

Homework 2 Report

Math 5185 - Artificial Intelligence for Clinical Data Analytics

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1. (1 %) Please describe your pre-processing process (normalizing, masking, cropping, resampling, etc.).

Before preprocessing, I removed 12 sets of CT image that are labeled incorrectly.

For preprocessing, first I transferred all CT images to Hounsfield units (HU). Then, normalize all images to 0~1 with lower threshold = -1000, upper threshold = 400.

2. (2 %)
 - a. Please print the network architecture of your best performance model and **describe your training config** (loss, optimizer, batch size, learning rate, early stopping config, etc.).

Layer (type)	Output Shape	Param #	Connected to
input_1 (InputLayer)	(None, 512, 512, 1)	0	
conv2d_1 (Conv2D)	(None, 512, 512, 8)	80	input_1[0][0]
batch_normalization_1 (BatchNor	(None, 512, 512, 8)	32	conv2d_1[0][0]
activation_1 (Activation)	(None, 512, 512, 8)	0	batch_normalization_1[0][0]
conv2d_2 (Conv2D)	(None, 512, 512, 16)	1168	activation_1[0][0]
batch_normalization_2 (BatchNor	(None, 512, 512, 16)	64	conv2d_2[0][0]
activation_2 (Activation)	(None, 512, 512, 16)	0	batch_normalization_2[0][0]
max_pooling2d_1 (MaxPooling2D)	(None, 256, 256, 16)	0	activation_2[0][0]
conv2d_3 (Conv2D)	(None, 256, 256, 16)	2320	max_pooling2d_1[0][0]
batch_normalization_3 (BatchNor	(None, 256, 256, 16)	64	conv2d_3[0][0]
activation_3 (Activation)	(None, 256, 256, 16)	0	batch_normalization_3[0][0]
conv2d_4 (Conv2D)	(None, 256, 256, 32)	4640	activation_3[0][0]
batch_normalization_4 (BatchNor	(None, 256, 256, 32)	128	conv2d_4[0][0]
activation_4 (Activation)	(None, 256, 256, 32)	0	batch_normalization_4[0][0]
max_pooling2d_2 (MaxPooling2D)	(None, 128, 128, 32)	0	activation_4[0][0]
conv2d_5 (Conv2D)	(None, 128, 128, 32)	9248	max_pooling2d_2[0][0]
batch_normalization_5 (BatchNor	(None, 128, 128, 32)	128	conv2d_5[0][0]
activation_5 (Activation)	(None, 128, 128, 32)	0	batch_normalization_5[0][0]

conv2d_6 (Conv2D)	(None, 128, 128, 64)	18496	activation_5[0][0]
batch_normalization_6 (BatchNor	(None, 128, 128, 64)	256	conv2d_6[0][0]
activation_6 (Activation)	(None, 128, 128, 64)	0	batch_normalization_6[0][0]
max_pooling2d_3 (MaxPooling2D)	(None, 64, 64, 64)	0	activation_6[0][0]
conv2d_7 (Conv2D)	(None, 64, 64, 64)	36928	max_pooling2d_3[0][0]
batch_normalization_7 (BatchNor	(None, 64, 64, 64)	256	conv2d_7[0][0]
activation_7 (Activation)	(None, 64, 64, 64)	0	batch_normalization_7[0][0]
conv2d_8 (Conv2D)	(None, 64, 64, 128)	73856	activation_7[0][0]
batch_normalization_8 (BatchNor	(None, 64, 64, 128)	512	conv2d_8[0][0]
activation_8 (Activation)	(None, 64, 64, 128)	0	batch_normalization_8[0][0]
cropping2d_1 (Cropping2D)	(None, 128, 128, 64)	0	activation_6[0][0]
conv2d_transpose_1 (Conv2DTrans	(None, 128, 128, 128)	65664	activation_8[0][0]
concatenate_1 (Concatenate)	(None, 128, 128, 192)	0	cropping2d_1[0][0] conv2d_transpose_1[0][0]
conv2d_9 (Conv2D)	(None, 128, 128, 64)	110656	concatenate_1[0][0]
batch_normalization_9 (BatchNor	(None, 128, 128, 64)	256	conv2d_9[0][0]
activation_9 (Activation)	(None, 128, 128, 64)	0	batch_normalization_9[0][0]
conv2d_10 (Conv2D)	(None, 128, 128, 64)	36928	activation_9[0][0]
batch_normalization_10 (BatchNo	(None, 128, 128, 64)	256	conv2d_10[0][0]
activation_10 (Activation)	(None, 128, 128, 64)	0	batch_normalization_10[0][0]
cropping2d_2 (Cropping2D)	(None, 256, 256, 32)	0	activation_4[0][0]
conv2d_transpose_2 (Conv2DTrans	(None, 256, 256, 64)	16448	activation_10[0][0]
concatenate_2 (Concatenate)	(None, 256, 256, 96)	0	cropping2d_2[0][0] conv2d_transpose_2[0][0]
conv2d_11 (Conv2D)	(None, 256, 256, 32)	27680	concatenate_2[0][0]
batch_normalization_11 (BatchNo	(None, 256, 256, 32)	128	conv2d_11[0][0]
activation_11 (Activation)	(None, 256, 256, 32)	0	batch_normalization_11[0][0]
conv2d_12 (Conv2D)	(None, 256, 256, 32)	9248	activation_11[0][0]
batch_normalization_12 (BatchNo	(None, 256, 256, 32)	128	conv2d_12[0][0]
activation_12 (Activation)	(None, 256, 256, 32)	0	batch_normalization_12[0][0]
cropping2d_3 (Cropping2D)	(None, 512, 512, 16)	0	activation_2[0][0]
conv2d_transpose_3 (Conv2DTrans	(None, 512, 512, 32)	4128	activation_12[0][0]
concatenate_3 (Concatenate)	(None, 512, 512, 48)	0	cropping2d_3[0][0] conv2d_transpose_3[0][0]
conv2d_13 (Conv2D)	(None, 512, 512, 16)	6928	concatenate_3[0][0]
batch_normalization_13 (BatchNo	(None, 512, 512, 16)	64	conv2d_13[0][0]
activation_13 (Activation)	(None, 512, 512, 16)	0	batch_normalization_13[0][0]
conv2d_14 (Conv2D)	(None, 512, 512, 16)	2320	activation_13[0][0]
batch_normalization_14 (BatchNo	(None, 512, 512, 16)	64	conv2d_14[0][0]
activation_14 (Activation)	(None, 512, 512, 16)	0	batch_normalization_14[0][0]
conv2d_15 (Conv2D)	(None, 512, 512, 1)	17	activation_14[0][0]
activation_15 (Activation)	(None, 512, 512, 1)	0	conv2d_15[0][0]
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Total params: 429,089			
Trainable params: 427,921			
Non-trainable params: 1,168			

Model: U-net 2D depth=3

Loss: binary_crossentropy

Optimizer: Adam

Batch size: 8

Learning rate: 1e-3

b. Please summarize what you have tried before and discuss the reason.

I have also tried resample and mask the data. Resampling the data to an isomorphic resolution to remove variance in scanner resolution; however, I have some trouble to deal with prediction, not sure about the relation of the images with the coordinate after resampling. As for masking, it is done for reducing the problem space by segment out the lungs. Though the masking works, some results are not quite good for this task. Take patient **1cjggtlk17z3yzmbu1sa94vueum4jqw3** for example, some labels take place outside the lung part (as Figure 1 shown), which may cause negative effect to learning.

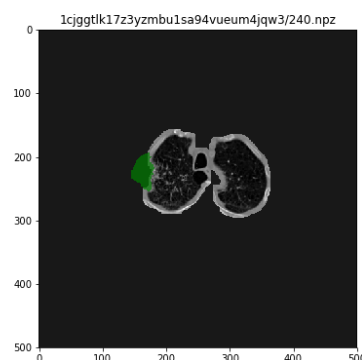


Figure 1 An example after masking

For the models that can pass medium-baseline, I only simply convert the images to Housefield Unit and normalize them between 0 and 1 with lower threshold = -1000, upper threshold = 400 due to the range we are interested in (Lung and soft tissue, reference from Figure 2).

Substance	HU
Air	-1000
Lung	-500
Fat	-100 to -50
Water	0
CSF	15
Kidney	30
Blood	+30 to +45
Muscle	+10 to +40
Grey matter	+37 to +45
White matter	+20 to +30
Liver	+40 to +60
Soft Tissue, Contrast	+100 to +300
Bone	+700 (cancellous bone) to +3000 (cortical bone)

Figure 2 Substance and HU table (from wiki)

Also, I also tried using to train a 3D model with only the central part of each patient because I can't figure out the way to crop samples yet. But again, I don't know how to deal with the coordinate for predictions and maybe try 3D model next time.

3. (1 %)

a. Please show the predicted image of

“52nd slice of patient **jdndkse8voi5t59sr8y1z9nuh1a4k09s**”,

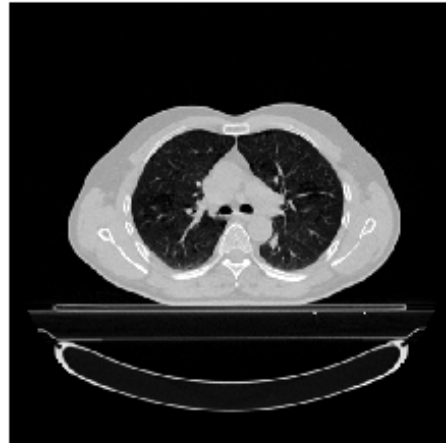
“59th slice of patient **ob3o558sc26crrdtv38b2z7fjl8xpqda**”, and

“58th slice of patient **k9plcilsqtwwwuu9oj2logl8ph5cmmmx**” during the early, middle, and the final stage in the training process. (For example, results of 1st, 100th, 10000th epoch). Epoch 5, 10, 20

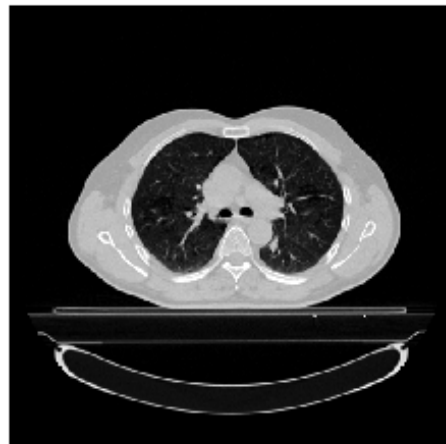
jdndkse8voi5t59sr8y1z9nuh1a4k09s_slice 52_epoch5



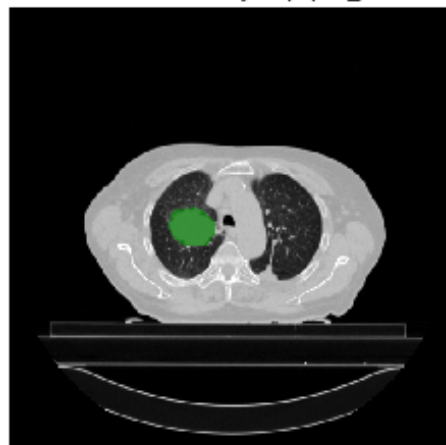
jdndkse8voi5t59sr8y1z9nuh1a4k09s_slice 52_epoch10



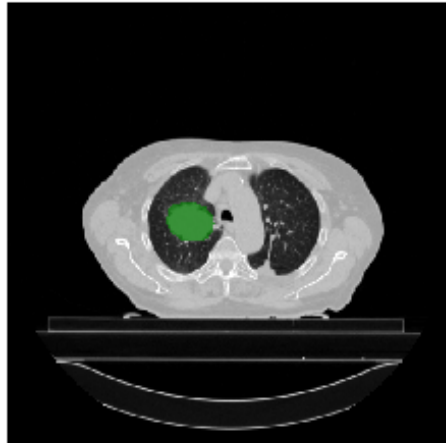
jdndkse8voi5t59sr8y1z9nuh1a4k09s_slice 52_epoch20



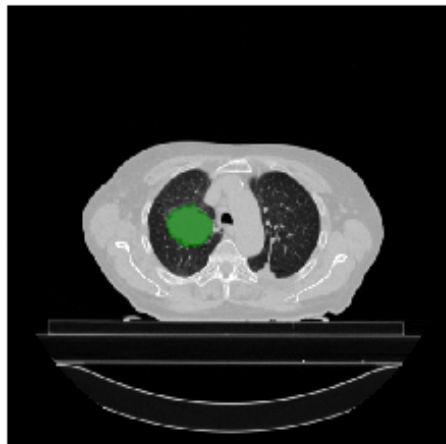
ob3o558sc26crrdtv38b2z7fjl8xpqda_slice 59_epoch5



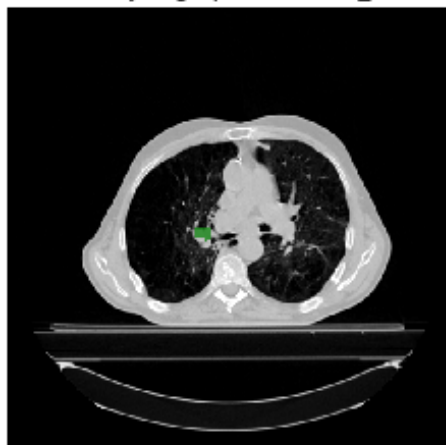
ob3o558sc26crrdtv38b2z7fjl8xpqda_slice 59_epoch10



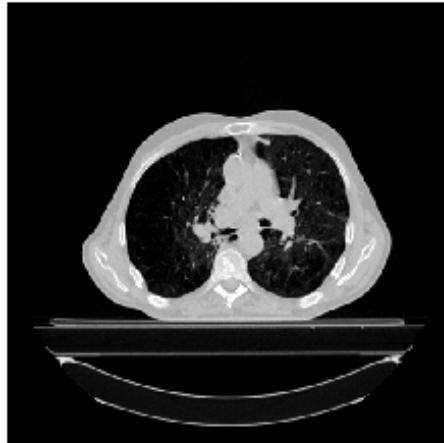
ob3o558sc26crrdtv38b2z7fjl8xpqda_slice 59_epoch20



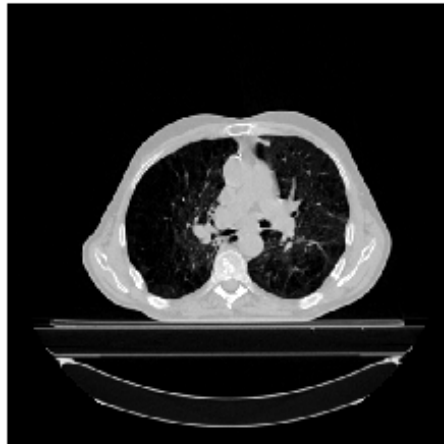
k9plcilsqtwwwuu9oj2logl8ph5cmmmx_slice 58_epoch5



k9plcilsqtwwwuu9oj2logl8ph5cmmmx_slice 58_epoch10



k9plcilsqtwwwuu9oj2logl8ph5cmmmx_slice 58_epoch20



- b. Please plot the training curve with training/validation loss and training/validation Dice coefficient.

