

Automatic Segmentation of COVID-19 from CT images



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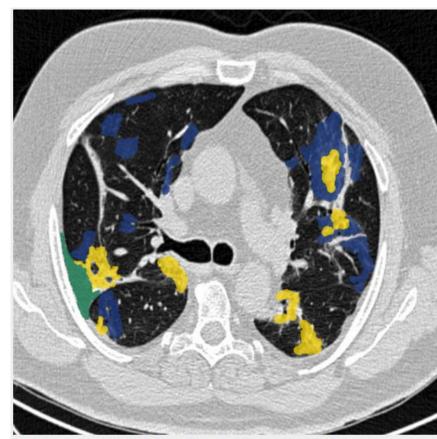


Outlier

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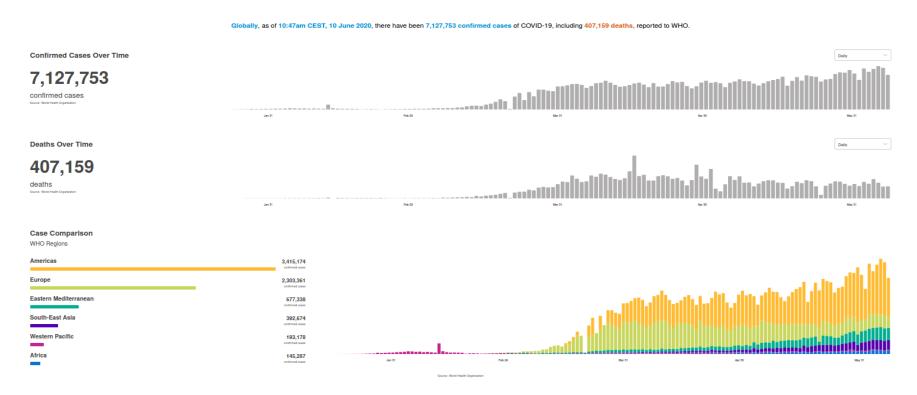
Introduction

- The coronavirus disease (COVID- na si (19 niarts wen a yb desuac esaesid suoitcefni surivanoroc fo
- This new virus and disease were unknown before the outbreak began in Wuhan, China, in December .2019
- This virus directly causes respiratory diseases, and this appears in the lungs.
- This virus has claimed many lives around the world and until now



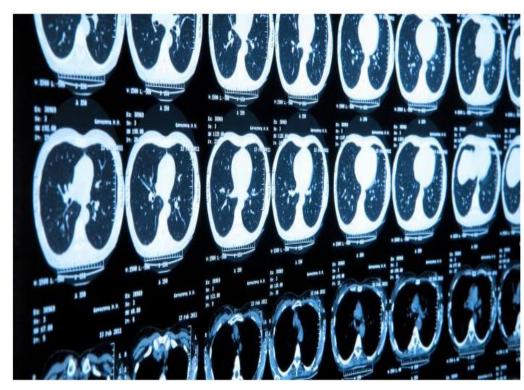
Example of one segmented COVID-19 CT axial slice. Ground-glass opacities in blue, consolidation in yellow and pleural effusion in green

COVID-19 World



Problem:

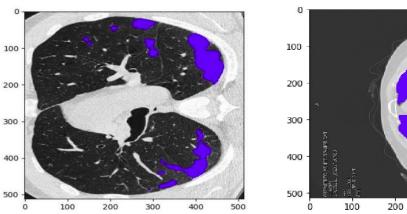
- For COVID-19 patients the common stage in diagnosis is computer tomography (CT).
- A radiologist is often asked to estimate the extent of damage with respect to lung volume.
- It is a time-consuming procedure, because radiologist should look through all axial slices on CT and segment each of them.



https://news.feinberg.northwestern.edu/-recnac-gnul-stops-metsys-ecnegilletni-laicifitra/2019/05/stsigoloidar-erofeb

Objective

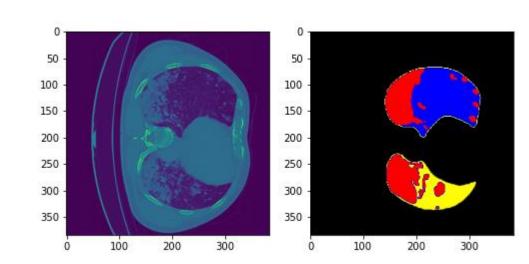
- Automatic Segmentation using Artificial intelligence to :
 - Left Lung
 - Right Lung
 - COVID-19 in CT images.
- Determine the location of diseases and the rate of occurrence in the lung.



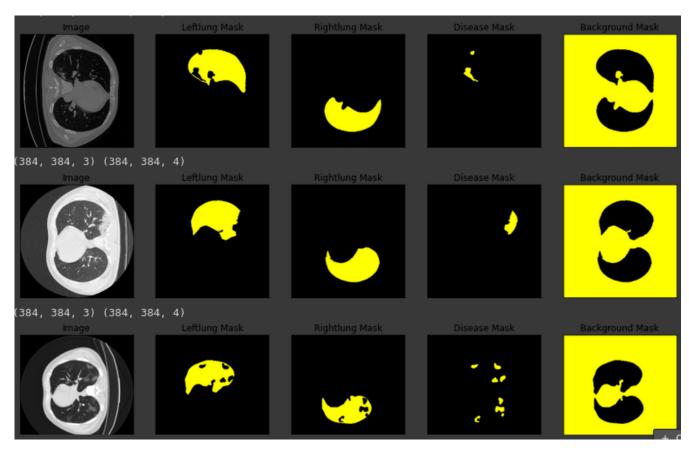
500

Dataset:

- 20lung CT scans from for Lung.
- Annotations to:
 - -1left lung.
 - -2right lung.
 - -3infections.



Sample of Dataset:



Solution

- There are several techniques used in the left ventricle segmentation.

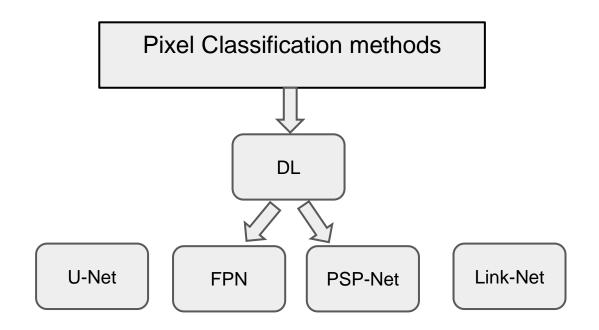
Techniques	Methods					
Image based methods	Thresholding, Region growing					
Pixel Classification methods	Clustering, Classification					
Deformable models	Active contour model					
model based methods	Active shape model [ASM], Active appearance model [AAM]					

Segmentation Methods

Let's focus on this method:

Techniques	Methods					
Image based methods	Thresholding, Region growing					
Pixel Classification methods	Clustering, Classification					
Deformable models	Active contour model					
model based methods	Active shape model [ASM], Active appearance model [AAM]					

Segmentation Models [Deep Learning]:



Deep learning method (U-net)

- It had been quite successful in biomedical segmentation tasks. U-net models are promising, as the authors were able to train their network with only 30 images by using aggressive image augmentation combined with pixel-wise reweighting. (Interested readers: here are reviews for CNN and conventional approaches.)
- The U-Net architecture is built upon the Fully Convolutional Network and modified in a way that it yields better segmentation in medical imaging.

U-net (Cont.)

U-Net architecture is separated in 3 parts:

: 1The contracting/downsampling path

: 2Bottleneck

: 3The expanding/upsampling path

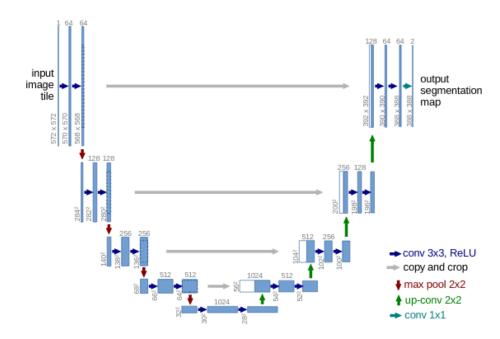


Fig. 1. U-net architecture (example for 32x32 pixels in the lowest resolution). Each blue box corresponds to a multi-channel feature map. The number of channels is denoted on top of the box. The x-y-size is provided at the lower left edge of the box. White boxes represent copied feature maps. The arrows denote the different operations.

Linknet:

 Deep neural network architecture which allows it to learn without any significant increase in number of parameters.

Efficient algorithm in real-time application.

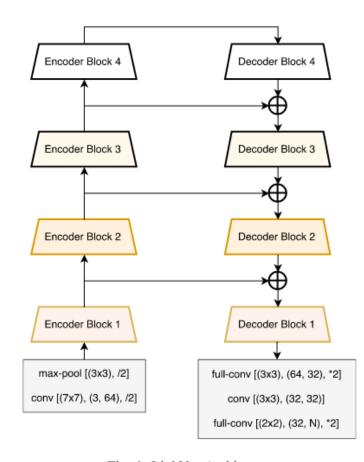
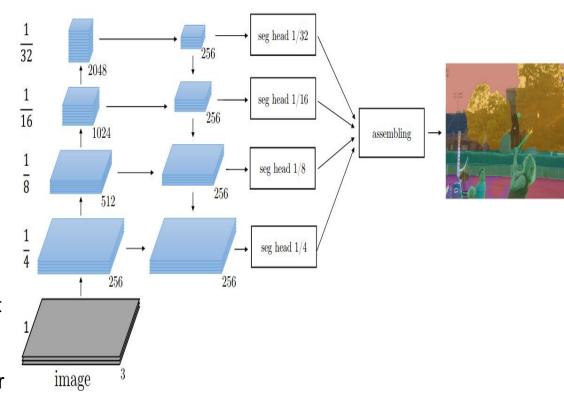


Fig. 1: LinkNet Architecture

Feature Pyramid Network(FPN)

- Feature pyramids inside the convolutional neural network (CNN).
- It combines low-resolution, semantically strong features with high-resolution, semantically weak features via a top-down pathway and lateral connections.
- Feature pyramid has rich semantics at all levels and is built quickly from a single input image scale, thereby without sacrificing representational power, speed, or memory.



Pyramid Scene Parsing Network(PNPnet)

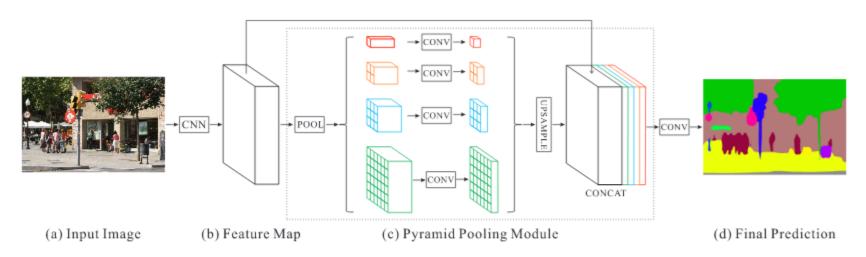


Figure 3. Overview of our proposed PSPNet. Given an input image (a), we first use CNN to get the feature map of the last convolutional layer (b), then a pyramid parsing module is applied to harvest different sub-region representations, followed by upsampling and concatenation layers to form the final feature representation, which carries both local and global context information in (c). Finally, the representation is fed into a convolution layer to get the final per-pixel prediction (d).

Transfer learning

- Transfer learning is a popular method in computer vision because it allows us to build accurate models in a timesaving way.
- With transfer learning, instead of starting the learning process from scratch, you start from patterns that have been learned when solving a different problem.

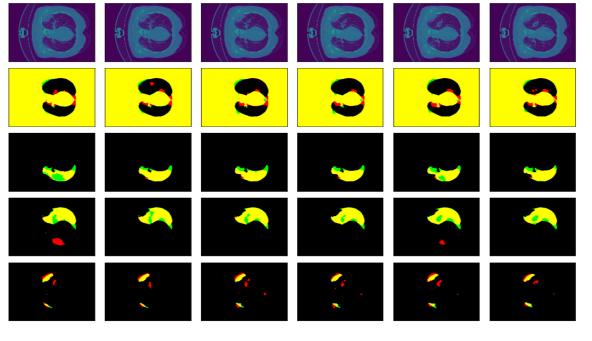
Pretrain models	Trained on	#Parameters	Input	Output	
U-Net		10,115,948			
LinkNet	Imagenet	6,096,780	(3*256*256)	(4*256*256)	
FPN	Dataset	7,041,964			
PSPNet		1,770,854	(3*384*384)	(4*384*384)	

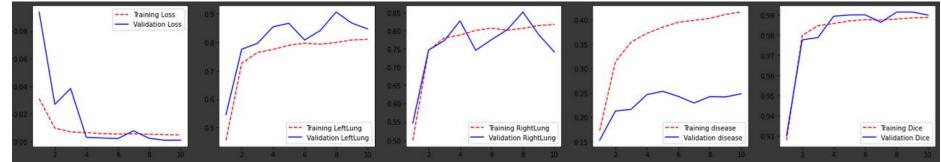
Train Models

- Using Google colab and Kaggle Notebooks
- Train models on [GPU]
- #Epoch = 10

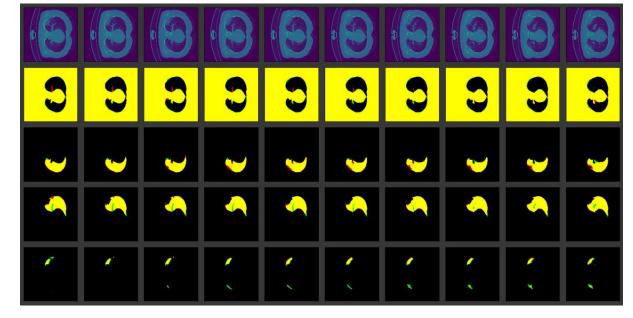
Pretrain models	Time of Train					
U-Net	4.5 ∼h					
LinkNet	3.5 ~h					
FPN	4 ~h					
PSPNet	2 ~h					

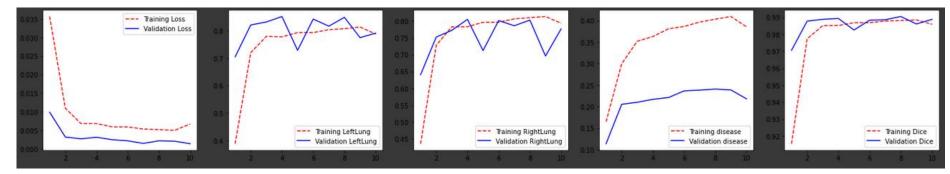
Results [U-net]



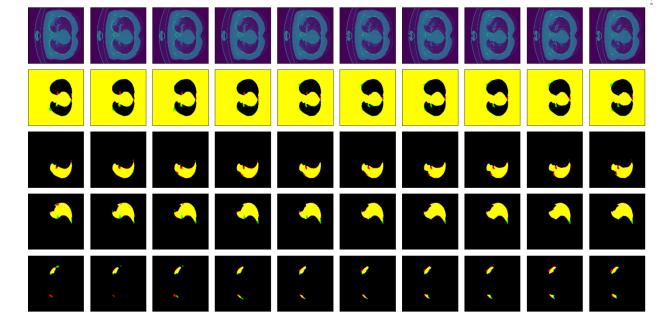


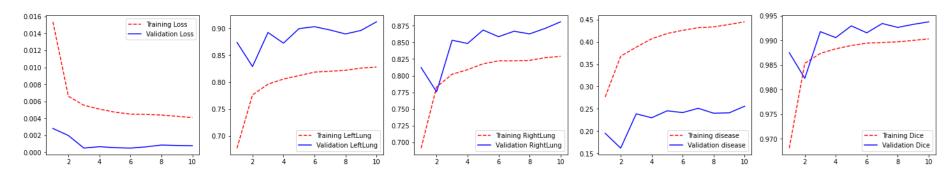
Results [Linknet]



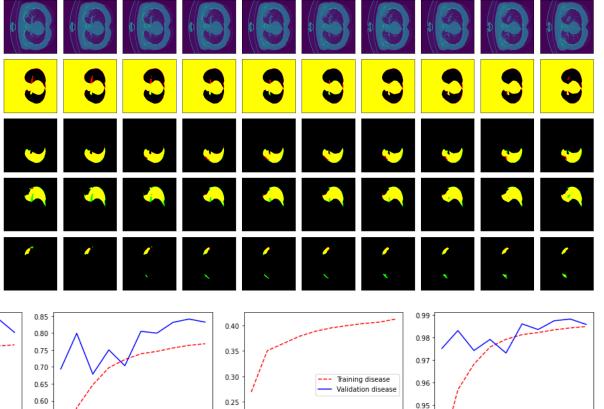


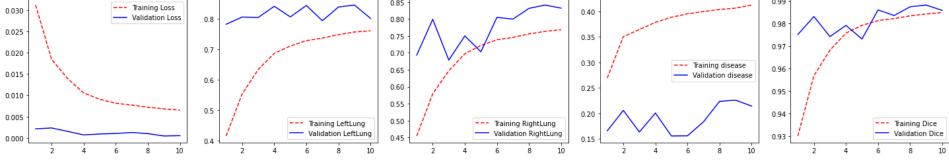
Results [FPN]





Results [PSPNet]





Evaluation:

- To evaluate the work, we calculate different parameters that used to measure the performance of the segmentation algorithm. These parameters are sensitivity, specificity, and dice metric..,
- Compared its values from the automatic segmentation algorithm, and the manual segmentation by different metric.

Evaluation(Accuracy):

True Positive (TP)	False Positive (FP)					
Patient has pneumonia Model predicts: pneumonia Number of occurrences: 1	Patient is healthy Model predicts: pneumonia Number of occurrences: 1					
False Negative (FN)	True Negative (TN)					
False Negative (FN) Patient has pneumonia Model predicts: healthy	True Negative (TN) Patient is healthy Model predicts: healthy					

 $\frac{accuracy}{accuracy} = \frac{\text{true positives} + \text{true negatives}}{\text{true positives} + \text{true negatives} + \text{false positives} + \text{false negatives}}$

Evaluation (sensitivity)

 The sensitivity is the proportion of true positives of the automatic segmentation output to the manual segmentation output (i.e. reference output).

$$S = \frac{TP}{TP + FN}$$

Evaluation (specificity)

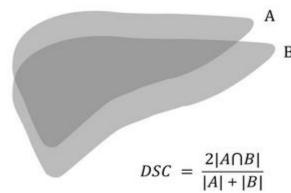
 The specificity is the proportion of true negatives of the automatic segmentation output to the manual segmentation output.

$$SP = \frac{TN}{FP + TN}$$

Evaluation (Dice Function)

 Dice similarity coefficient, which is a measure of how well two objects overlap.

The Dice index ranges from
) 0 complete mismatch (
 To .(hctam tcefrep)1



DSC: Dice similarity coefficient

Evaluation(Positive predictive value (PPV))

- Positive predictive value (PPV) is the probability that subjects with a positive screening test truly have the disease.

$$PPV = \frac{\text{true positives}}{\text{true positives} + \text{false positives}}$$

Evaluation(Negative predictive value (NPV))

 Negative predictive value (NPV) is the probability that subjects with a negative screening test truly don't have the disease.

$$NPV = \frac{\text{true negatives}}{\text{true negatives} + \text{false negatives}}$$

Evaluat [U-net]

	TP	TN	FP	FN	Accuracy	Prevalence	Sensitivity	Specificity	PPV	NPV	Dice	Threshold
RightLung	883021	138376	19127	8052	97.408	84.9793	99.0964	87.8561	97.8798	94.5011	97.9415	0.5
LeftLung	39628	982328	2624	23996	97.4613	6.06766	62.2847	99.7336	93.7896	97.6155	65.3197	0.5
Disease	63988	954467	11194	18927	97.1274	7.90739	77.173	98.8408	85.1108	98.0556	74.3531	0.5
										1	odo -	Toxt

Evaluat [LinkNet]

	TP	TN	FP	FN	Accuracy	Prevalence	Sensitivity	Specificity	PPV	NPV	Dice	Threshold
RightLung	883723	154309	3194	7350	98.9944	84.9793	99.1752	97.9721	99.6399	95.4534	98.9193	0.5
LeftLung	61759	980026	4926	1865	99.3524	6.06766	97.0687	99.4999	92.613	99.8101	89.4522	0.5
Disease	78520	962857	2804	4395	99.3134	7.90739	94.6994	99.7096	96.5521	99.5456	90.5323	0.5

Evaluat [FPN]

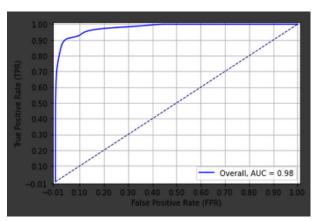
		TP	TN	FP	FN	Accuracy	Prevalence	Sensitivity	Specificity	PPV	NPV	Dice	Threshold
R	ightLung	882851	155145	2358	8222	98.991	84.9793	99.0773	98.5029	99.7336	94.9672	99.1084	0.5
	LeftLung	63119	980031	4921	505	99.4825	6.06766	99.2063	99.5004	92.7675	99.9485	94.2097	0.5
	Disease	79998	963618	2043	2917	99.527	7.90739	96.4819	99.7884	97.5098	99.6982	95.2581	0.5

Evaluat [PSPNet]

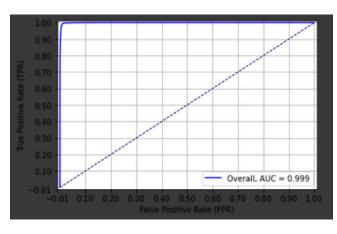
	TP	TN	FP	FN	Accuracy	Prevalence	Sensitivity	Specificity	PPV	NPV	Dice	Threshold
RightLung	2002388	323843	30813	2252	98.5985	84.9677	99.8877	91.3119	98.4845	99.3094	98.889	0.5
LeftLung	133180	2210674	5194	10248	99.3455	6.07927	92.855	99.7656	96.2464	99.5386	92.0179	0.5
Disease	164429	2171278	1428	22161	99.0002	7.90872	88.1232	99.9343	99.139	98.9897	91.6287	0.5

ROC Curve:

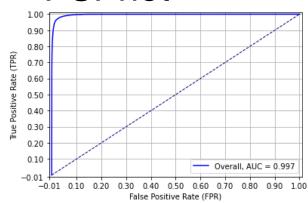
U-net



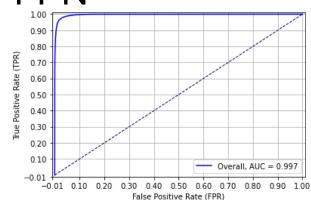
Linknet



PSPnet

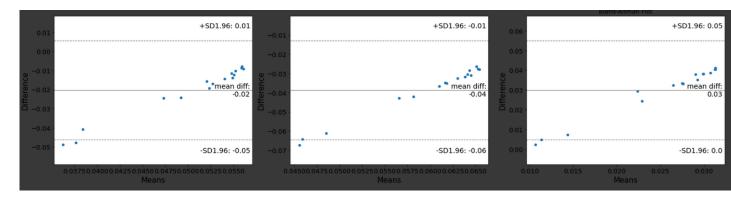


FPN



Bland-Altman Plot:

U-net



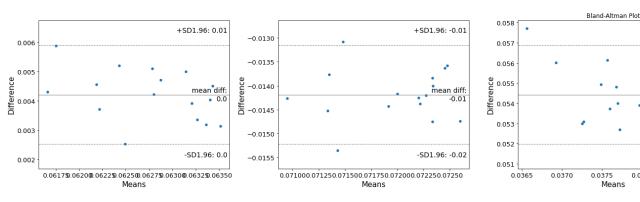
Link-net

+SD1.96: 0.06

-SD1.96: 0.05

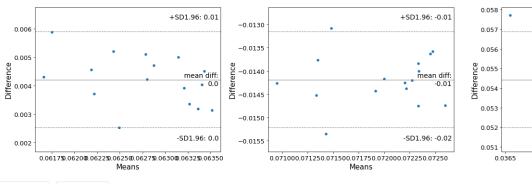
0.0385

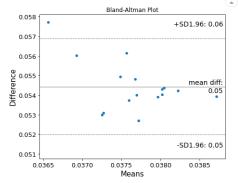
0.0380



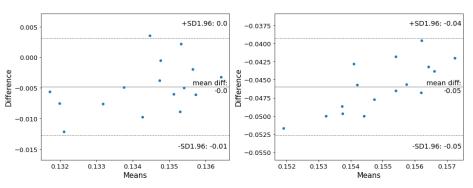
Bland-Altman Plot:

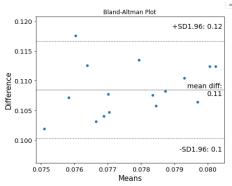
FPN





PSPnet





Hausdorff Distance

#images = 16

Pretrain models	HD	HD95		
U-Net				
LinkNet	15.5 ~ - 10.5~	12~ - 8~		
FPN	15.5 ~ - 10.5~			
PSPNet				

Conclusion:

- In this project we mork on multiclass segmentation problem for CT images to segment [Left Lung, Right Lung and COVID-.[19
- Applied different model to solve this problem like [U-Net, LinkNet, FPN and PSPNet].
- Evaluate the result using several method like [Dice, ROC, Hausdorff, Sensitivity and specificity, ...].

Implementation:

- Python
- Keras
- Tensorflow
- Albumentations
- Sklearn
- Google Colab, Kaggle Notebooks:
 - : [ten-U] -1 https://colab.research.google.com/drive/1FkkU2wApXPvI977olGR3kiFlhyr3jj5TBOiCGQF=oTllorcs#31BCP
 - : [tenkniL] -2https://colab.research.google.com/drive/3uRTK_12o2TckyjMSGTRt0hVJEXuOVw7g#scrollTo=NkMbeYuwSwD6
 - : [NPF] -3 https://colab.research.google.com/drive/1ZUR-cL6fWYv-D1ELxlpjAi4X9F7nploE#scrollTo=Lr7OzGMzuDuZ

1/evird/moc.elgoog.hcraeser.baloc//:sptth: [tenPSP] -4w7dQ2TaA-w-B2461sXbWpN1RQcNsUz3k#scrollTo=rlxGm79W7mAK

References:

- -1 https://arxiv.org/pdf/[noitatnemgeS egaml lacidemoiB rof skrowteN lanoitulovnoC :teN-U] fdp.1505.04597
- -2 https://arxiv.org/pdf/[noitatnemgeS citnameS tneiciffErof snoitatneserpeR redocnE gnitiolpxE :teNkniL] fdp.1707.03718
- -3https://arxiv.org/pdf/[(teNPSP) krowteN gnisraP enecS dimaryP] fdp.1612.01105
- -4http://presentations.cocodataset.org/COCO[(NPF) krowteN dimaryP erutaeF] fdp.RIAF-ffutS-17
- -5https://segmentation-models.readthedocs.io/en/latest/index.html
- -6https://gitee.com/junma 2#kramhcneB-geS-TC-19-DIVOC/11
- -7 http://medicalsegmentation.com/covid /19
- -8https://github.com/EMIDEC-Challenge/Evaluation-metrics

THANK YOU FOR YOUR ATTENTION!

