Assembling Existing Labels from Public Datasets to Diagnose Novel Diseases: COVID-19 in Late 2019

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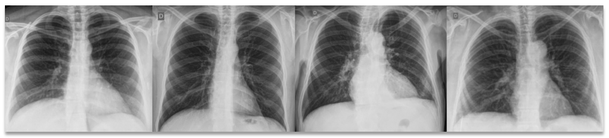
Introduction

Despite the grand success of deep learning in a few medical applications, its prohibitively ***high annotation costs*** raise doubts about the feasibility of applying it to those medical specialties that lack such magnitude of annotation.

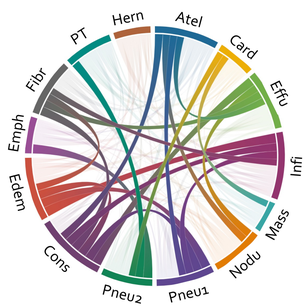
- For Pancreas tumors detection in ***FELIX***[1], it needs ***5038*** examples to get high performance. But This annotation took ***15 human-year*** to create.
- it is impossible to acquire sufficient annotation or even to gather sizable data for novel diseases and emerging pandemics during the outbreak.
- We ask: ***can we exploit these existing, large, annotated datasets to facilitate computer-aided diagnosis of novel diseases?***

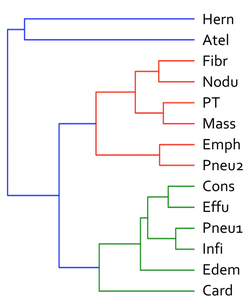
Materials

- COVIDx CXR-2 provides about 15,000 subjects from at least 51 countries.



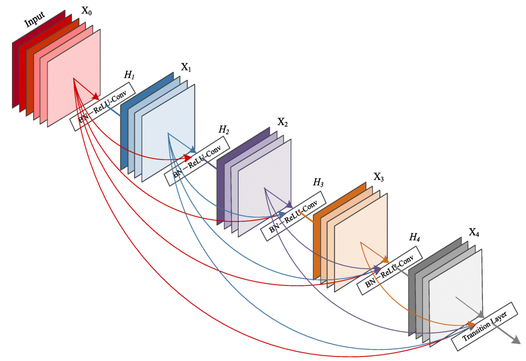
- ChestX-ray14[2] provides 112,120 frontal-view X-ray images of 30,805 unique patients with the text-mined 14 disease image labels.



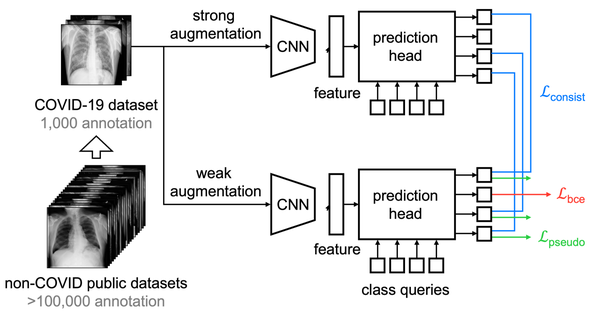


Method

- We used ***DenseNet121***[3] as the classification backbone. This classifier contains 1+N output headers. One of the output headers is to predict whether it is a COVID-19 positive or not, and the other N output headers are used to predict assembled labels.



- Label-Assemble comes in two different types: ***fully-supervised Label-Assemble*** and ***semi-supervised Label-Assemble***. The semi-supervised component consists of three loss functions are as the figure below.



Reference

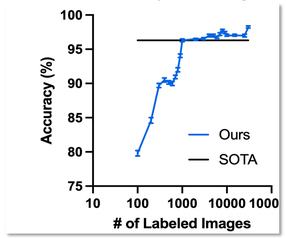
[1] Xia, Yingda, Qihang Yu, Linda Chu, Satomi Kawamoto, Seyoun Park, Fengze Liu, Jieneng Chen et al. "The FELIX Project: Deep Networks To Detect Pancreatic Neoplasms." medRxiv (2022).
[2] Xiaosong Wang, Yifan Peng, Le Lu, Zhiyong Lu, Mohammadhadi Bagheri, and Ronald M Summers. Chestx-ray8: Hospital-scale chest x-ray database and benchmarks on weakly-supervised classification and localization of common thorax diseases. In Proceedings of the IEEE conference on computer vision and pattern recognition, pages 2097–2106, 2017.
[3] G. Huang, Z. Liu, K. Q. Weinberger, and L. van der Maaten, "Densely connected convolutional networks," in Proceedings of the IEEE Conference on Computer Vision and Pattern Recognition, vol. 1, no. 2, 2017, p. 3.
[4] Linda Wang, Zhong Qiu Lin, and Alexander Wong. Covid-net: a tailored deep convolutional neural network design for detection of covid-19 cases from chest x-ray images. Scientific Reports, 10(1):19549, Nov 2020.

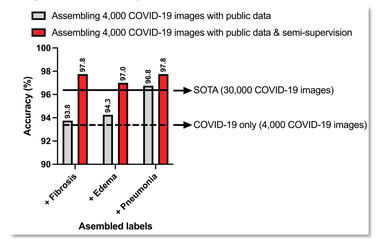
Results

(1) Compared with the current state-of-the-art[4], we only use ***1000*** images (***3%***) to achieve the effect of it.

(2) For fully-supervised Label-Assemble, the more similar the diseases, the better the model.

(3) Semi-supervised Label Assemble can better improve the effect on classification by learning more negative sample features of different





(4) Exceeding Prior Arts of COVID-19 Classification

Assembled Label	# Images	Accuracy [95% CI]	Specificity [95% CI]	Sensitivity [95% CI]
Fibrosis	4,000	97.8 [97.6 – 97.9]	98.4 [98.3 – 98.7]	97.8 [97.8 – 98.2]
	30,850	99.3 [99.1 – 99.3]	99.5 [99.4 – 99.6]	99.0 [98.8 – 99.1]
Edema	4,000	97.0 [96.8 – 97.1]	97.5 [97.0 – 97.5]	96.5 [96.4 – 97.0]
	30,850	98.8 [98.6 – 99.2]	99.0 [98.8 – 99.1]	99.5 [99.3 – 99.6]
Pneumonia	4,000	97.8 [97.6 – 97.9]	99.0 [98.9 – 99.2]	96.5 [96.2 – 96.7]
	30,850	98.8 [98.7 – 98.8]	100	99.3 [99.3 – 99.6]

Conclusion

Label-Assemble shows a good prospect in disease diagnosis: ***we can use common pneumonias to improve the accuracy of rare pneumonias and reduce the cost of labeling.*** Semi-supervised Label-Assemble not only improves accuracy, but also eliminates the effects of category similarity. Although our paper focuses on COVID-19, the proposed method and discovery are applicable to many novel diseases, e.g., Silicosis. Note that for novel diseases, we still need many labeled data for evaluation.