset dilakukan dengan pembagian data latih 0.8 dan data latih 0.2 (Muhammad Chowdhury; & Khandakar, 2021). Dilanjutkan dengan proses costum layer, history training dan validasi.
4. Evaluation of Model Performance



Source : Research Results (2023)

Figure 1. Research process flow

Figure 1 is process evaluation for presisi (1), recall (2) dan f1-skor (3). Where TP is true positif, FP is false negatif.

- $$Precision = \frac{TP}{TP+FP} \quad (1)$$
- $$Recall = \frac{TP}{TP+FN} \quad (2)$$
- $$F1 - Score = 2\,x\,\frac{Precision\ x\ Recall}{Precision+\ Recall} \quad (3)$$

In the context of this study, it is important for the parameter evaluation process. The main focus of this study is the accurate detection of viral pneumonia cases. The F1-score provides a comprehensive picture of the precision-to-recall ratio. A high F1-score value shows that the model has a good balance in accurately recognising viral pneumonia. Figure 1 depicts the process of this investigation.

5. RestNet-152

2015 was the beginning of the ResNet-152 artificial neural network, which won the ImageNet competition (Canziani et al., 2016). Several convolutional layers, each integrated with each other, create a residual network from the residual block concept. Advanced structures, obstacle residual blocks, and basic residual blocks are types of residual blocks in ResNet-152. The core formula of ResNet-152 is contained in the remaining blocks. Each remaining block is the core of the ResNet-152 formula. The mapping of x to another feature space is a function, and the remaining block inputs are assumptions of $F(x)$. The output of the remaining block can be represented as follows:

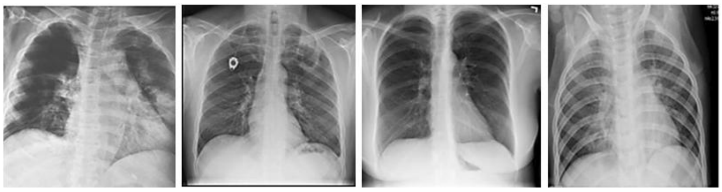
$$y = F(x) + x \quad (4)$$

y is the output and expectation of the residual block. The original representation (x) is a change that must be made when providing a network approach; (y) is the desired representation and target. $(F(x))$ is the difference estimated in the learning process experiment in each residual block. (y) is the actual representation, (x) is the expected representation, and (x) to be added back (y) is the expectation of the target outcome. The deep neural network depth of ResNet-152 enables better learning results through the use of residual blocks and deep structures, which is a major contribution. Image recognition and a high level of accuracy are possible when implementing the ResNet-152 neural network.

Conceptually, the pseudocode learning process in ResNet-152 can be explained as follows:

Pseudocode RestNet-152

```
function ResidualBlock(input, filters, strides):
   x = Convolution(input, filters=filters, kernel_size=(3, 3), strides=strides, padding='same')
   x = BatchNormalization(x)
   x = ReLU(x)
   x = Convolution(x, filters=filters, kernel_size=(3, 3), strides=1, padding='same')
   x = BatchNormalization(x)
   if strides > 1 or input.shape[-1] != filters:
      input = Convolution(input, filters=filters, kernel_size=(1, 1), strides=strides, padding='same')
      input = BatchNormalization(input)
   x = Add(x, input)
   x = ReLU(x)
   return x
function ResNet152(input_shape, num_classes):
   inputs = Input(input_shape)
   x = Convolution(inputs, filters=64, kernel_size=(7, 7), strides=2, padding='same')
   x = BatchNormalization(x)
   x = ReLU(x)
   x = MaxPooling(x, pool_size=(3, 3), strides=2, padding='same')
   x = ResidualBlock(x, filters=64, strides=1)
   x = ResidualBlock(x, filters=128, strides=1)
   x = ResidualBlock(x, filters=256, strides=1)
   x = ResidualBlock(x, filters=512, strides=1)
   x = GlobalAveragePooling(x)
   x = Dense(x, units=num_classes, activation='softmax')
   model = Model(inputs, x)
   return model
```


(a) (b) (c) (d)

Source : Research Results (2023)

Figure 2. X-ray images from the dataset: (a) COVID-19; (b) lung opacity; (c) normal; (d) viral pneumonia

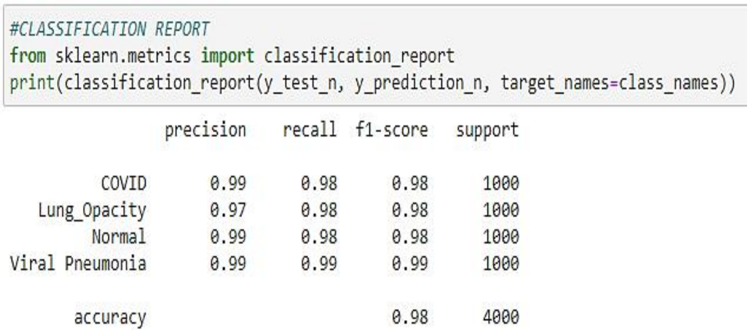
Figure 2 is a representation of the dataset from Kaggle.com (Muhammad Chowdhury; & Khandakar, 2021).

3. Results and Discussion

In the analysis of artificial neural network training results, as presented with a train loss value of 0.3702, a training accuracy value of 0.9988, a validation loss value of 0.4873, and a validation accuracy value of 0.9388, there are several aspects that can be interpreted in depth:

- The low train loss value (0.3702) indicates that the model has succeeded in reducing prediction errors on the training data.
- This low value indicates that the model has a good ability to adapt to the patterns in the training data.
- The very high accuracy of the training data (0.9988) indicates that the model is almost perfect at predicting classes based on the data used to train it.
- However, keep in mind that very high accuracy on training data can also be an indication of overfitting if validation does not reflect the same performance.
- The validation loss value (0.4873), which is slightly higher than the train loss, indicates that the model may be slightly overfitting.
- This usually occurs when the model overfits the training data and is unable to generalise well to data it has never seen before.
- Even though the validation loss value is slightly higher than the train loss, the accuracy validation value is still high (0.9388), indicating that this model is able to make good predictions on data that was not used during training.
- High accuracy on validation data is an indication that the model is able to generalise well to new data.
- Models that are able to generalise well on validation data are highly desirable for real-world applications where the model needs to be able to generalise on data that has never been seen before.

Analysing these values in depth allows us to understand how well our model can generalise and how we can improve or optimise it for better performance in the real world.



```
#CLASSIFICATION REPORT
from sklearn.metrics import classification_report
print(classification_report(y_test_n, y_prediction_n, target_names=class_names))
```

```
                 precision    recall  f1-score   support

           COVID       0.99      0.98      0.98      1000
    Lung_Opacity       0.97      0.98      0.98      1000
          Normal       0.99      0.98      0.98      1000
 Viral Pneumonia       0.99      0.99      0.99      1000

        accuracy                           0.98      4000
```

Source : Research Results (2023)

Figure 3. Report classification results

Figure 3 is the results of the study obtained a high precision value, which is a category and an indicator that the model that has been built can identify images that are close to correct. The accuracy value reaches 0.99, indicating that predictions from viral pneumonia images can be identified with very good results, reaching 99%. It can be said that the model that has been built has a small error rate. Figure 3 depicts the report classification results

4. Conclusion

This study has succeeded in building an excellent model where the results for predicting chest x-ray images in the viral pneumonia category can be identified well. As a result of achieving high precision, it has succeeded in identifying cases with minimal errors. Accurately and consistently identified is a representation of the model with high precision values. A minimal error rate in the classification process is a representation of a model that has been built in the very good category. False positive cases in each category can be reduced with high-precision value indicators. Finally, achieving high precision values is a good aspect to support and provide confidence in the prediction process for quality medical diagnosis.

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