# CAPSULE NETWORK BASED COVID-19 DETECTION WITH CLASS WEIGHT MODIFICATION

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## ABSTRACT

Nowadays, a year after the corona hit the world, the existing corona detection technique also boasts excellent functions. Still, the need for a diagnostic method to judge more accurately and efficiently with an automated technique has emerged. Although the CNN-based algorithm has been widely used in several studies, it has a disadvantage. It does not consider the spatial layer, so in this project, the capsule network-based approach is adopted as an alternative to increasing the accuracy. In this project, after segmenting the CT image of the lung for the CAPSULE Network, labeling is performed according to the detection result of the patient of the CT image to prepare input data for training. The model used in this project consists of two stages. In the first stage, the normal data are filtered out, and in the second stage, the CAP and COVID data are separated. In the model's training process, we devise to give different weight values to reduce the performance degradation due to the imbalance of the data ratios among the normal, CAP, and COVID data.

***Index Terms***— Segmentation, Capsule Network, Imbalanced train dataset, Class weights modification, COVID detection

## 1. INTRODUCTION

COVID broke out in 2019 and hit the world by 2020, paralyzing all healthcare and infrastructure. Coronavirus is infected by exposure to respiratory droplets when in close contact with an infected person, and its transmission power is very high. Currently, the number of confirmed patients worldwide is 111,073,319, and the number of deaths is 2,460,286.

RT-PCR is the most commonly used type of coronavirus test [1], and saliva PCR and rapid antigen tests have been newly added. RT-PCR extracts RNA, amplifies it, and determines whether two or more genes characteristic of COVID-19 are positive. However, it takes a long time, and when it fails to collect a sufficient amount of viral cells during the sample collection process, even if it is infected with the virus, it may produce negative. The specificity is high, but the sensitivity is somewhat low. Saliva PCR had a lower sensitivity value than RT-PCR, and the rapid antigen test method was faster, but if no symptoms were included in the evaluation, the actual sensitivity was only 50-60 %.

With the rapid increase in the number of people in need of COVID-19 testing, it is essential for medical professionals to quickly and accurately determine whether an outbreak occurs in ending the pandemic. In some studies, detection techniques using CNN are applied, but CNN has limitations because it fails to consider spatial layers [2, 3]. For this reason, one needs to train on various transformations of objects. In other words, in order to solve this shortcoming, it is necessary to obtain extensive data. Unfortunately, it is not easy to access large data sets due to its privacy restrictions. Therefore, to increase the accuracy, we devised a model by modifying the COVID-FACT [4], which is based on the capsule network, with detailed algorithms. The model consists of two stages. The first stage distinguishes the infected slices from the input slices. In the second stage, the infected slices determined in the first stage are relabeled for the COVID and CAP.

This report is organized as follows. The following section introduces the dataset given in the competition and how to avoid data imbalancing. In Section 3, the main algorithm is presented, and the weight adjustment and the training and testing results are described. Finally, the report is concluded in Section 4.

## 2. DATASET

The data given at the competition were for 60 pneumonia patients, 171 corona-positive patients, and 76 normal patients. However, if they are used as they are, the amount of the infected slices is relatively small compared to the entire slices, so learning was not performed well due to data imbalance. To cope with this problem, through several trials and errors, the ratios of 54.5% for positive corona patients, 27.3 % for pneumonia patients, and 18.2 % for normal persons were selected and processed for the data set. The validation data was constructed to determine the accuracy of learning, and 90 % of the total data was randomly selected as training data and 10 % as validation data slices determined in the first stage are relabeled for COVID and CAP.

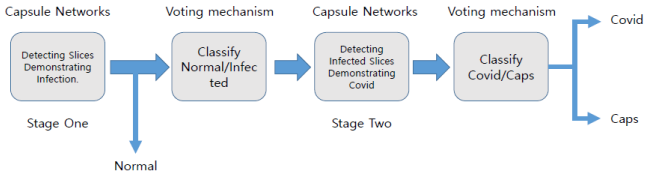


**Fig. 1**. Schematic flow chart of the model employed in the project.

## 3. MAIN ALGORITHM AND RESULTS

The overall model devised in this project consists of two stages, and the submodel used in each stage relies on that of Stage two of COVID-FACT [4]. In fact, COVID-FACT was developed to determine COVID using chest radiographs. The flowchart of the model employed in the project is illustrated in Fig. 1.

This model consists of four convolutional layers and 2 capsule layers. After the first convolution layer, batch normalization, the maxpooling layer after the second convolution layer, and the dropout layer after the fourth convolution layer were used. Next, two capsule layers were placed, which were sequentially performed the routing process. As input, segmented CT-slices are entered. The model is used to create the weights used in stage one and stage two, respectively.

### 3.1. Weights for Stages 1 and 2

In Stage 1, the input is a set of CT slices corresponding to the patient; 30 COVID-19 , 15 CAP, and 10 NORMAL. To avoid excessive data imbalance, fewer NORMAL patients were enrolled than infected patients. Of the total 8261 CT slices, 90 % were used as train data, and 10 % were randomly selected and used as validation data.

To cope with the data imbalance in the training data set, the class weights were modified to give a higher weight ratio to the minority class [5]. A class weight of 0.34 was assigned to the majority class and 0.66 to the minority class according to the following rules;

$$w_0 = N_1/(N_1 + N_0) \quad (1)$$

$$w_1 = N_0/(N_1 + N_0), \quad (2)$$

where $N_1$ and $N_0$ are the numbers of majority and minority classes, respectively, while $w_1$ and $w_0$ are the weight ratios assigned to the majority class and the minority class, respectively.

When creating the weights of Stage 2, the input is the infected CT slices for the patients with 10 COVID-19 and 10 CAPs. Among the infected slices of COVID-19 patients and CAP patients, the label of COVID-19 patients was 1. In contrast, the CAP patients' label was 0. 80 % of them were used as training data, and 20 % were randomly selected and used as validation data. We modified class weights by giving a higher weight ratio to the minority classes to cope with the data imbalance in the training dataset. The weight ratio of the majority class was 0.47, while that of the minority class was 0.53. The training result demonstrates the validation accuracy of 72 %.

### 3.2. Stage 1

Stage 1 determines whether the input data is normal with trained weights. The input is the CT slice set corresponding to the patient. According to the ratio of the output infected slices, it is decided on whether the patient is NORMAL or not. When the number of infected slices is less than 30 % of the total volume of the test output, the patient is considered normal. In the following, the infected slices produced by Stage 1 is fed into Stage 2.

### 3.3. Stage 2

Stage 2 determines whether the patient is COVID-19 or CAP. The input is the infected slices that are detected in Stage 1. The output of Stage 2 indicates the percentage of infected slices of COVID-19 for the entire volume. To distinguish between COVID-19 and CAP, we chose the threshold probability of 0.6. Note that the higher the cut-off value is, the more cases can be identified as COVID-19.

### 3.4. Test Results

Among the data given in the competition, the accuracy was 46 % when we tested the model with the remaining data, which are other than the data used to train. The test input included 25 COVID-19 patients, 10 CAP patients, and 15 NORMAL patients. The test results are summarized in Table 1.

**Table 1**. Summary of the test results.

| Label | Sensitivity | Accuracy |
|---|---|---|
| COVID | 36 % | 46 % |
| CAP | 50 % | |
| Normal | 60 % | |

## 4. CONCLUSION

This report focuses on the algorithm for determining each patient's disease through CT pictures of patients with COVID-19, CAPS, and Normal. We utilized 30 COVID-19,15 CAP,10 Normal patients to train the model and observed 73 percent accuracy in Stage 1 and 72 percent accuracy in Stage 2, respectively. For the model test, the total accuracy was 46 percent. Although the accuracy is somewhat lower, we tried to increase accuracy by giving different weights compared to

previous studies(COVID-FACT). We observed that the accuracy increased for the case that we tried different weights than equal ones. Besides, according to the previous work, when the ratio of the abnormal slices is less than 3 percent, they are classified as normal patients. But, in our work, we observed that 30 percent is optimal through trial and error. The amount of data was insufficient, and all data could not be used for training and testing because the amount of data specified in the infected slice was small. However, the appropriate proportions are found through many trials and utilized for learning to produce results.

## 5. REFERENCES


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