Imperial College
London

IMPERIAL COLLEGE LONDON

DEPARTMENT OF COMPUTING

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Author:
Tianyang Sun

Supervisor:
Dr Benny Lo

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Abstract

Your abstract.

Acknowledgments

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Chapter 1

Introduction

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In this project, we dealt with two common scenario in medical imaging on segmentation task: (1)only a small set of labelled samples are collected, and (2) a small set of labelled data is available and in addition, a relatively larger amounts of data is collected but not labelled.

For case 1, we explored transfer learning using different pretraining method or available pretrained models. We also tried to understand the network behaviour during transfer learning.

1. First, we pretrained the model on non-Covid Lung volumes to get a pretrained model $F_{pretrained}$, and we also obtained the available pretrained model of Model Genesis [1].
2. Then we perfrom transfer learning using Covid dataset on the two pretrained model weights.
3. We analyzed the results using SVCCA tool to get a further understanding of the Fine-tuned model.

For case 2, we further explored the semi-supervise learning under this typical semisupervise setup. For psuedo labeling, we proposed a method that assign the segmentation label using cosine similarity score from the labelled datset.

1. First, given a pretrained model A, we fine-tune to get A' on the small set of Covid dataset until the model gives relatively good performance (e.g Dice coefficient over 0.75).

2. Next, we random crop 120 68 * 68 patches P_{img} from the labelled datset and store the labels P_{label}. We randomly crop 32 68 * 68 slices from each volume of the unlabelled dataset.

3. Then, we take the encoder part of A'. Given an unlabelled patch $p_{unlabelled}$, we calculate its cosine similarity with each data in P_{img} in the encoded latent space and get the top two most similar labels P_{label_i}, P_{label_j} with similarity score S_i, S_j. We assign the mask with the weighted combinatino of the labels to the unlablled image **Only if both the similarity score is larger than 0.90**.

4. We treated those fake labels in step 3 as 'soft-mask'. We made a copy of A' as A'_{copy} as the student network and trained using the same way as mean-teacher training skeme.

5. We obtained an improvement of ??? percent compared with the transfer learning method.

1.4 Outline of this report

Chapter 2

Background

2.1 Scanning CT

2.1.1 CT and HU values

Computed Tomography (CT) scan leverages X-rays to generate images of the body through rapid rotation of the X-ray tube. Then **attenuation value** of the tissue can be calculated from the intensity reading of the tissue of each voxel to reconstruct the pixels in the images.

Hounsfield units (HU) represents the average attenuation value of each voxel compared to the attenuation value of water. CT numbers can take value between -1000 and 1000 while 2000 shades of grey is out of the capacity of human eyes can distinguish. Thus, only a limited number of HU are displayed for human interpretation. Lung window is normally set to [-1250, 250].

2.1.2 Thick and thin slices

Thin slices are generally regarded as planes representing thickness of less than 3mm [1] In our work, we experienced slice thickness from 1mm to 8mm.
In medical CT scanning, considering the dose of CT, and the equipment limitation, CT slice this varies a lot

[1] http://tech.snmjournals.org/content/36/2/57

2.2 Deep learning fundamentals

In this section, we briefly mention some of the fundementals of Deep Learning and some layer structures used in our experiment, note that most of our notation follows book[2].

2.2.1 Optimizers in training neural network

Batch Gradient Desent
Adam op

2.2.2 Convolutional Neural Network

Convolutional neural networks (CNN) improved deep learning with respect to **Sparse interactions, parameter sharing and equivariant representations** that employ mathematical convolution operation denoted with asterisk symbol $*$. The imaging domain usually make use of discrete convolution:

$$s(t) = (x * w)(t) = \sum_{a=-\infty}^{\infty} x(a)w(t-a)$$

We here clarify that in our following notation, we call x the **input**, w **kernel** or **weight**, and s **output** or **feature map**.
In two dimensional case:

$$S(i,j) = (I * K)(i,j) = \sum_m \sum_n I(m,n)K(i-m, j-n)$$

2.2.3 Activation function

Activation function ϕ (usually non-linear) introduce non-linearity into neural networks. In modern Neural Networks, some of the activation functions are:

- Recitified Linear Unit (RelU): $\sigma(x) = \max(0, x)$
- Eponential Linear Unit (Elu): $\sigma(x) = \begin{cases} \alpha\,(e^x - 1) & \text{for } x < 0 \\ x & \text{for } x \geq 0 \end{cases} \mid \alpha \geq 0$
- Leaky Relu: $\sigma(x) = \begin{cases} 0.01x & \text{for } x < 0 \\ x & \text{for } x \geq 0 \end{cases}$
- Sigmoid: $\sigma(x) = \frac{1}{1+e^{-x}}$
- Softmax: $\sigma(\boldsymbol{x})_i = \frac{e^{x_i}}{\sum_{j=1}^{n} e^{x_j}} \mid i \in \{1, \ldots, n\}$ Softmax scale the layer output between 0 and 1 and its sum = 1.

2.2.4 Pooling

Pooling function modify the output of a layer at a specific location through summarizing its neighboring outputs that helps an approximate invariant. Max pooling is simply the maximum output within a neighborhood. Average pooling takes the average of the neighborhood as output instead of the maximum. An illustration of pooling is shown in figure 2.1 [2]

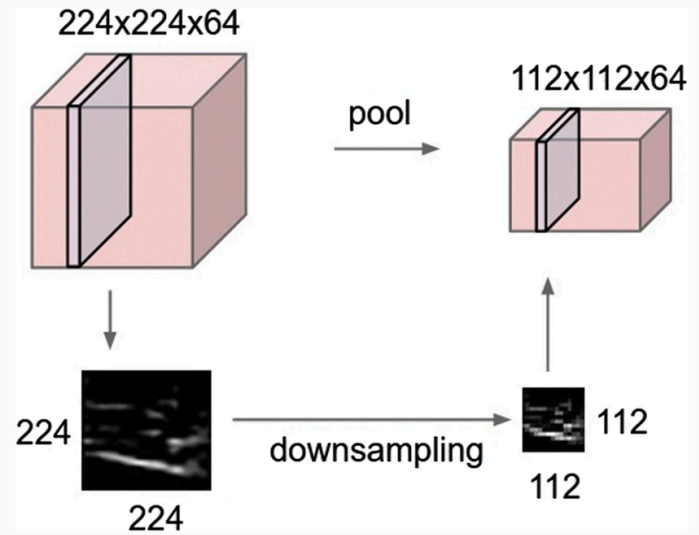


Figure 2.1: Downsampling using pooling

2.2.5 Batch Normalization

Batch normalization (BN) was proposed to mitigate **internal covariate shift** by fixing the mean and variance of each layer's inputs so that it allows each layer of the network to learn more independently from the rest of the layers.

Batch Normalization adds two trainable parameters to each of the layer. The process of BN is shown below: Define empirical mean and variance of a batch of the training set as:

$$\mu_B = \frac{1}{m}\sum_{i=1}^{m} x_i$$

$$\sigma_B^2 = \frac{1}{m}\sum_{i=1}^{m} (x_i - \mu_B)^2$$

2.2.6 Attention Gate

Attention Gate proposed in [] provided a way that we can train the network for segmentation with extra localization objective. Let $\mathbf{x}^l = \{\mathbf{x}_i^l\}_{i=1}^n$ denotes the activation

[2]https://link.springer.com/article/10.1007/s00521-019-04296-5/figures/1

Algorithm 1 Batch Normalisation

Input: Values x over a mini-batch: $Batch = x_{1...m}$, γ, β
Output: $BN_{\gamma,\beta}(x_{1...m})$
$\mu_{\mathcal{B}} \leftarrow \frac{1}{m}\sum_{i=1}^{m} x_i$
$\sigma^2_{\mathcal{B}} \leftarrow \frac{1}{m}\sum_{i=1}^{m} (x_i - \mu_{\mathcal{B}})^2$
▷ Normalizing
$\widehat{x}_i \leftarrow \frac{x_i - \mu_{\mathcal{B}}}{\sqrt{\sigma^2_{\mathcal{B}} + \epsilon}}$
▷ Scale and shift
$y_i \leftarrow \gamma \widehat{x}_i + \beta \equiv \mathrm{BN}_{\gamma,\beta}(x_i)$

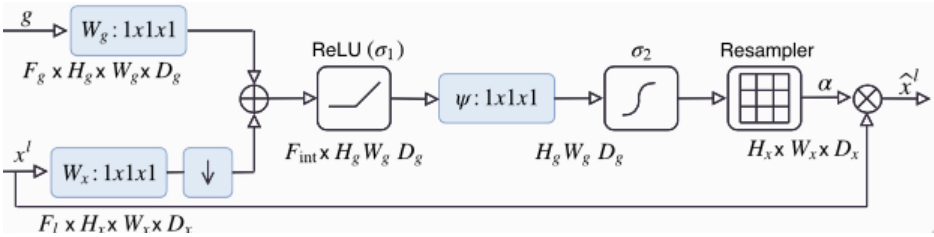


Figure 2.2: Attention Gate structure proposed in []

map over a layer such that x_i^l is the pixel-wise feature vector with dimension equals to the number of feature maps of the output. Attention Gate learn a scaling vector α_i^l as the weight to scale the feature vector, more formally:

$$\hat{\mathbf{x}}^l = \left\{\alpha_i^l \mathbf{x}_i^l\right\}_{i=1}^n$$

The additive attention in the paper, can then be written as:

$$q_{att,i}^l = \psi^T\left(\sigma_1\left(\boldsymbol{W}_x^T \boldsymbol{x}_i^l + \boldsymbol{W}_g^T \boldsymbol{g} + \boldsymbol{b}_{xg}\right)\right) + b_\psi$$

$$\alpha^l = \sigma_2\left(q_{att}^l\left(\boldsymbol{x}^l, \boldsymbol{g}; \boldsymbol{\Theta}_{att}\right)\right)$$

in which σ_1 denotes a non-linear activation function such as ReLU and σ_2 is a normalizing function so that $\sum_i e^{q_{att,i}^l} = 1$. In the paper, the author used sigmoid as activation function. Note the the attention gate is usually obtained from a coarser feature map. Figure 2.2 shows the attention gate structure

2.2.7 Encoder decoder architecture

2.2.8 Unet & Friends

This section we introduce several well known methods in medical segmentation. Unet [3] and its variations plays a dominant role in current medical segmentation tasks, and it is often used as a baseline model for performance evaluation in the literature.

Unet [3] is among one of the most widely used medical segmentation models since the day it was proposed. The original Unet consists of a contracting path followed

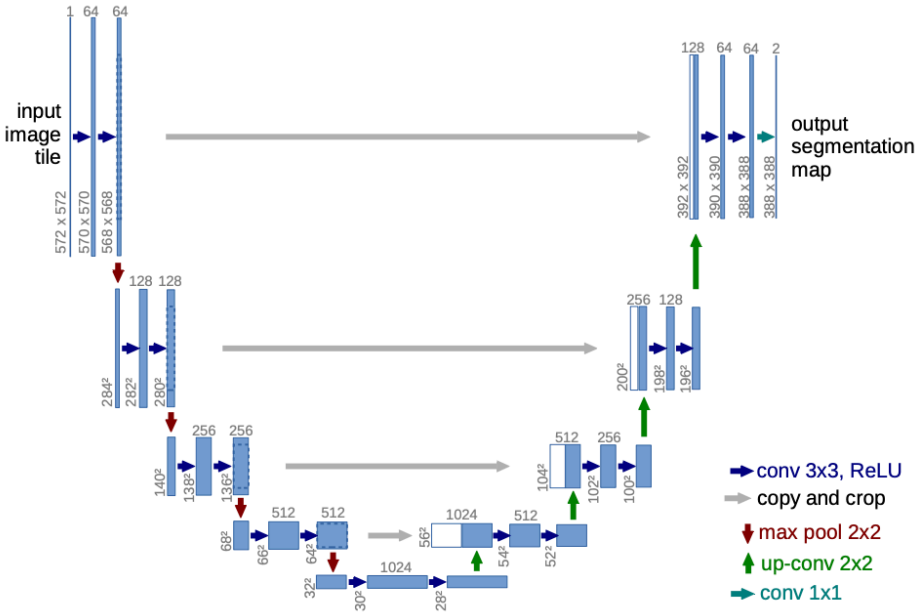


Figure 2.3: Original Unet architecture in [3]

by an expansive path that gives a ”U” shaped architecture. The network architecture is shown in figure 2.3. Later this 2D model was extended to 3D version in [4] for for Kidney segmentation tasks so that the model learn features from information implicated between slices.

VNet [5] is another 3D variation of Unet, and the network performed evaluation on prostate dataset. Each block of convolution has a residual feature that the input of the block is added to the last convolutional layer. The author argued that leverage residual structure enables network convergence in a fraction of the amount of time other network used.

2.3 Small Sample Segmentation

2.3.1 Data augmentation

In medical domain, huge dataset consists of large numbers of carefully labelled samples is rarely available due to heavy workload for annotations, rarity of disease, ethic issues of data acquire process and data privacy. Furthermore, different data acquire protocols (i.e. CT machines used by different hospitals) brings difficulties to clinical practice for good accuracy of existing pre-trained models. As a result, few shot learning and/or few shot segmentation has been explored in recent years. In this section, we focus on a few approaches that has been used in current literature which aim to explore the potential of existing training samples through various augmentation methods to alleviate the insufficient training samples in medical imaging. We discuss data augmentation method as well as the amount of data used in each work.

Table 2.1 provide an overview of each method.

2.3.2 Traditional Data Augmentation

Traditional Data augmentation method in imaging domain refers to the process that does not require such training data to learn a transformation.

[6] investigated data augmentation methods under 3D medical domain of MR and ultrasound images. The data augmentation process consists of a sequence of traditional transformation techniques. The paper argued that sharpness in medical images during training process limits model generalization thus applying gaussian filter to images take noise into consideration. Brightness and contrast difference caused by variations in scanning protocols brings potential domain shift thus a sequenced random shift followed gamma correction and random linear transform in intensity are reasonable data augmentation methods. Finally spatial transformations including rotation, flipping, scaling and deformation is added to the augmentation process. The source domain in this method is Prostate dataset [3] which consists 48 4D volumes. We argue here that the stacked transformation is a physical transformation process independent to the size of dataset because no learning or training process is required in this augmentation method thus might bring benefits to our task. However, although Deep learning models (Convolutional Neural Networks) are scale and rotation invariant, medical images differs from natrual images that scanning was conducted with a certain position, i.e. patients usually lie on a CT bed facing up for CT scanning. Thus flipping the lung volumes or rotating the lungs more than 5 degrees seems too 'violent'.

Another method "mixup" by [7] based on generic vicinal distribution, which generates new samples through interpolation between two existing data. The author argued that this method works as a regularizer which encourages linear behavior between training samples. In terms of imaging, the augmentation is applied to CIFAR 10 (2D non medical) Dataset. The calculation method in paper follows the following equations where x_i and x_j are training examples and λ is usually sampled from beta distribution.

$$\tilde{x} = \lambda x_i + (1 - \lambda) x_j$$

$$\tilde{y} = \lambda y_i + (1 - \lambda) y_j$$

The work was originally implemented on training GANs. Later in medical domain, [8] further investigated mixup method on Knee MR images on OIA database [4] that consists of 88 3D MRI scans. The work showed mixup improves generalization under their experiment setup while having risk of slight underfitting due to to the strong regularization. The author further mentioned not using weight decay in the experiment solve the underfitting issue. [9] summarized mixup augmentation method

[3] http://medicaldecathlon.com/index.html#tasks
[4] http://www.oai.ucsf/.edu/

Paper	Method	Dataset	Number of samples
[6]	Stacked traditional transform	Prostate dataset	48 4D volumes
[7]	mixup	CIFAR 10	Huge
[8]	mixup	Knee MR images	88 3D MRI
[10]	Asymmetric mixup	BraTS	not specified

Table 2.1: Data Augmentation methods

gives ”soft labels”. Variations of the mixup method utilize asymmetric is further explored in [10] trained on Brain MR images, and the method reports huge gain under their experiment setup.

2.3.3 Network

2.3.4 Transfer Learning

In medical domain, few shot learning mainly focus on transfer learning from pre-trained networks that leverage both medical and non-medical datasets.

In Lung CT segmentation area, Sports-1M dataset has been used as source domain to train a multi-task learning model for nodule malignancy prediction and rating [11]. The author reported significant improvement in the prediction accuracy, however, did not mention the proportion of data used for transfer training.

People tend to choose datasets from closer domain for transfer learning. It is reasonable to consider methods that transfer across disease in the same structure under the same modality. In our case, we might want to investigate transfer learning from NSCLC Dataset to Covid segmentation set given that both of them are lung CT scans.

Recent work explored several across disease transfer learning training techniques under MRI domain [12]. The paper evaluated three transfer learning methods trained on 3D U-Net by Fine tuning the last three layers, Fine tuning the decoder and Fine tuning all model parameters. The Source Dataset: Multiple Sclerosis Dataset consists 3630 MRI volumes and used Brain Tumor Dataset as Target dataset including 210 high-grade glioma (HGG) and 75 low-grade glioma (LGG) Brain MRI scans. The training target is a decaying weighted categorical cross entropy loss weighted by relative voxel. Their best validation performance of pre-trained network achieved validation performance AUC 0.77. Experiment result on 20, 50, 100 and 150 samples during Fine tuning respectively showed that Fine tuning all parameters out performed the rest methods in most cases.

One potential drawback is that compared to the our task, the target training set is relatively larger, the performance is expected to be less ideal when using ”fine tune all” method using 4 or less volumes in our case.

Paper	Method	Domain Details	Task
[13]	Design Conditional Branch	Target PASCAL-5	Few shot segmentation
[14]	Guidance network	Target PASCAL VOC	Few shot segmentation
[11]	Non medical to medical transfer	Source: Sports-1M; Target: Lung nodule	Multi-task learning: prediction and rating
[12]	Across domain transfer	Source: MSD; Target: Brain Tumor Dataset	Segmentation
[13]	Augmentation+pixel dense segmentation	Only trained on 7 brain Volumes	Dense segmentation
[15]	Branch network design	–	Segmentation

Table 2.2: Small sample methods in medical and non-medical domain

2.3.5 Learning with unlabelled data

Another common scenario with medical imaging is that, a small set of labelled annotations is available and a relatively larger set of data was collected but not labelled. In this section, we briefly mention three types of work that leverage unlabelled data: training encoder, noise removing, and semi-supervise learning. Both training encoder and noise removing serves as a pretrained network that are usually fined-tuned using the methods we described in the previous section. Semi-supervise learning however, How to describe this

Training encoder as initialization

Training encoder part without expert labeling usually make use of spatial information of the image such as slice order [**?**] and direction [**?**].

In the work [**?**], authors trained a network to predict a transformation of orientation by rotating or flipping the input slice, and then fine tune the network to classify retinal imaged of diabetes patients. One potential use of this type of initialzation for segmentation task is that we can append the Up-Convolution then transfer on segmentation labels.

Paper [**?**] trained a encoder that, given a reference slice and a prediction slice, predict the prediction slice is above of behind the reference slide so that the network can learn spatial information using the unlabelled images.

Noise removing

Instead of training a surrogate task such as training encoder leveraging spatial or location information as a pretraining task, Zongwei Zhou [1] provided another probability for pretraining both encoder and decoder that used together can serve as

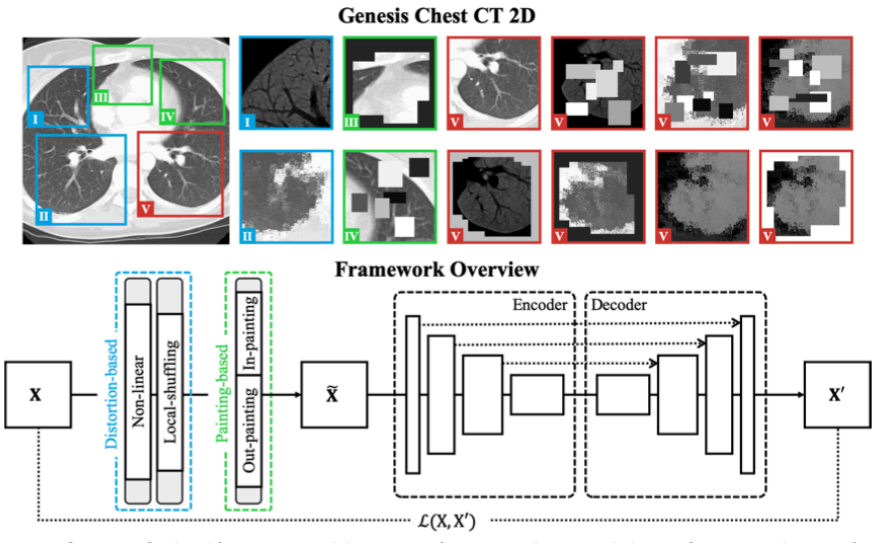


Figure 2.4: An illustration of Model Genesis pre-training (Figure from the original paper [1])

weight initialization for a segmentation model, and encoder used on its own is a pretrained feauture extractor for classification task.

The work trained a Unet-style network that given a randomly cropped and sliced image, first destroy the image through a sequence of random non-linear transformation, local shifting, out/in-painting then forward the image to restore the original image by minimizing the mean-square-error during training. The author argue that in that way, both the generalizability and the detail feature encoding can be learnt which can be leveraged in later transfer learning process. Figure 2.4 showed the restoration process. The model was trained on Lung CT images which is close to our task while the provided model was in 3D version, later in the experiment stage, we actually flattened the pretrained weight into 2D for future training.

Semi-supervise

Semi supervise approach usually add a prediction consistency loss during training. [16] propsed a teacher-student training strategt such that two networks are train together. The proposed so called 'Mean-teacher' network trained two network simultaneusly. First the author train a model on the fully labeled dataset, that serve as the teacher model. In the beginning of the semi-supervise training, a copy of the teacher model is also created called the student network. Now given a new set of unlabelled raw images, the student network are trained using the weight of psuedo-label cost and the prediction consistency cost. The teacher model weights are updated periodically using an exponential moving average of the student network. Figure 2.5 explains the training process.

We here further gives the defnition in the original work [16]. More formally, define

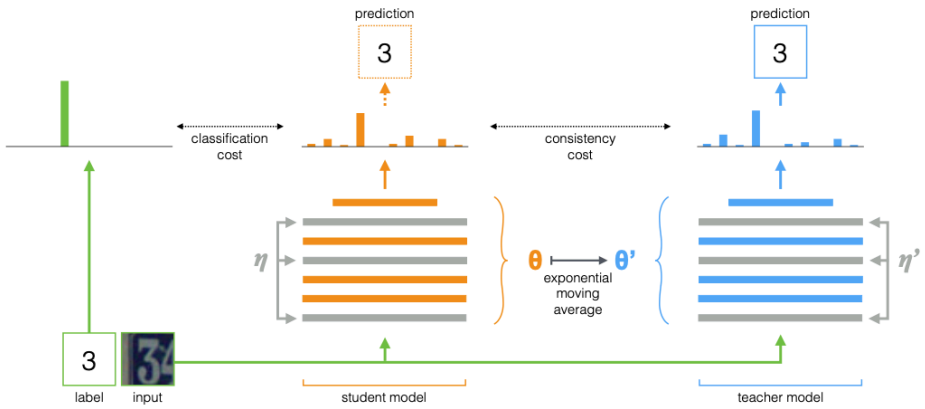


Figure 2.5: An illustration of mean teacher for semi-supervise learning (Figure from the original paper [16])

the consistency of the prediction as:

$$J(\theta) = \mathbb{E}_{x,\eta',\eta}\left[\|f\left(x,\theta',\eta'\right) - f(x,\theta,\eta)\|^2\right]$$

where x is the input data (image), θ, η denotes the weight and noise in the teacher model and θ', η' denotes the weight and noise in the student model. The weight update in the teacher model can then be written as:

$$\theta'_t = \alpha\theta'_{t-1} + (1-\alpha)\theta_t$$

in which α is the smoothing parameter showing how much the teacher want to move given the new student network.

We argue here that this training strategy can help our task 2 given a relatively larger amount of unlabelled samples are available.

2.4 Evaluation

2.4.1 Quantifying Segmentation prediction

Loss function or objective function is a crutial component in neural network training. Segmentation tasks usually make use of *Distribution loss*, *Region based loss* and *boundary-based* loss for training and evaluation of segmentation performance. Recent work in [17] summarized some common loss functions for segmentation.

Cross entropy (CE) measures the dissimilarity between the learned distribution and target distribution.

$$CE = -\frac{1}{N}\sum_{i=1}^{N}\sum_{c=1}^{C} w_c \cdot (y_i^c \log p_i^c)$$

where y_i^c indicates the prediction result (correct or wrong) and p_i^c denotes the predicted probability of pixel i for class c, w_c is now 1 for original cross entropy loss. Unet [3] training extend the CE by adding weight w_c. A common example for weight measurement is through the inverse proportion of observed class frequency. This modification potentially deal with imbalance class which is very common in medical domain.

Dice loss is a region based loss function that learn to optimize the Dice Coefficient (D). Vnet [5] first brought the Dice loss into machine vision community to solve the problem of highly biased prediction towards dominant area (e.g background) in medical segmentation.

$$D = \frac{2\sum_i^N p_i g_i}{\sum_i^N p_i^2 + \sum_i^N g_i^2}$$

Assume we segment N samples, p_i denotes the prediction volume and g_i denotes the ground-truth volume. Dice loss usually require the label to be one hot encoded during training. One benefit is that Dice loss does not requires class balance methods such as weighting method in CE loss.

Hausdorff Distance loss(HD) aims to minimize the boundary distance between prediction and ground-truth segmentation masks. Similar to Dice loss, it also alleviate the class imbalance issue during training. However,directly minimizing Hausdorff Distance is intractable while an approximation (HD Loss) through distance transform (gray-level intensities of points inside foreground regions are changed to show the distance to the closest boundary from each point [5]).

$$L_{HD_{DT}} = \frac{1}{N}\sum_{i=1}^{N}\left[(s_i - g_i)\cdot\left(d_{Gi}^2 + d_{Si}^2\right)\right]$$

Paper [17] proposed that so far none of the papers in the literature provide a comprehensive comparison of the loss functions for segmentation task. Selecting loss function is still based on empirical comparison. For example, [**?**] used compound loss function that combined CE and Dice together as training objectives overall gives good performance compared to individual loss functions.

2.4.2 Evaluating Transfer Learning

Loss function quantifies the transfer learning prediction accuracy. We further want to understand the model behaviours. For example: How weights are updated during fine tuning? Is Pretraining compared to random initialization result in different weights such that the the latent space are apart from each other?

Singular Vector Canonical Correlation Analysis (SVCCA) [18] developed by Google Brain provide a method that compares the latent space of different models or different layers. The method is more quite simple while useful for comparing high

[5] https://homepages.inf.ed.ac.uk/rbf/HIPR2/distance.htm

dimensional latent features.

First let l denotes the output of layer over a dataset D, The paper perform the following SVCCA steps:

- Given two layers of output l_1, l_2 that represent the learnt subspace on the dataset, perform singular value decomposition then select the new subspace l_1', l_2' which preserve 99% of the original variance.
- Perform Canonical Correlation Analysis on the two subspace l_1', l_2' so that the two new subspaces are as correlated as possible through transfomation. Each direction has a correlation ρ_i
- The correlation of two subspaces is the average of each output correlation $\rho_{l_1,l_2} = \frac{1}{N}\sum_{i=0}^{N}\rho_i$

SVCCA interpret the result of any two learnt subspace over a dataset. Later in work [19], the author utilized the method to understand the behavior of transfer learning in rather larger amounts of data on medical classification task.

2.5 Ethics and professional considerations

Chapter 3

Data

3.1 Data description

One of the most straightforward way to deal with the limit amount of available data is to leverage as much related Medical Data as possible. We thus investigated several public available dataset for Lung CT scans in addition to the Covid-CT dataset.

3.1.1 NSCLC Dataset

NSCLC Dataset contains 402 Lung CT scans, of which 78 cases are anotated with left lung, right lung and pleural effusion area. A sample annotation is shown in figure 3.1

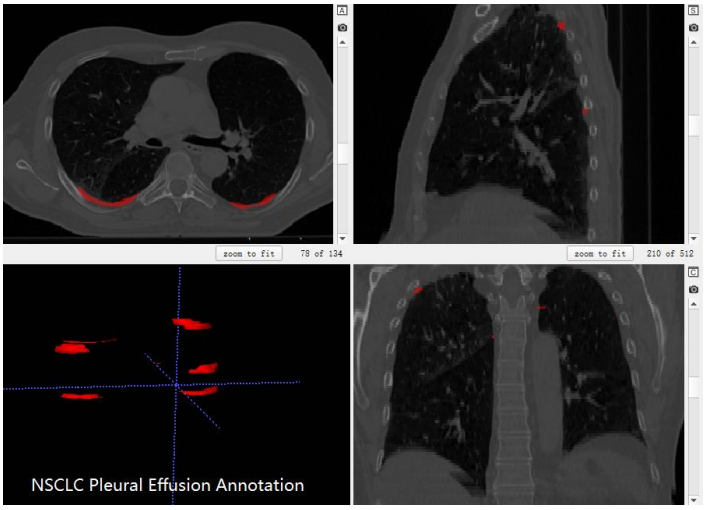


Figure 3.1: An example volume from NSCLC Dataset with its annotation

3.1.2 MSD Lung Tumor

MSD Lung Tumor contains 63 Lung CT scans, annotating the Lung Cancer area. An example shown in figure 3.2

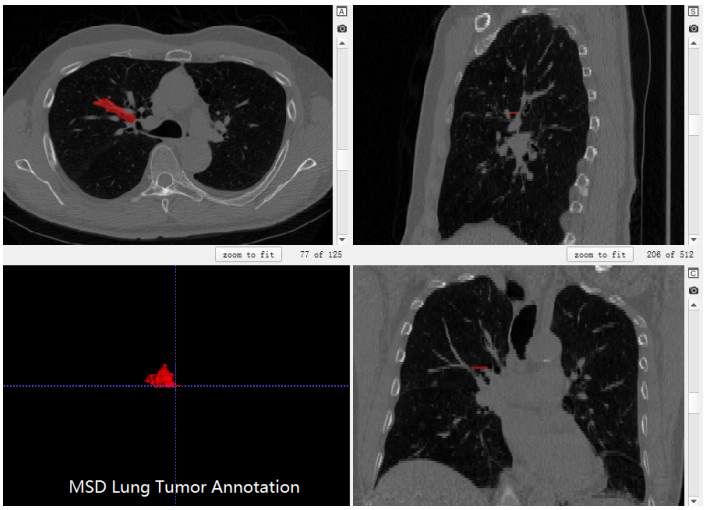


Figure 3.2: An example volume from MSD Dataset with its annotation

3.1.3 MosMed Dataset

MosMed Dataset Contains 50 Annotated thick-slice Covid CT scans, as well as around 300 unannotated Lung CTs. We'd like to report here that we used only 200 unannotated slices because downloading keep giving me error due to location restriction. An example shown in figure 3.3

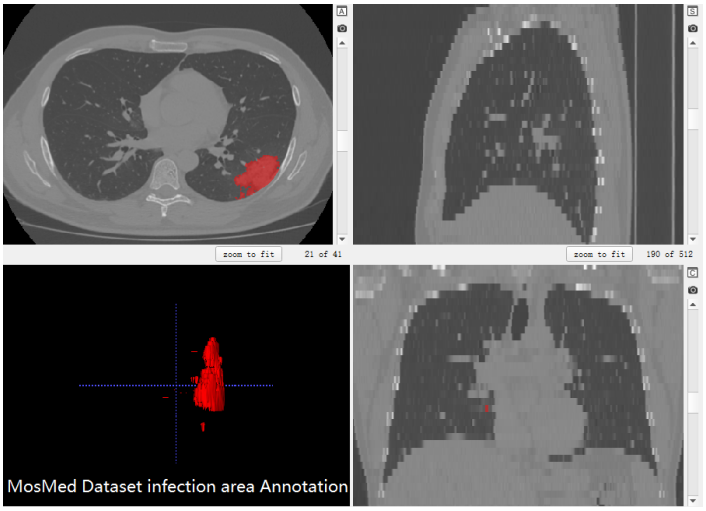


Figure 3.3: An example volume from MosMed Dataset with its annotation

3.1.4 Covid Segmentation Benchmark

Covid Segmentation Benchmard contains 20 CT scans from 2 radiometric centers, of which 10 volumes thin-slice CT volumes and 10 thick slice CT volumes.

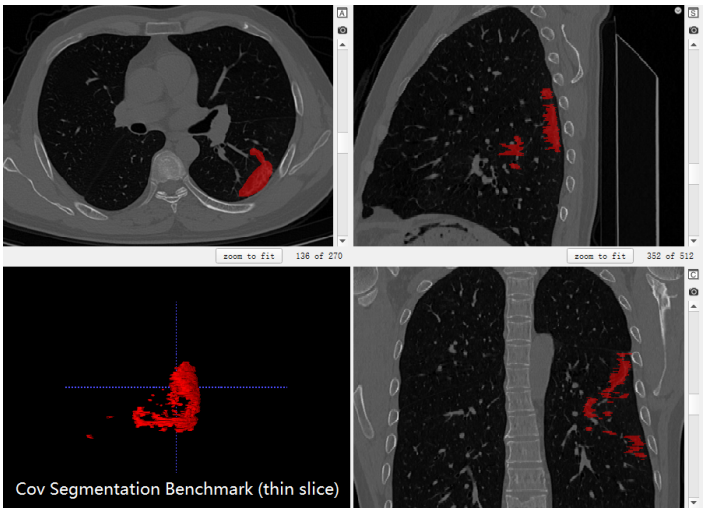


Figure 3.4: An example volume from Cov Segmentation Benchmark (thin slice) with its annotation

3.2 Data preprocessing

The dataset used in this paper was collected from multiple centers with different equipment setup. Structseg2019, NSCLC, MSD Lung Tumor set are thin slice CT scans. MosMed contained 50 thick slice scans and the Covid segmentation benchmark are multi-center dataset from different centers. We argue that deep learning algorithms, especially segmentation tasks are sensitive to this difference. To make most use of the data, we first extract the lungs from the CT volumes. Then a sequence of preprocessing was performed including resampling, histogram equalization, and mean variance normalization. Most implementation used SimpleITK dataset

3.2.1 Data gathering and cleaning

3.2.2 Processing into functional features

Lung CT scans images includes the lung tissue as well as bones and meshes that influence the preprocessing such as normalization as well as future segmentation. We intended to first segment the lung tissue out for better focus.
Lung segmentation using watershed algorithm

Lung segmentation Using pre-trained Deep learning models
Deep learning method provide finer results when facing severe pathology. Work in [20] provided a promising result for Lung segmentation. In addition, they further improve their lung segmentation model with Covid-19 Lung data.

We leveraged their models provided in their github repository [1]. Original volumes from the Lung datasets went through the model, we threshold the lung out and

[1]https://github.com/JoHof/lungmask

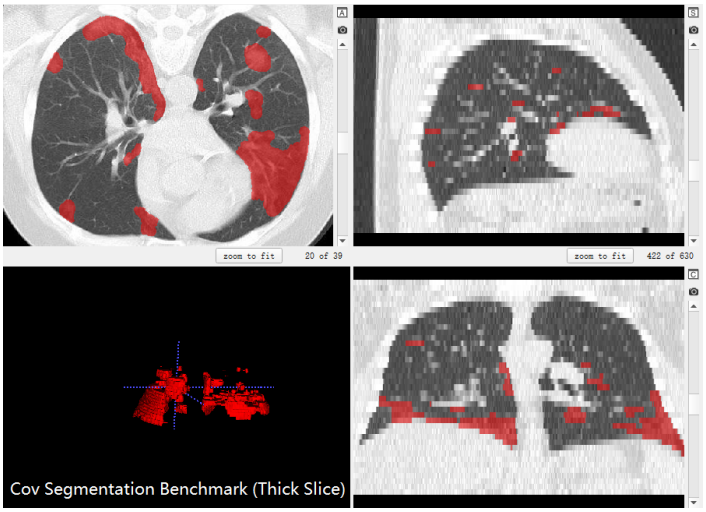


Figure 3.5: An example volume from Cov Segmentation Benchmark (thick slice) with its annotation

set the uninterested area (background) as 0. Figure 3.6 showed and example lung volume before and after filtering the lung tissue.

3.2.3 Resampling

Figure 3.7 showed the diveristy in spacing from different datsets. To deal with the different spacing for multi-domain data, we resampled the data to spacing (1, 1) in the Axial view and remain not changed in the Z axis.

3.2.4 Mean Variance Normalization

We performed Mean Variance Normalization (Z score normalization) for the lung tissue voxels by subtracting each volume with its mean and divided by its standard deviation. So that the data has zero mean and standard deviation of 1.

$$z = \frac{x - \mu}{\sigma}$$

of which μ is the mean and σ is the variance. Figure 3.8 showed the intensity range before and after normalization

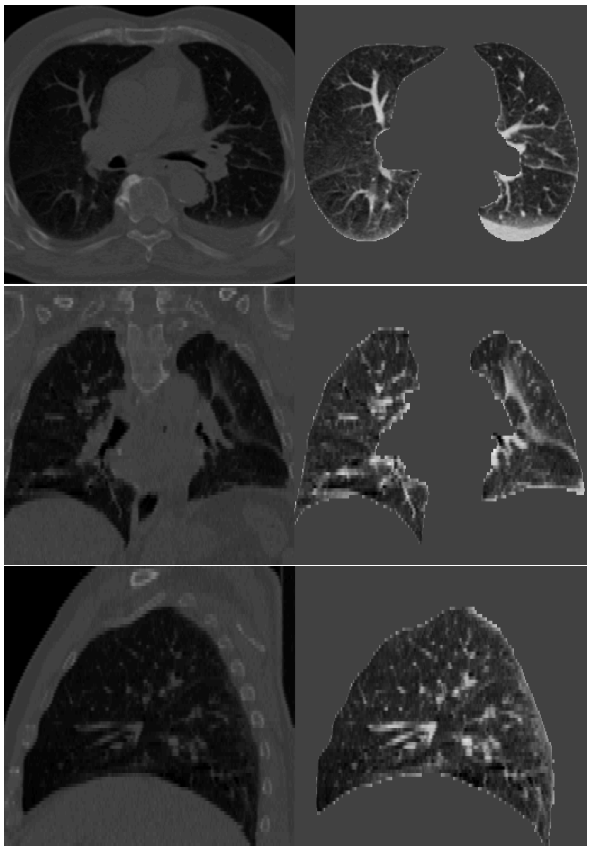


Figure 3.6: An example from NSCLC Pleural Effusion dataset showing the volumes before and after lung filtering. (Top: Axial view, Middle: Coronal view, Bottom: Saggital View)

3.3 Data Augmentation

For data augmentation, we investigated some of the augmentation techniques in medical imaging domain, each of the augmentation techniques was carefully chosen matching real medical situation.

Rotation: We performed a small random rotation between [-3, 3] degree considering the pose variation when lying down on the scanner.

Elastic Transformation: We performed a small elastic transformation considering lying down and holding breath when scanning Lung CT might brings shape change to the lungs tissue.

Random Gamma and Gaussian Noise: We performed a random gamma correction to simulate the variation generate due to different equipment. We also added a random gaussian noise for a more robust training.

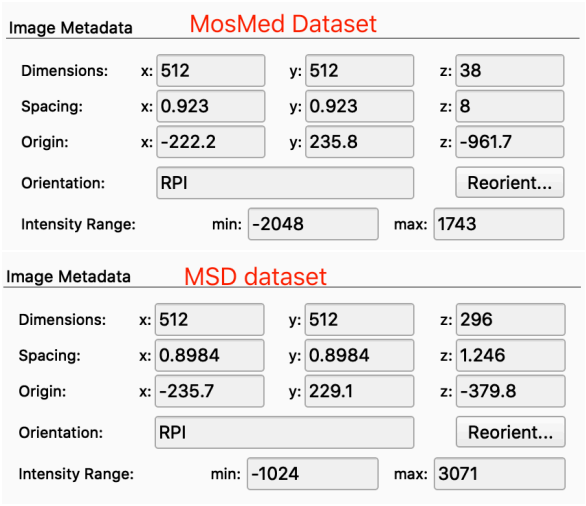


Figure 3.7: An example of different spacing information from MosMed and MSD dataset

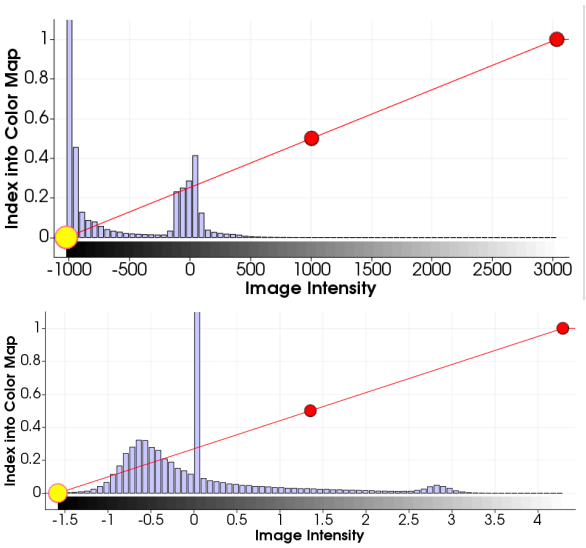


Figure 3.8: An example showing the intensity range before and after normalization (Top: before normalization; Bottom: after normalization)

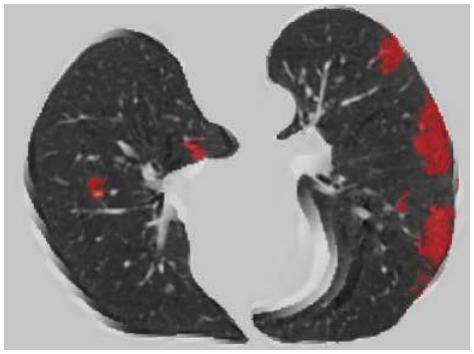


Figure 3.9: An example of rotation using MosMed Dataset

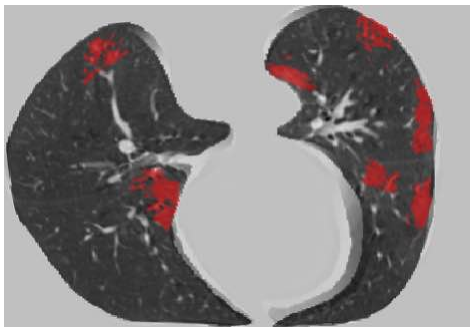


Figure 3.10: An example of elastic transformation using MosMed Dataset

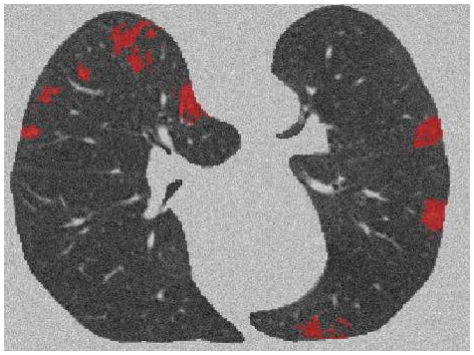


Figure 3.11: An example of random Gamma and Gaussian Noise using MosMed Dataset

Chapter 4

Deep learning architecture

4.1 Network Architecture and Methodology

4.1.1 Unet

4.1.2 Attention Gate

4.2 presenting with unlabelled data

4.2.1 Psuedo labeling

4.2.2 Semi-supervise architecture

As we described in Chapter 2, we designed a Mean-teacher style model for the semi-supervise task.

Layer	input	output	channel
Conv 3x3 + RELU	572	570	64
Conv 3x3 + RELU	570	568	64
Max Pool 2 × 2	568	284	64
Conv 3x3 + RELU	284	282	128
Conv 3x3 + RELU	282	280	128
Max Pool 2 × 2	280	140	128
Conv 3x3 + RELU	140	138	256
Conv 3x3 + RELU	138	136	256
Max Pool 2 × 2	136	68	256
Conv 3x3 + RELU	68	66	512
Conv 3x3 + RELU	66	64	512
Max Pool 2 × 2	64	32	512
Conv 3x3 + RELU	32	30	1024
Conv 3x3 + RELU	30	28	1024
up-conv 2 × 2	28	56	512
convs 1x1	56	54	512
convs 1x1	54	52	512
up-conv 2 × 2	52	104	256
convs 1x1	104	102	256
convs 1x1	102	100	256
up-conv 2 × 2	100	200	128
convs 1x1	200	198	128
convs 1x1	198	196	128
up-conv 2 × 2	196	392	64
convs 1x1	392	390	64
convs 1x1	388	388	2

Table 4.1: The Original Unet Architechture

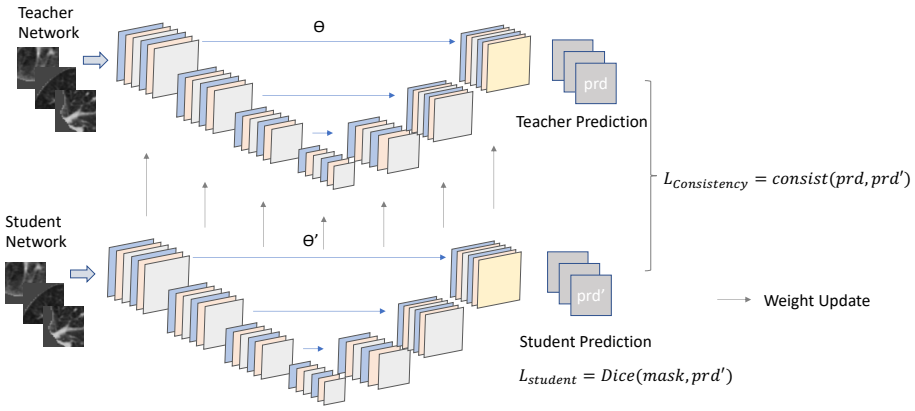


Figure 4.1: The design of network model for our semi-supervise setup

Chapter 5

Experiment

5.1 Experiment

A good model, especially facing with small sample segmentation, should generalize well instead of overfitting on a small number of training data. The whole point of data augmentation, adding noise, etc, is to improve the generalizability of the trained neural network so that for the unseen data, the model predict reasonably well.

Due to the limited ability of the GPU resource available, tuning hyper-parameters using grid search is too inefficient. Thus in our experiment, we leveraged the optimizer scheduler in pytorch so that starting from the learning rate starts from $lr = 2 \times 10^{-4}$ and decreased to 0.8 * lr every 25 epochs so that the learning rate approach 0 in the later training stage.

1. **learning rate**

2. **Optimizer:** We used Adam optimizer considering that Model Genesis, winning solution for NSCLC segmentation as well as other well known solutions used the model optimizer.

3. **Epochs:** The maximum number of epochs for training is 500. However, each epoch we validate the result and the best model was saved throughout the training process. We count the number of continued non-improving epochs, and when it reached 30 epochs, the training progress terminated automatically.

5.2 With Fully labelled data

We first consider training on a small dataset and all of them are labelled with segmentation masks, because this is the case during the first few months of this project when only 20 volumes of the Covid lungs from the Covid Segmentation benchmark were publicly available, later in July 2020, MosMed published a new dataset containing 50 labeled slices.

5.2.1 Experiment Setup

To fully leverage the Covid Dataset, we combined the 20 volumes in Covid Segmentation bechmark and the 50 volumes MosMed Dataset. We randomly selected 20 volumes for testing, and further split the 50 remaining volume into 5 fold for cross validation. Smaller sample: One fold (10 volumes) for training; Normal training: Four fold (40 Volumes) for training. Note that since we cannot do anything to the various slice thickness, we sliced the volume into 2D.

5.2.2 Best results

For the segmentation of infection area using **fully labelled sample only**, we achieved Dice score (DSC) on the training set (50 volumes sliced in 2D) of 99.0321%, 80.3601% on the validation set and 79.9356% on the testing set. All the volumes was preprocessed as described in Section 3 and augmented the data using random rotating, and elastic transformation and mix up augmentation on the training set only.

5.2.3 Training

We experimented two transfer learning intialization in this section. First we trained the Binary segmentation task with the images from NSCLC and MSD dataset, then the model was fine tuned using two different methods suggested in work [12]: Fine-Tuning all layers (reinitialize the last layer), and Fine-Tuning only the Decoder, shown in figure 5.1.

Pretraining with NSCLC and MSD Dataset

First the we pretrained the segmentation model using non-Covid dataset based on the assumption that the weights serves as good starting point for the fine-tuning stage. Figure 3.6 plots the validation loss every 10 epochs.

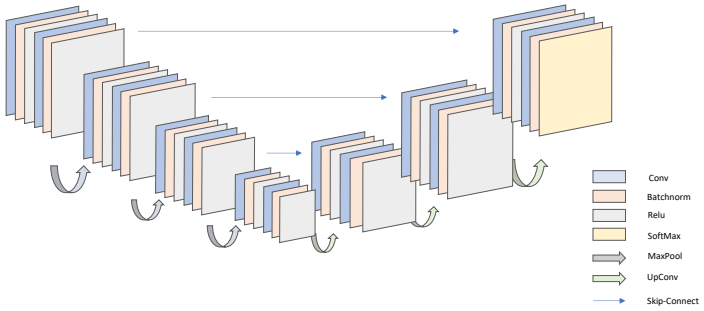
Fine Tuned with Model Genesis:

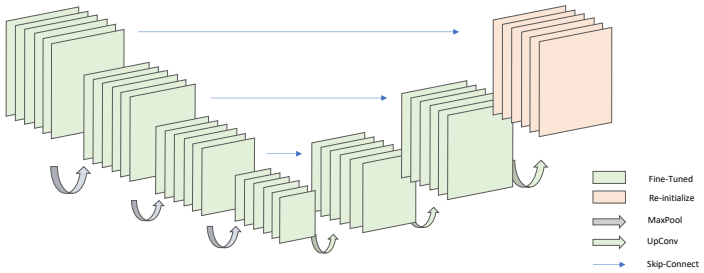
Paper [1] pretrained a 3D Unet-like model using several public dataset in the way that trained the model to restore image using destroyed image. The model was published in 3D [1]. Since we did out experiment in 2D, we first load the 3D model and extract the layer weight. Then we flatten the weights into 2D as the initialization.

Freezing encoder: We freeze the first half of the encoder, and fine tuned the decoder except that we re-initialized the output layer.

Fine-Tune-All: The whole network is fine tuned and the last block of convolutional layers was reinitialized.

[1] https://github.com/MrGiovanni/ModelsGenesis/tree/master/pytorch





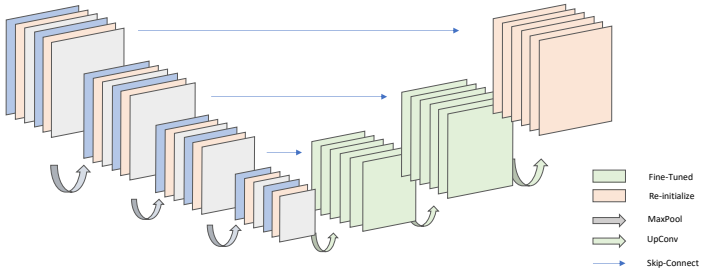


Figure 5.1: An illustration of Network structure used for pretraining and transfer-learning

Unet		Train	Validation	Test
From Scratch	10-40 split	0.9894	0.7012	0.6893
	40-10 split	0.9705	0.8119	0.8012
Fine Tune Decoder	10-40 split	0.9771	0.7963	
	40-10 split	0.9693	0	
Fine Tune All	10-40 split	0.9802		
	40-10 split	0.9562		
Attention gated Unet		Train	Validation	Test
From Scratch	10-40 split	0.9904		
	40-10 split	0.9710		
Fine Tune	10-40 split	0.9521		
	40-10 split	0.9512		
Fine Tune All	10-40 split	0.9608		
	40-10 split	0.9611		

Table 5.1: Training with fully labeled Dataset

5.2.4 SVCCA analysis on transfer learning

Network convergence during training

We compared the convergence on each layer throughout the training process on the segmentation model. [**?**] reported that the network converged bottom up for a classification task during training. However, this is not exactly the case in our segmentation model.

Network convergence with random initialization

We first want to analyze the change of network layers from random initialization towards convergence using the SVCCA tool. We iterate through the dataloader and validate every 100 epochs and save the model if the result yield better performance.

Figure 5.3 plots the similarity of latent space of each network layer using random initialization.

- We observed that, in general, encoder converged faster than decoder.
- Suprisingly, the first down convolution layer moved less comparing the initialization to the converged model.
- The similarity score in the output layer converged slightly faster than the other decoder part. Our explanation is that, the model performance (accuracy) increased faster in the first few number of iterations then slowly improved throughout the training.
- Although the similarity of the several Up-Convolution in the decoder part kept changing in the later stage of training, the output layer(out_tr.finalconv in figure 5.3) did not moved much. One implication is that, Neural Network may

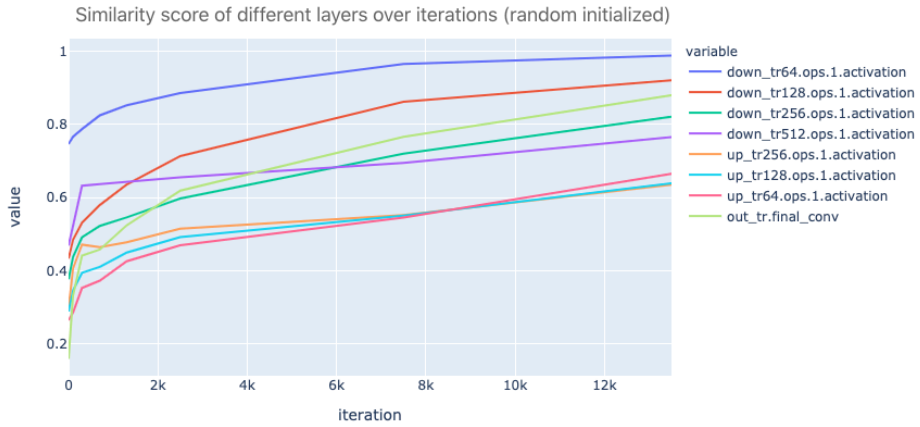


Figure 5.2: CCA similarity score of each layer over training iterations (randomly initialized)

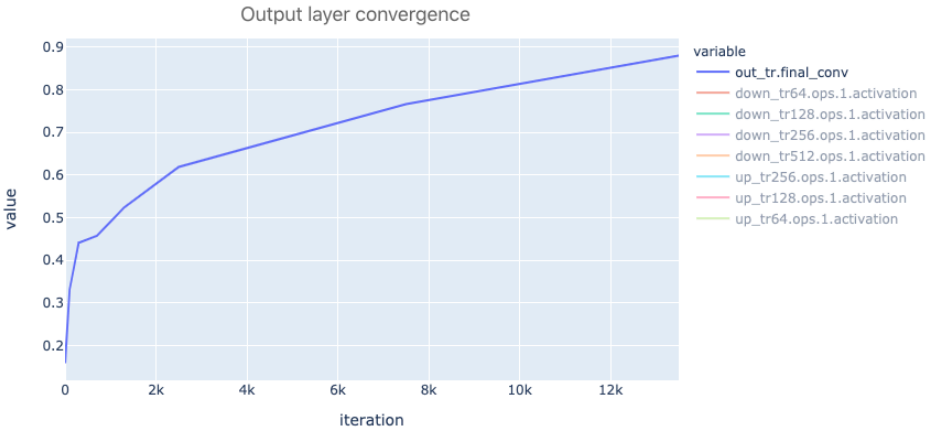


Figure 5.3: Filtering out the output layer convergence

learn different latent feature space while giving similar performance with respect to the accuracy.

Network convergence during Fine-tuning

The question we asked is: **Is the convergence similar to random initialization when we have a pre-trained model?** To test the convergence, we repeated the experiment in the previous section: Starting from a pre-trained model, we iterate through the Dataloader (containing 40 volumes sliced into 2D from the Axis view) and validate every 100 iterations. We saved the model of that epoch if the validation accuracy reported a better performance. Figure 5.4 plots the CCA similarity score of each saved model compared with the converged model.
Comparing the similarity of feature map in the segmentation model, we observed the following behaviour:

- In the Encoder part, lower layers converged faster compared to higher layers. Specifically, down covolution reported higher similarity score from the

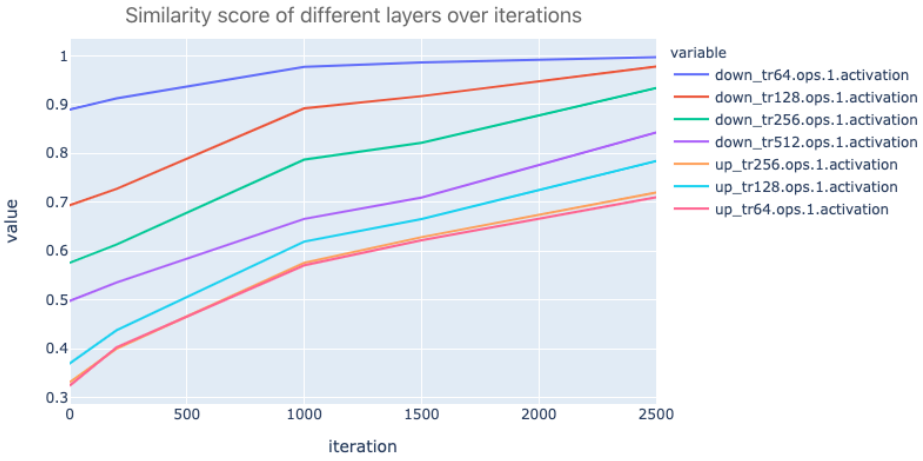


Figure 5.4: CCA similarity score of each layers over iterations during Fine-tuning

beginning compared with the similarity score obtained when we trained from scratch

- Layers in the Decoder observed convergence almost at the same time.

Feature space comparison for transfer learning

Another question we want to discuss is: **How much did the model move given the amount of data it observed during the Fine-Tuning?**

A larger amounts of data:
Figure 5.4 shows that, although all layers output seen a higher similarity score as the iteration number increase, Down-Convolution layers in the Encoder moved much less compared to the rest of the model, yielding a slightly better feature reuse during Fine-Tuning, and the feature reuse decreased from lower layers to higher layers. The Decoder, however, gives a much lower similarity score (lower than 0.5) comparing the pre-trained initialization to the converged model. Figure 5.5 compared the layer-wise feature space similarity which showed the similar obeservation.
We then trained the model using only 5 volumed sliced into 2D.....

5.3 With unlabeled data

We then consider leveraged unlablled data because in mid July, MosMed published unlabelled CT volumes. Thus, we continued our experiment to leveraged the unlabeled dataset. We first fine tune a pre-trained model on the annotated dataset, take the encoder of the network. We cropped patches from the unannotated images, assign noisy label to them and train a mean-teacher style network using those cropped patches

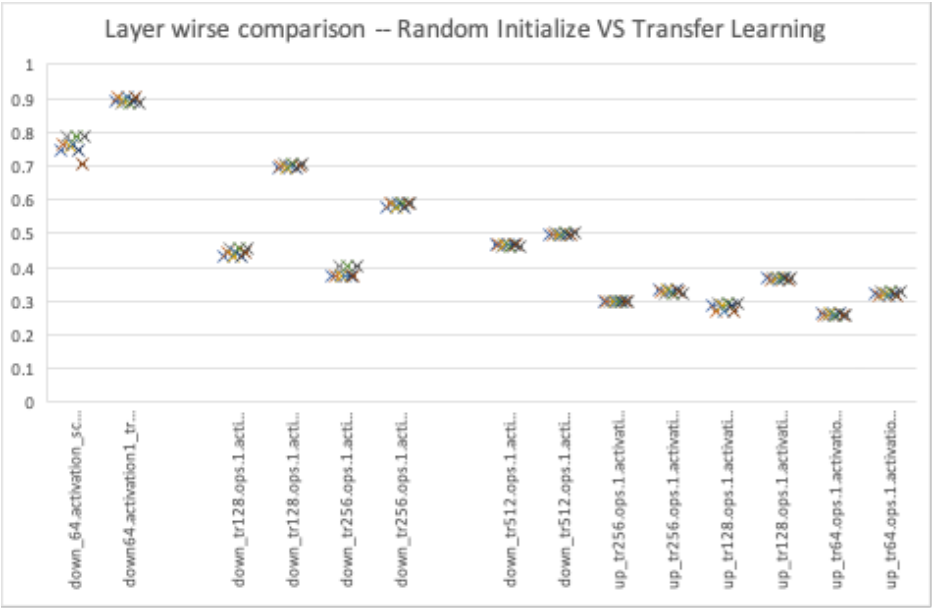


Figure 5.5: Layer-wise Comparison during training

5.3.1 Experiment Setup

Apart from the labelled datset described in section 5.2, we downloaded 200 unlabeled volumes and first preprocessed the CT volumed as we described in chapter 3.

5.3.2 Training a coarse 3D segmentation

The purpose of leveraging unlabelled data during training is to improve the generalization of the network so that it generalize better on unseen data. We want to crop more infection area to guide the segmentation model, so we first train a coarse 3D segmentation to generate a 'rough mask' of the image to guide the segmentation.

5.3.3 Transfer learning 2D segmentation

5.3.4 Psuedo Label Assignment – Cosine Similarity in the feature space

We sampled both the labelled samples and the unlabelled images. For the labeled samples, we first get the bounding box of the segmentation mask, then enlarge the mask by a maximum of 10 pixels each side, and we sampled images within that bounding box. For unlabeled images, we use the coarse 3D segmentation to generate the bounding box, and the bounding box was enlarged maximum of 15 pixels, we sample patches within the coarse bounding box. To assign a noisy psuedo label to the cropped images, we take the encoder part of the trained 2D segmentation model and append a Global Average Pooling function. We then encode a dictionary of the

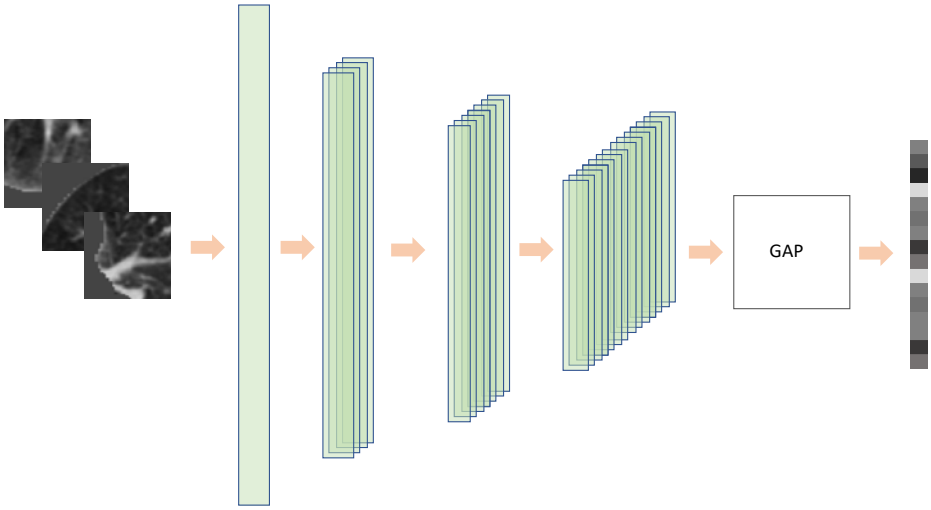


Figure 5.6: An illustration of feature encoding process

annotated samples in the feature space.

For assigning noisy psuedo labels, given an unlabeled sample $I_{unlabeled}$ and its latent representation $Latent(I_{unlabelled})$, we calculated the pairwise cosine similarity and return the maximum cosine similarity score as the weight for this sample.

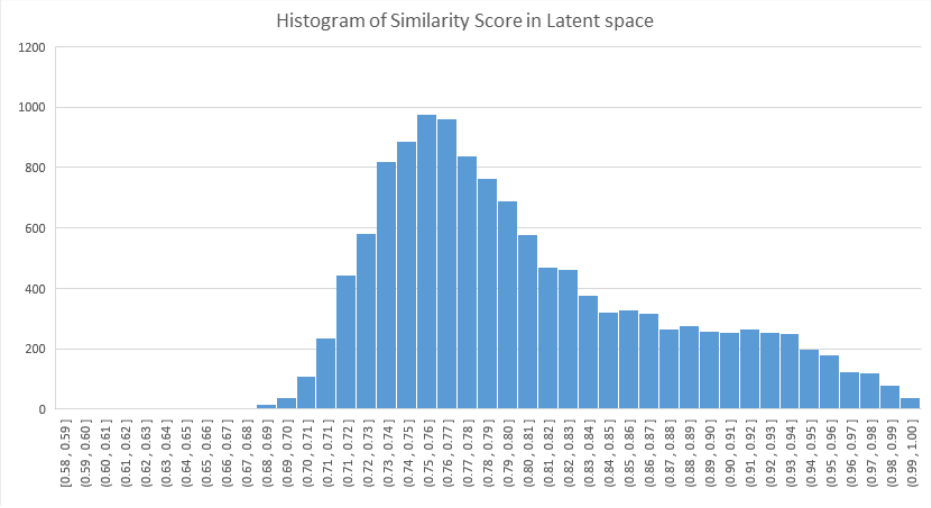


Figure 5.7: Histogram of Cosine Similarity score

Figure 5.7 counts the occurence of similarity score over all sampled unlabeled patches. We took those samples with similarity score between 0.87 and 0.96 (sim $\in$ [0.87, 0.96]), and we assign the label of the annotated samples with highest similarity score. Figure 5.8 showed some examples of noisy labels assigned using this method.

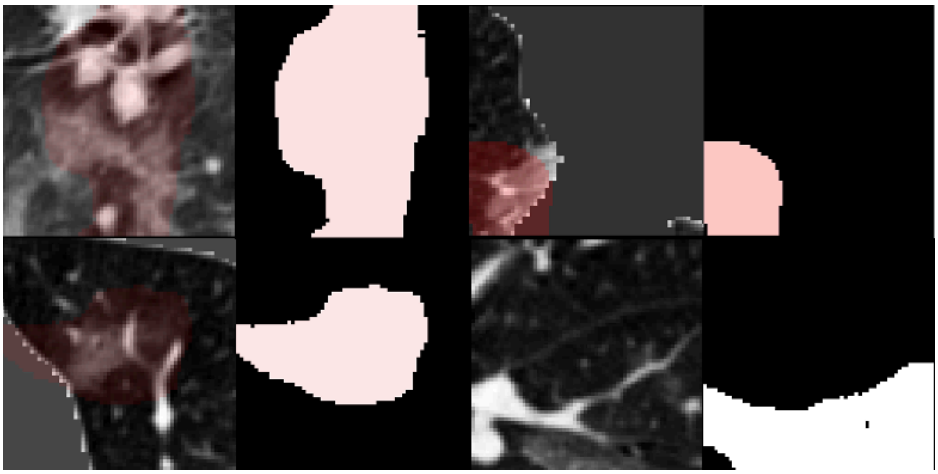


Figure 5.8: Example patches and noisy masks

5.3.5 Mean teacher training

Chapter 6

Discussion and conclusion

6.1 Conclusion

6.2 Future work

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