# COVID-CAPS: A CAPSULE NETWORK-BASED FRAMEWORK FOR IDENTIFICATION OF COVID-19 CASES FROM X-RAY IMAGES

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## ABSTRACT

Novel Coronavirus disease (COVID-19) has abruptly and undoubtedly changed the world as we know it at the end of the 2nd decade of the 21st century. COVID-19 is extremely contagious and quickly spreading globally making its early diagnosis of paramount importance. Early diagnosis of COVID-19 enables health care professionals and government authorities to break the chain of transition and flatten the epidemic curve. The common type of COVID-19 diagnosis test, however, requires specific equipment and has relatively low sensitivity and high false-negative rate. Computed tomography (CT) scans and X-ray images, on the other hand, reveal specific manifestations associated with this disease. Overlap with other lung infections makes human-centered diagnosis of COVID-19 challenging. Consequently, there has been an urgent surge of interest to develop Deep Neural Network (DNN)-based diagnosis solutions, mainly based on Convolutional Neural Networks (CNNs), to facilitate identification of positive COVID-19 cases. CNNs, however, are prone to lose spatial information between image instances and require large datasets. This paper presents an alternative modeling framework based on Capsule Networks, referred to as the COVID-CAPS, being capable of handling small datasets, which is of significant importance due to sudden and rapid emergence of COVID-19. Our initial results based on a dataset of X-ray images show that COVID-CAPS has advantage over previous CNN-based models. COVID-CAPS achieved an Accuracy of $95.7\%$, Sensitivity of $90\%$, Specificity of $95.8\%$, and Area Under the Curve (AUC) of $0.97$, while having far less number of trainable parameters in comparison to its counterparts.

***Index Terms*: COVID-19 Pandemic, X-ray Images, Deep Learning, Capsule Network.**

## 1. INTRODUCTION

Novel Coronavirus disease (COVID-19), first emerged in Wuhan, China [1], has abruptly and significantly changed the world as we know it at the end of the 2nd decade of the 21st century. COVID-19 seems to be extremely contagious and quickly spreading globally with common symptoms such as fever, cough, myalgia, or fatigue resulting in ever increasing number of human fatalities. Besides having a rapid human-to-human transition rate, COVID-19 is associated with high Intensive Care Unit (ICU) admissions resulting in an urgent quest for development of fast and accurate diagnosis solutions [1]. Identifying positive COVID-19 cases in early stages helps with isolating the patients as quickly as possible [2], hence breaking the chain of transition and flattening the epidemic curve.

Reverse Transcription Polymerase Chain Reaction (RT-PCR), which is currently the gold standard in COVID-19 diagnosis [1], involves detecting the viral RNA from sputum or nasopharyngeal swab. The RT-PCR test is, however, associated with relatively low sensitivity (true positive rate) and requires specific material and equipment, which are not easily accessible [1]. Moreover, this test is relatively time-consuming, which is not desirable as the positive COVID-19 cases should be identified and tracked as fast as possible [2]. Images [3] in COVID-19 patients, on the other hand, have shown specific findings, such as ground-glass opacities with rounded morphology and a peripheral lung distribution. Although imaging studies and theirs results can be obtained in a timely fashion, the previously described imaging finding may be seen in other viral or fungal infections or other entities such as organizing pneumonia which limits the specificity of images and reduces the accuracy of a human-centered diagnosis.

**Literature Review:** Since revealing the potentials of computed tomography (CT) scans and X-ray images in detecting COVID-19 and weakness of the human-centered diagnosis, there have been several studies [5–7] trying to develop automatic COVID-19 classification systems, mainly using Convolutional Neural Networks (CNNs) [4]. Xu *et al.* [1] have first adopted a pre-trained 3D CNN to extract potential infected regions from the CT scans. These candidates are subsequently fed to a second CNN to classify them into three groups of COVID-19, Influenza-A-viral-pneumonia, and irrelevant-to-infection, with an overall accuracy of $86.7\%$. Wang *et al.* [2] have first extracted candidates using a threshold-based strategy. Consequently, for each case two or three regions are randomly selected to form the dataset. A pre-trained CNN is fine-tuned using the developed dataset. Finally, features are extracted from the CNN and fed to an ensemble of classifiers for the COVID-19 prediction, reaching an accuracy of $88\%$. CT scans are also utilized in Reference [8] to identify positive COVID-19 cases, where all slices are separately fed to the model and outputs are aggregated using a Max-pooling operation, reaching a sensitivity of $90\%$. In a study by Wang and Wong [9], a CNN model is first pre-trained on the ImageNet dataset [10], followed by fine-tuning using a dataset of X-ray images to classify subjects as normal, bacterial, non-COVID-19 viral, and COVID-19 viral infection, achieving an overall accuracy of $83.5\%$. In a similar study by Sethy and Behera [11], different CNN models are trained on X-ray images, followed by a Support Vector Machine (SVM) classifier to identify positive COVID-19 cases, reaching an accuracy of $95.38\%$.

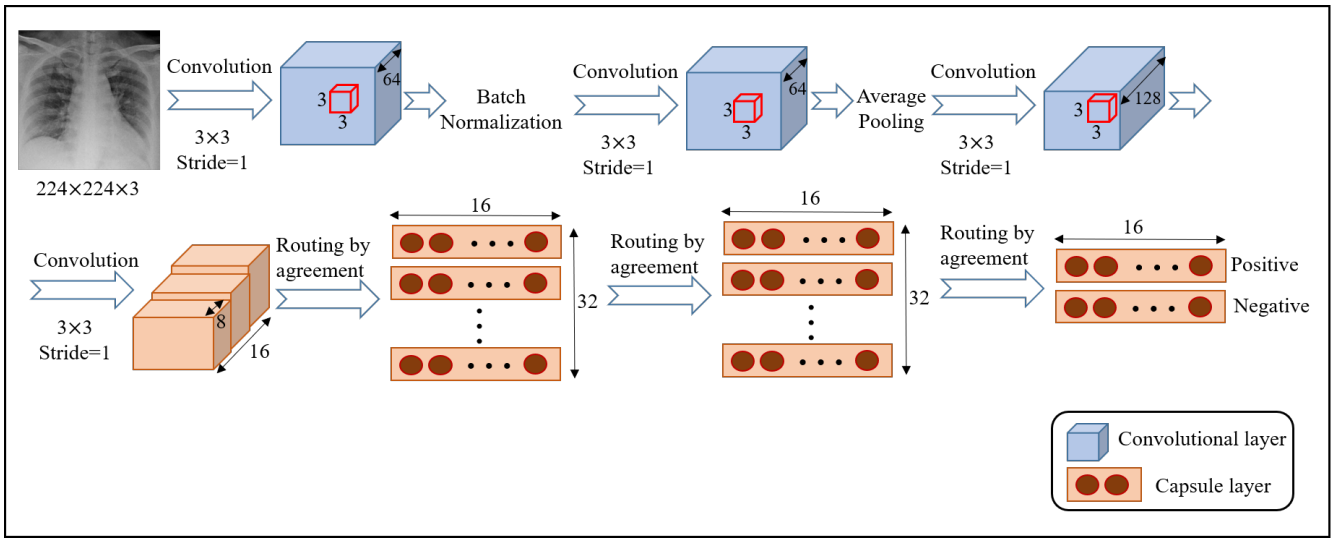



**Fig. 1**. The proposed COVID-CAPS architecture.

**Contributions:** All the studies on deep learning-based COVID-19 classification have so far utilized CNNs, which although being powerful image processing techniques, are prone to an important drawback. They are unable to capture spacial relations between image instances. As a result of this inability, CNNs cannot recognize the same object when it is rotated or subject to another type of transformation. Adopting a big dataset, including all the possible transformations, is the solution to this problem. However, in medical imaging problems, including the COVID-19 classification, huge datasets are not easily accessible. In particular, COVID-19 has been identified only recently, and large enough datasets are not yet developed. Capsule Networks (CapsNets) [12] are alternative models that are capable of capturing spatial information using routing by agreement, through which Capsules try to reach a mutual agreement on the existence of the objects. This agreement leverages the information coming from instances and object parts, and is therefore able to recognize their relations, without a huge dataset. Through several studies [13–18], we have shown the superiority of the CapsNets for different medical problems such as brain tumor [13–17] and lung tumor classification [18]. In this study, we propose a Capsule Network-based framework, referred to as the COVID-CAPS, for COVID-19 identification using X-ray images. The proposed COVID-CAPS achieved an accuracy of 95.7%, a sensitivity of 90%, specificity of 95.8%, and Area Under the Curve (AUC) of 0.97. Trained COVID-CAPS model is available publicly for open access at https://github.com/ShahinSHH/COVID-CAPS. To the best of our knowledge, this is the first study investigating applicability of the CapsNet for the problem at hand.

The rest of the manuscript is organized as follows: Section 2 briefly introduces the Capsule networks. The COVID-CAPS is presented in Section 3. Utilized dataset for evaluation of the proposed COVID-CAPS, and our initial results are presented in Section 4. Finally, Section 5 concludes the work.

## 2. CAPSULE NETWORKS

Each layer of a Capsule Network (CapsNet) consists of several Capsules, each of which represents a specific image instance at a specific location, through several neurons. The length of the Capsule determines the existence probability of the associated instance. Similar to a regular CNN, each Capsule $i$, having the instantiation parameter $\boldsymbol{u}_i$, tries to predict the outputs of the next layer's Capsules, using a trainable weight matrix $\boldsymbol{W}_{ij}$, as follows

$$\hat{\boldsymbol{u}}_{j|i} = \boldsymbol{W}_{ij}\boldsymbol{u}_i, \tag{1}$$

where $\hat{\boldsymbol{u}}_{j|i}$ denotes the prediction of Capsule $i$ for Capsule $j$. The predictions, however, are taken into account based on a coefficient, through the "routing by agreement" process, to determine the actual output of the Capsule $j$, denoted by $\boldsymbol{s}_j$, as follows

$$a_{ij} = \boldsymbol{s}_j.\hat{\boldsymbol{u}}_{j|i}, \tag{2}$$

$$b_{ij} = b_{ij} + a_{ij}, \tag{3}$$

$$c_{ij} = \frac{\exp(b_{ij})}{\sum_k \exp(b_{ik})}, \tag{4}$$

$$\text{and } \boldsymbol{s}_j = \sum_i c_{ij}\hat{\boldsymbol{u}}_{j|i}, \tag{5}$$

where $a_{ij}$ denoted the agreement between predictions and outputs, and $c_{ij}$ is the score given to the predictions. In other words, this score determines the contribution of the prediction to the output. Routing by agreement is what makes the CapsNet different from a CNN and helps it identify the spatial relations.

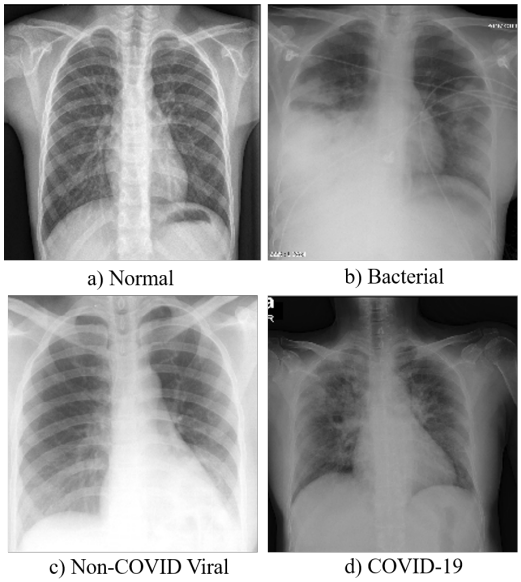
The CapsNet loss function, $l_k$, associated with Capsule $k$, is calculated as follows

$$l_k = T_k \max(0, m^+ - ||\boldsymbol{s}_k||)^2 + \lambda(1 - T_k)\max(0, ||\boldsymbol{s}_k|| - m^-)^2, \tag{6}$$

where $T_k$ is one whenever the class $k$ is present and zero otherwise. Terms $m^+$, $m^-$, and $\lambda$ are the hyper parameters of the model. The final loss is the summation over all the $l_k$s.

## 3. THE PROPOSED COVID-CAPS

The proposed COVID-CAPS is shown in Fig. 1, which consists of 4 convolutional layers and 3 Capsule layers. The inputs to the network are 3D X-ray images. The first layer is a convolutional one, followed by batch-normalization. The second layer is also a convolutional one, followed by average pooling. Similarly, the third and



a) Normal b) Bacterial

c) Non-COVID Viral d) COVID-19

**Fig. 2**. Labels available in the dataset.

forth layers are convolutional ones, where the forth layer is reshaped to form the first Capsule layer. Consequently, three Capsule layers are embedded in the network to perform the routing by agreement process. The last Capsule layer contains the instantiation parameters of the two classes of positive and negative COVID-19. The length of these two Capsules represents the probability of each class being present.

Since we have developed a Capsule Network-based architecture, which does not need a large dataset, we did not perform any data augmentation and/or used a pre-trained model. However, since the number of positive cases, $N^+$, are less than the negative ones, $N^-$, we modified the loss function to handle the class imbalance problem. In other words, more weight is given to positive samples in the loss function, where weights are determined based on the proportion of the positive and negative cases, as follows

$$\begin{aligned} l_k = &\frac{N^+}{N^+ + N^-} T_k \max(0, m^+ - ||\boldsymbol{s}_k||)^2 \\ &+ \frac{N^-}{N^+ + N^-} \lambda (1 - T_k) \max(0, ||\boldsymbol{s}_k|| - m^-)^2. \end{aligned} \tag{7}$$

We used Adam optimizer with an initial learning rate of $10^{-5}$, 100 epochs, and a batch size of 16. We have split the training dataset, described in Section 4, into two sets of training (90%) and validation (10%), where training set is used to train the model and the validation set is used to select a model that has the best performance. Selected model is then tested on the testing set, for the final evaluation. The following four metrics are utilized to represent the performance: Accuracy; Sensitivity; Specificity, and Area Under the Curve (AUC). Next, we present the obtained results.

## 4. EXPERIMENTAL RESULTS

To conduct our experiments, we used the same dataset as Reference [9]. This dataset is generated from two publicly available chest X-ray datasets [19, 20]. As shown in Fig. 2, the generated dataset contains four different labels, i.e., Normal; Bacterial; Non-COVID Viral, and; COVID-19. As the main goal of this study is to identify positive COVID-19 cases, we binarized the labels as either positive or negative. In other words, the three labels of normal, bacterial, and non-COVID viral together form the negative class.

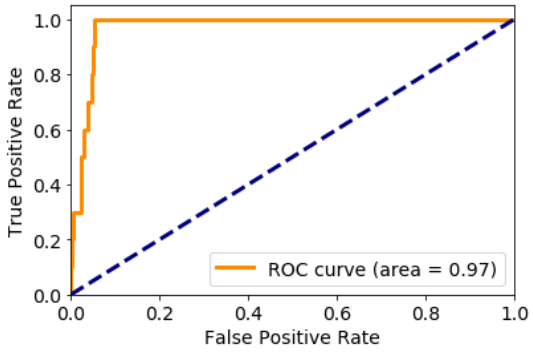



**Fig. 3**. ROC curve from the proposed COVID-CAPS.

Using the aforementioned dataset, the proposed COVID-CAPS achieved an accuracy of 95.7%, a sensitivity of 90%, specificity of 95.8%, and AUC of 0.97. The obtained receiver operating characteristic (ROC) curve is shown in Fig. 3. *In particular, false positive cases have been further investigated to have an insight on what types are more subject to being mis-classified as COVID-19. It is observed that* 54% *of the false positives are normal cases, whereas bacterial and non-COVID cases form only* 27% *and* 19% *of the false positives, respectively.*

Finally, as shown in Table 1 we compare our results with Reference [11] that has used the binarized version of the same dataset. COVID-CAPS outperforms its counterpart in terms of accuracy and specificity. Sensitivity is higher in the model proposed in Reference [11], that contains 23 million trainable parameters. *It is worth mentioning that the proposed COVID-CAPS has only* 295,488 *trainable parameters. Compared to* 23 *million trainable parameters of the model proposed in Reference [11], therefore, COVID-CAPS can be trained and used in a more timely fashion, and eliminates the need for availability of powerful computational resources.*

Reference [6] is another study on the binarized version of the same X-ray images. However, as the negative label contains only normal cases (in contrast to including all normal, bacterial, and non-COVID viral cases as negative), we did not compare the performance of the COVID-CAPS with this study.

## 5. CONCLUSION

In this study, we proposed a Capsule Networks-based framework, referred to as the COVID-CAPS, for diagnosis of COVID-19 from X-ray images. The proposed framework consists of several Capsule and convolutional layers, and the lost function is modified to account for the class-imbalance problem. The obtained results show that the COVID-CAPS has a satisfying performance with a low number of trainable parameters. Trained COVID-CAPS model is available publicly for open access at https://github.com/ShahinSHH/COVID-CAPS. As more and more COVID-19 cases are being identified all around the world, larger datasets are being generated. We will continue to further modify the architecture of the COVID-CAPS and incorporate new available datasets. New versions of the COVID-CAPS will be released upon development through the aforementioned link.

**Table 1**. Results obtained from the proposed COVID-CAPS, along with the results from Reference [11].

| Method | Accuracy | Sensitivity | Specificity | Number of Trainable Parameters |
|---|---|---|---|---|
| **Proposed COVID-CAPS** | **95.7%** | 90% | **95.8%** | **295,488** |
| **Reference [11]** | 95.38% | **97.29%** | 93.47% | 23,000,000 |

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