A Teacher-Student Framework with Fourier Augmentation for COVID-19 Infection Segmentation in CT Images

Han Chen\textsuperscript{a}, Yifan Jiang\textsuperscript{a}, Hanseok Ko\textsuperscript{a,\ast}, Murray Loew\textsuperscript{b}

\textsuperscript{a}School of Electrical Engineering, Korea University, Seoul, South Korea
\textsuperscript{b}Biomedical Engineering, George Washington University, Washington D.C., USA

Abstract
Automatic segmentation of infected regions in computed tomography (CT) images is necessary for the initial diagnosis of COVID-19. Deep-learning-based methods have the potential to automate this task but require a large amount of data with pixel-level annotations. Training a deep network with annotated lung cancer CT images, which are easier to obtain, can alleviate this problem to some extent. However, this approach may suffer from a reduction in performance when applied to unseen COVID-19 images during the testing phase due to the domain shift. In this paper, we propose a novel unsupervised method for COVID-19 infection segmentation that aims to learn the domain-invariant features from lung cancer and COVID-19 images to improve the generalization ability of the segmentation network for use with COVID-19 CT images. To overcome the intensity shift, our method first transforms annotated lung cancer data into the style of unlabeled COVID-19 data using an effective augmentation approach via a Fourier transform. Furthermore, to reduce the distribution shift, we design a teacher-student network to learn rotation-invariant features for segmentation. Experiments demonstrate that even without getting access to the annotations of COVID-19 CT during training, the proposed network can achieve a state-of-the-art segmentation performance on COVID-19 images.

Keywords: COVID-19, Infection Segmentation, Computed Tomography, Teacher-Student Network, Fourier Transform

1. Introduction
The pandemic caused by the novel coronavirus disease (COVID-19) that emerged at the start of 2020 has had significant worldwide medical and economic impacts \[1\textsuperscript{,}2\]. A recent report by the World Health Organization found that there had been more than 198 million confirmed cases and more than 4 million deaths globally by July 2021 \[3\]. To diagnose COVID-19, real-time reverse transcription-polymerase chain reaction (RT–PCR) tests and radiological imaging techniques, such as computed tomography (CT) and X-rays, are widely used. In particular, CT imaging plays a critical role in the early diagnosis and evaluation of COVID-19 \[4\textsuperscript{,}5\], with the segmentation of infected regions in CT scans providing essential information that can be used in the quantitative assessment of the progression of the disease \[6\textsuperscript{,}7\].

Recently, deep-learning-based automatic segmentation methods \[8\textsuperscript{,}9\textsuperscript{,}10\textsuperscript{,}11\textsuperscript{,}12\] have been proposed for use in COVID-19 CT image analysis, and these have achieved excellent results. Despite the promising results, however, these approaches all rely on large datasets with pixel-level annotations, and it is time-consuming and laborious to collect a sufficient number of COVID-19 CT images with annotations due to concerns over patient privacy and the lack of experts \[13\textsuperscript{,}14\textsuperscript{,}15\]. In contrast, collecting lung cancer datasets...

\textsuperscript{\ast}Corresponding author
Email address: hsko@korea.ac.kr (Hanseok Ko)
is relatively easy. Therefore, it is possible to utilize publicly available lung cancer databases to train a deep network for the detection of COVID-19 infections. For example, Jin et al. [16] developed a system using a large dataset from the Lung Image Database Consortium and Image Database Resource Initiative (LIDC-IDRI) [17] to achieve multi-class classification diagnoses. Chen et al. [18] also proposed a contrastive learning method and trained an encoder that could be used to capture expressive feature representations in large lung datasets; they then employed a prototypical network for COVID-19 classification.

However, these approaches were not able to produce any significant improvement in segmentation performance for COVID-19 infections, and few other studies have attempted to utilize lung cancer datasets for this purpose. Even though COVID-19 infection and lung cancer nodule exhibit similar manifestations to some degree in CT scans, models trained using CT images with lung nodules do not perform well when tested on COVID-19 CT images due to the domain shift between the two. The difference between pulmonary nodules and COVID-19 infection in CT scans is presented in Fig. [1] and can be categorized as follows: (1) In terms of distribution, COVID-19 presents as a bilateral, patchy infection, while early-stage lung cancer is unilateral and oval in shape [19]; (2) While there is also a clear difference in intensity due to the use of different scanners, scanning protocols, and subject populations [20].

In this paper, we consider infection segmentation in the context of the wide availability of lung cancer CT images with annotations, the limited availability of unlabeled COVID-19 CT images, and the domain shift between the two. We hypothesize that the features learned from pulmonary nodules in lung cancer CT can improve the segmentation performance for COVID-19 diagnosis through alignment. For our segmentation network, we design a novel data augmentation method and training scheme. In order to address the intensity shift, we transform the lung cancer CT images into the style of COVID-19 CT images using an effective augmentation approach via a Fourier transform, which replaces the low-level frequencies in the lung cancer CT images with those of COVID-19 CT images. Because lung cancer CT images are labeled at pixel-level, the augmented images and corresponding annotations are used to train the end-to-end infection segmentation network. To overcome the distribution shift, we introduce a teacher-student learning paradigm to achieve robust features learning. We treat our base network as a student network and introduce another teacher network. We then impose the same type of image transformation (e.g., rotation and affine transformation) on the input to the student network and the output of the teacher network, respectively. The output predictions of these two networks are forced to be consistent with these transformations. We validate the effectiveness of our proposed method using public COVID-19 CT images. Experimentally, it outperforms various competing state-of-the-art approaches.

The contributions of our work can be summarized as follows:

- We propose a novel unsupervised COVID-19 infection segmentation network to distinguish the infected regions in the COVID-19 CT images, of which the training process requires a large-scale labeled lung cancer CT dataset and unlabeled COVID-19 CT images.
- We propose an effective data augmentation method to overcome the intensity shift between the lung cancer data and COVID-19 data using a Fourier transform and its inverse.
- We build a segmentation framework that collaborates with a teacher-student network based on transformation-consistency learning, thus alleviating the distribution shift and allowing the network to learn the robust features.
- The experimental results show that our proposed method can achieve a state-of-the-art performance for COVID-19 CT images. We also provide a comprehensive analysis of our approach.

2. Related Works

**COVID-19 Infection Segmentation.** Deep-learning-based segmentation methods have played an essential role in the fight against COVID-19. For example, Oulefki et al. [21] presented a multilevel thresholding process based on Kapur entropy to improve the COVID-19 segmentation performance. Zhou et al. [22] proposed to use spatial and channel attention to improve the representation ability of the network. Ouyang et al. [23] developed a 3D CNN network for COVID-19 infection segmentation and proposed a dual-sampling attention mechanism. To address the scarcity of well-labeled data, some studies constructed new networks suitable for small-scale or point-level labeled data. Fan et al. [8] presented a semi-supervised segmentation method based on a random selection propagation strategy, which required only a few labeled images and primarily utilizes unlabeled data. Laradji
Our method is designed to compensate for the scarcity of COVID-19 data by utilizing a large-scale lung cancer dataset. Specifically, we propose an unsupervised COVID-19 infection segmentation network with robust invariant-feature learning. We propose to transform the lung cancer data into the style of COVID-19 CT images for data augmentation to overcome the intensity shift. By constructing a teacher-student network with consistency learning and entropy minimization, our network can then learn those features that are robust to transformations. As a consequence, the distribution shift is alleviated to some degree.

3. Proposed Method

In this section, we provide an overview of our proposed method. We then illustrate our Fourier transformation-based data augmentation method. Finally, we describe our teacher-student training strategy and optimization objection.

3.1. Overview

Fig. 2 overviews our unsupervised COVID-19 infection segmentation network. The labeled lung cancer image and unlabeled COVID-19 CT image are denoted as \{X^L, Y^L\} and \{X^U\}, respectively. We first augment the input data by replacing the low-frequency information of \(\mathcal{F}(X^L)\) with that of \(\mathcal{F}(X^U)\). After the use of the inverse Fourier transformation, we obtain \{X_{\rightarrow T}, Y^L\} which retains the semantic information for lung cancer but in COVID-19 style. A teacher and a student network are employed in our framework, with the former acting as an ensemble network and the latter acting as the base network. After data augmentation, we feed \(X_{\rightarrow T}\) into the student network and obtain the pixel-wise segmentation prediction. \(X^U\) is sent to both the student and teacher networks. Here, we apply the same transformation to the input of the student network and to the output of the teacher network, then align the two-stream outputs with the consistency loss. Back-propagation only occurs for the student network, and the weights of the teacher network are updated using the exponential moving average (EMA) for the student network.

3.2. Data augmentation using frequency space transformation

To address the intensity shift between the lung cancer and COVID-19 CT images, our solution employs a Fourier transform and replaces the low-frequency spectrum information of the lung cancer images with that of the COVID-19 images. In this way, we make it possible to disentangle the low-level distribution (i.e., the intensity information) from the high-level semantic information (i.e., the object content) of an image and transfer the former to another image.
Specifically, given image $X \in \mathbb{R}^{H \times W \times C}$ ($C = 1$ for a single-channel input), we can calculate its Fourier transform using the FFT algorithm as,

$$\mathcal{F}(X)(u, v) = \sum_{h=0}^{H-1} \sum_{w=0}^{W-1} X(h, w) e^{-j2\pi \frac{h u}{H} + \frac{w v}{W}}$$  \hspace{1cm} (1)$$

We further decompose $\mathcal{F}(X)$ into an amplitude spectrum $\mathcal{A}(X) \in \mathbb{R}^{H \times W \times C}$ and a phase spectrum $\mathcal{P}(X) \in \mathbb{R}^{H \times W \times C}$, which respectively represent the intensity distribution and semantic content of the image, respectively. We then denote a binary mask $M = \mathbb{I}_{(h, w) \in \mathbb{R}^{H \times W \times C}}$, which controls the scale of the amplitude spectrum to be replaced. Given $\mathcal{A}(X_T)$ from the lung cancer image and $\mathcal{A}(X_T)$ from the COVID-19 image, we apply the mask $M_n$ to them and generate a new amplitude spectrum:

$$\mathcal{A}(X_{S \rightarrow T}) = M_n \mathcal{A}(X_T) + (1 - M_n) \mathcal{A}(X_T)$$  \hspace{1cm} (2)$$

After obtaining the transformed amplitude spectrum $\mathcal{A}(X_{S \rightarrow T})$, we combine it with the phase spectrum $\mathcal{P}(X_S)$ for lung cancer image $X_S$ and conduct the inverse Fourier transform $\mathcal{F}^{-1}$ to generate augmented image $X_{S \rightarrow T}$.

$$X_{S \rightarrow T} = \mathcal{F}^{-1}(\mathcal{A}(X_{S \rightarrow T}), \mathcal{P}(X_S))$$  \hspace{1cm} (3)$$

where the semantic content of $X_{S \rightarrow T}$ is the same as $X_S$, but follows the intensity distribution of $X_T$. In this way, we obtain the augmented lung cancer data $\{X_{S \rightarrow T}, Y_S\}$ with a similar intensity to that of COVID-19 images; this augmented data is utilized for further training and can effectively alleviate the intensity distribution between the two domains.

3.3. Teacher-student network and entropy minimization

Even though the augmented data $X_{S \rightarrow T}$ have a similar style to $X_T$, a difference in distribution remains. To account for this distribution shift between the nodule of lung cancer nodules and COVID-19 infection, we build a teacher-student network with a transformation-consistency learning strategy. The teacher and student networks follow the same U-Net architecture [45] but are updated in different ways.

Specifically, the $X_{S \rightarrow T}$ for lung cancer is only sent to the student network to output the pixel-wise segmentation result $\hat{Y}_S$, which is then utilized to calculate the following dice loss [46]:

$$\mathcal{L}_{\text{dice}} = \frac{2 \sum_{n=1}^{N} p_n g_n}{\sum_{n=1}^{N} p_n + \sum_{n=1}^{N} g_n + \epsilon}$$  \hspace{1cm} (4)$$

where $g_n$ and $p_n$ represent the ground truth for the input and the predicted probabilistic map, respectively, with a background class probability of $1 - p_n$. The term $\epsilon$ is used to avoid being divided by zero.

Updating the base student network with the segmentation loss in Equation (4) leads to good segmentation performance for lung cancer images. However, when testing on the COVID-19 images, the performance will be significantly lower due to the distribution shift. To resolve this problem, we introduce a teacher network and utilize the unlabeled COVID-19 CT images to guide the student network to learn the robust features. As shown
in Fig 2 we first impose an elastic transformation $\tau(\cdot)$ on $X_T$, then the student network takes the transformed $\tau(X_T)$ as input and produce the predicted segmentation map. For the teacher network, we apply the same transformation $\tau(\cdot)$ on its prediction map. We then define the consistency loss for the predictions:

$$L_{\text{con}} = -\frac{1}{HW} \sum_{h=0}^{H-1} \sum_{w=0}^{W-1} \|f_t(\tau(X_T))^{(h,w)} - \tau(f_t(X_T))^{(h,w)}\|^2$$

(5)

To more firmly bridge the gap between the labeled lung cancer image and the COVID-19 image, we introduce entropy minimization to force the model's decision boundary toward a high prediction certainty for the teacher network's prediction from the COVID-19 input. Given a COVID-19 CT image $X_T$, the entropy loss is calculated as follows:

$$L_{\text{ent}} = -\frac{1}{HW} \sum_{h=0}^{H-1} \sum_{w=0}^{W-1} f_t(X_T) \log(f_t(X_T))$$

(6)

We update the student network with a combination of the dice loss, consistency loss and entropy loss. The optimization objection can thus be formulated as follows:

$$L_{\text{student}} = L_{\text{dice}} + \lambda L_{\text{con}} + L_{\text{ent}}$$

(7)

where $\lambda$ is the hyper-parameter acting as a weight for the consistency loss. Unlike the student network, the teacher network does not participate in the backpropagation and is updated via the exponential moving average (EMA) of the weights for the current student network at each step,

$$\theta_{t,i} = \beta \theta_{t,i-1} + (1 - \beta) \theta_{s,i}$$

(8)

where $\theta_{t,i}$ and $\theta_{s,i}$ represent the weights for the teacher and student networks at training step $i$, respectively, and $\beta$ is a hyper-parameter for exponential moving average decay.

The ensemble of the teacher and student network makes it possible to train the network with the unlabeled COVID-19 CT images. Moreover, through the regularization of the consistency loss, the student network can learn from the teacher network output. The networks are then regularized to be transformation-consistent thus increasing the generalization capacity and robustness to the distribution shift between the lung cancer images and the unlabeled COVID-19 images.

4. Experiments

4.1. Experimental settings

Datasets. The lung cancer data comes from the LIDC-IDRI lung cancer dataset [17], which is currently the largest CT dataset for pulmonary nodule detection. It provides a large number of chest CT images that share similarities with COVID-19 CT images. The LIDC-IDRI dataset contains 1018 cases, each of which includes images from a clinical thoracic CT scan along with pixel-wise annotations from experienced radiologists. The COVID-19 CT images come from [http://medicalsegmentation.com/covid19] which has been collected by the Italian Society of Medical and International Radiology. It contains 26 CT volumes from confirmed COVID-19 patients, and each volume contains ~200 slices.

The data processing for the above two datasets is detailed as follows. For LIDC-IDRI, we select subjects with lung nodules and generate a corresponding ground truth mask based on the patient’s XML file. We exclude the scans where the pixel number for every nodule is less than 200 for robust training. This leaves a total of 2,438 slices from lung cancer CT images with annotations that are used as source data for training. For the COVID-19 CT images, we reformat all of the 3D volumes into 2D slices with a size of 512×512 to produce a total of 1,616 slices. We employ 70% of these slices as the unlabeled target data for training, while the remaining 30% are used to test segmentation performance. We follow the patient-level split rule when separating the target data into the training and test sets.

Implementation details. Our network is implemented using PyTorch on an NVIDIA RTX 2080Ti and an Intel(R) Core i7-9700K CPU. The batch size is set to 1. We use an Adam optimizer with the initial learning rate of 6e-4 and weight decay of 0.0005. The hyper-parameters are set at $\alpha = 0.005$ and $\beta = 0.99$. The consistency weight is updated using a sigmoid ramp-up of $\lambda = 1.5e^{-5(1-p)^2}$, where $p$ is the progress of the training epochs normalized to a range of 0 to 1. The structure of the student and teacher networks follows U-Net architecture [45].

Evaluation metrics. For quantitative evaluation, we adopt the three most commonly used metrics in medical imaging analysis: the dice similarity coefficient (Dice), sensitivity (Sen), and specificity (Spe) [47, 46]. The dice similarity coefficient is an overlap index that indicates the similarity between the prediction and the ground truth. Sensitivity and specificity are two statistical measures for the performance of binary medical image segmentation tasks. The former measures the per-
Table 1: Segmentation performance for COVID-19 CT images. The highest evaluation score is marked in bold. ↑ indicates that a higher number is better.

| Method      | Dice (%) ↑ | Sen (%) ↑ | Spe (%) ↑ |
|-------------|------------|-----------|-----------|
| Source-only | 40.06±8.26 | 33.68±8.55| 99.86±0.03|
| FDA [31]    | 41.55±8.75 | 38.28±7.33| 99.96±0.01|
| MinEnt [37] | 43.86±6.43 | 40.65±6.06| 99.95±0.02|
| AdvEnt [37] | 44.11±7.35 | 40.76±6.54| 99.95±0.02|
| Ours        | 49.51±6.48 | 44.70±9.38| 99.75±0.06|

Percentage of actual positive pixels correctly predicted to be positive, while the latter measures the proportion of actual negative pixels correctly predicted to be negative. These metrics are defined as follows:

\[
\text{Dice} = \frac{2 \times TP}{2 \times TP + FP + FN} \tag{9}
\]

\[
\text{Sen} = \frac{TP}{TP + FN} \tag{10}
\]

\[
\text{Spe} = \frac{TN}{TN + FP} \tag{11}
\]

where \(TP\), \(FP\), \(TN\), and \(FN\) represent the number of true positive, false positive, true negative, and false negative pixels in the prediction, respectively.

4.2. Experimental results

In this section, we compare the COVID-19 infection segmentation performance of the proposed method with the source-only (baseline) model and the state-of-the-art segmentation methods FDA [31], MinEnt [37], and AdvEnt [37].

Quantitative results. Table 1 shows the quantitative results for each method, reported as the mean± error interval (calculated based on a 95% confidence interval). Our proposed method outperforms the other methods across most metrics. For example, our method produces a 9.54% improvement in the dice similarity coefficient compared with that of the source-only method, which trains the U-Net using lung cancer data in a supervised manner, which confirms the effectiveness of our data augmentation and consistency learning. FDA [31] also transforms lung cancer images into the style of COVID-19 images, which helps to reduce the intensity shift to some degree, but it still suffers from poor generalization because it does not consider the distribution shift. Unlike the entropy-based methods MinEnt [37] and AdvEnt [37], our method attempts to learn the domain-invariant features for segmentation. Fig.3 shows that our proposed method produces the most impressive results overall, proving that the teacher-student structure can yield a more robust segmentation performance.

Qualitative results. Fig.4 presents the segmentation results (red regions) for our method and other approaches as a comparison. The source-only method is able to distinguish small infected regions but suffers from poor generalization for large-scale infections, such as case (b), because it is only trained with the LIDC-IDRI lung cancer dataset, in which the pulmonary nodules are relatively small and oval in shape. Similar to our method, FDA [31] also utilizes unlabeled data and transforms the labeled images into the style of unlabeled images for supervised training, thus overcome the intensity shift. However, it cannot account for distribution shift, thus it performs poorly for case (d). MinEnt [37] utilizes entropy minimization with the segmentation map to overcome the shift between the labeled data and unlabeled data but fails to capture the fine-grained details in case (b). AdvEnt [37] relies on the adversarial training with the entropy map and is unable to handle the large-scale infections in cases (b) and (d). Overall, our proposed method performs better than the other methods and is consistently closer to the ground-truth COVID-19 infected region, demonstrating that our method effectively utilizes the unlabeled COVID-19 images and improves segmentation performance.

4.3. Ablation analysis

This section describes the ablation analysis, of which the purpose is to assess the importance of each component and visualize the feature distribution learned by our method.

Contribution of each component. We validate the effect of each component of our method by analyzing the performance of the following setups: (1) Source-only,
Figure 4: Qualitative results for the segmentation task. Columns 1 presents the input COVID-19 CT images with the ground truth marked in red, while columns 2 to 6 are the segmentation results for the Source-only approach, FDA [31], MinEnt [37], AdvEnt [37], and our proposed method.

| Method     | Dice (%)  | Sen (%)  | Spe (%) |
|------------|-----------|----------|---------|
| Source-only| 40.06±8.26| 33.68±8.55| 99.86±0.03 |
| w/o aug.   | 48.40±6.82| 43.59±11.33| 99.63±0.11 |
| w/o con.   | 46.94±7.70| 39.13±8.56| **99.89±0.04** |
| w/o ent.   | 47.98±7.07| 44.45±9.92| 99.72±0.05 |
| Ours       | **49.51±6.48** | **44.70±9.38** | 99.75±0.06 |

Table 2: Ablation analysis of the components in the proposed network. The highest evaluation score is marked in bold. ↑ indicates that a higher number is better.

which includes only the student network and is trained with the lung cancer data in a supervised manner; (2) w/o aug., in which the data augmentation process that is essential for overcoming the intensity shift is removed; (3) w/o con., in which the teacher network is removed, corresponding to \( \lambda = 0 \) and the consistency loss not being used to update the student network; (4) w/o ent., in which the entropy minimization is not calculated, which corresponds to \( \lambda = 0 \). As shown in Table 2, the exclusion of any of the components, especially the teacher network, leads to a drop in performance, thus confirming that these components play an important role in the performance of our proposed method. In particular, data augmentation lays a foundation for alleviating the intensity shift, while the teacher-student training scheme allows robust transformation-invariant features to be effectively exploited.

Visualization of feature distributions via t-SNE. We analyze our proposed method by visualizing the feature representations using t-SNE [48]. We input the lung cancer and COVID-19 images to the trained baseline model of our proposed network and visualize the output feature maps for these two groups of data. As shown in Fig 5 for the baseline model, the feature distributions of lung cancer images are separated from those of the COVID-19 images because supervision only occurs with the lung cancer data. Thus, the learned features from the baseline cannot improve the segmentation performance for COVID-19 images. In contrast, our method projects the feature distributions of the two
5. Conclusion

In this paper, we proposed a novel teacher-student based framework for unsupervised COVID-19 infection segmentation in CT images. We attempted to address a challenging situation where there are no annotations for COVID-19 CT images, but the annotations for lung CT with pulmonary nodules are available. Given the differences between the pulmonary nodules with the COVID-19 infection, we introduced a Fourier transform-based augmentation method to alleviate the intensity shift. We further constructed a teacher-student network that utilizes the consistency loss and entropy loss to allow the network to learn the robust features, thus overcoming the distribution shift to some extent. Experiments on the COVID-19 CT dataset demonstrated that the proposed method produces a competitive performance when compared with the state-of-the-art methods.

References

[1] C. Wang, P. W. Horby, F. G. Hayden, G. F. Gao, A novel coronavirus outbreak of global health concern, The Lancet 395 (10223) (2020) 470–473.
[2] F. Shi, J. Wang, J. Shi, Z. Wu, Q. Wang, Z. Tang, K. He, Y. Shi, D. Shen, Review of artificial intelligence techniques in imaging data acquisition, segmentation, and diagnosis for covid-19, IEEE reviews in biomedical engineering 14 (2020) 4–15.
[3] Who coronavirus (covid-19) dashboard, [https://covid19.who.int/](https://covid19.who.int/).
[4] J. Lei, J. Li, X. Li, X. Qi, Ct imaging of the 2019 novel coronavirus (2019-ncov) pneumonia, Radiology 295 (1) (2020) 18–18.
[5] L. Li, L. Qin, Z. Xu, Y. Yin, X. Wang, B. Kong, J. Bai, Y. Lu, Z. Fang, Q. Song, et al., Artificial intelligence distinguishes covid-19 from community acquired pneumonia on chest ct, Radiology.
[6] L. Huang, R. Han, T. Ai, P. Yu, H. Kang, Q. Tao, L. Xia, Serial quantitative chest ct assessment of covid-19: a deep learning approach, Radiology: Cardiothoracic Imaging 2 (2) (2020) e200075.
[7] Y. Cao, Z. Xu, J. Feng, C. Jin, X. Han, H. Wu, H. Shi, Longitudinal assessment of covid-19 using a deep learning–based quantitative ct pipeline: illustration of two cases, Radiology: Cardiothoracic Imaging 2 (2) (2020) e200082.
[8] D.-P. Fan, T. Zhou, G.-P. Ji, Y. Zhou, G. Chen, H. Fu, J. Shen, L. Shao, Inf-net: Automatic covid-19 lung infection segmentation from ct images, IEEE Transactions on Medical Imaging 39 (8) (2020) 2626–2637.
[9] G. Wang, X. Liu, C. Li, Z. Xu, J. Ruan, H. Zhu, T. Meng, K. Li, N. Huang, S. Zhang, A noise-robust framework for automatic segmentation of covid-19 pneumonia lesions from ct images, IEEE Transactions on Medical Imaging 39 (8) (2020) 2653–2663.
[10] K. Gao, J. Su, Z. Jiang, L.-L. Zeng, Z. Feng, H. Shen, P. Rong, X. Xu, J. Qin, Y. Yang, et al., Dual-branch combination network (dcn): Towards accurate diagnosis and lesion segmentation of covid-19 using ct images, Medical image analysis 67 (2021) 101836.
[11] I. Laradji, P. Rodriguez, O. Manas, K. Lensink, M. Law, L. Kurzman, W. Parker, D. Vazquez, D. Nowrouzezahrai, A weakly supervised consistency-based learning method for covid-19 segmentation in ct images, in: Proceedings of the IEEE/CVF Winter Conference on Applications of Computer Vision, 2021, pp. 2453–2462.
[12] N. Paluru, A. Dayal, H. B. Jenssen, T. Sakinis, L. R. Cenkeramaddi, J. Prakash, P. K. Yalavarthy, Anam-net: Anamorphic depth embedding-based lightweight cnn for segmentation of
[44] J. Choi, T. Kim, C. Kim, Self-ensembling with gan-based data augmentation for domain adaptation in semantic segmentation, in: Proceedings of the IEEE/CVF International Conference on Computer Vision, 2019, pp. 6830–6840.

[45] O. Ronneberger, P. Fischer, T. Brox, U-net: Convolutional networks for biomedical image segmentation, in: International Conference on Medical image computing and computer-assisted intervention, Springer, 2015, pp. 234–241.

[46] F. Milletari, N. Navab, S.-A. Ahmadi, V-net: Fully convolutional neural networks for volumetric medical image segmentation, in: 2016 fourth international conference on 3D vision (3DV), IEEE, 2016, pp. 565–571.

[47] A. Fenster, B. Chiu, Evaluation of segmentation algorithms for medical imaging, in: 2005 IEEE Engineering in Medicine and Biology 27th Annual Conference, IEEE, 2006, pp. 7186–7189.

[48] L. Van der Maaten, G. Hinton, Visualizing data using t-sne., Journal of machine learning research 9 (11).