

COVID-19 Image Data Collection: Prospective Predictions are the Future

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Abstract

Across the world's coronavirus disease 2019 (COVID-19) hot spots, the need to streamline patient diagnosis and management has become more pressing than ever. As one of the main imaging tools, chest X-rays (CXRs) are common, fast, non-invasive, relatively cheap, and potentially bedside to monitor the progression of the disease. This paper describes the first public COVID-19 image data collection as well as a preliminary exploration of possible use cases for the data. This dataset currently contains hundreds of frontal view X-rays and is the largest public resource for COVID-19 image and prognostic data, making it a necessary resource to develop and evaluate tools to aid in the treatment of COVID-19. It was manually aggregated from publication figures as well as various web based repositories into a machine learning (ML) friendly format with accompanying dataloader code. We collected frontal and lateral view imagery and metadata such as the time since first symptoms, intensive care unit (ICU) status, survival status, intubation status, or hospital location. We present multiple possible use cases for the data such as predicting the need for the ICU, predicting patient survival, and understanding a patient's trajectory during treatment. Data can be accessed here: <https://github.com/ieee8023/covid-chestxray-dataset>

1. Introduction

In the times of the rapidly emerging coronavirus disease 2019 (COVID-19), hot spots and growing concerns about a second wave are making it crucial to streamline patient diagnosis and management. Many experts in the medical community believe that artificial intelligence (AI) systems could lessen the burden on hospitals dealing with outbreaks by processing imaging data [Kim, 2020; Rubin et al., 2020]. Hospitals have deployed AI-driven computed tomography (CT) scan interpreters in China [Simonite, 2020] and Italy [Lyman, 2020], as well as AI initiatives to improve triaging of COVID-19 patients (i.e., discharge, general admission, or ICU care) and allocation of hospital resources [Strickland, 2020; Hao, 2020].

Carefully curated and annotated data is the first step to developing any diagnostic or management tool. While there exist large public datasets of more typical chest X-rays (CXR) [Wang et al., 2017; Bustos et al., 2019; Irvin et al., 2019; Johnson et al., 2019; Demner-Fushman et al., 2016], there was no public collection of COVID-19 CXR or CT scans designed to be used for computational analysis. We first made data public in mid February 2020 and the dataset has rapidly grown [Cohen et al., 2020c]. More recently, in June, the BIMCV COVID-19+ dataset [De La Iglesia Vayá et al., 2020] was released. While it has more samples than the dataset we present, we complement their work with a focus on prospective metadata from multiple medical centers and countries.

Many physicians remain reluctant to share their patients’ anonymized imaging data in open datasets, even after obtaining consent, due to ethical concerns over privacy and confidentiality and a hospital culture that, in our experience, does not reward sharing [Keen et al., 2013; Lee and Yoon, 2017; Kostkova et al., 2016; Floca, 2014]. In order to access data in one hospital, researchers must submit a protocol to the hospital’s institutional review board (IRB) for approval and build their own data management system. While this is important for patient safety, such routines must be repeated for every hospital, resulting in a lengthy bureaucratic process that hurts reproducibility and external validation.

The ultimate goal of this project is to aggregate all publicly available radiographs, including papers and other datasets that can be combined. For research articles, images are extracted by hand, while for websites, such as Radiopaedia and Eurorad, data collection is partially automated using scrapers that extract a subset of the metadata while we hand review case notes to determine clinical events. This work provides three primary contributions:

- We create the first public COVID-19 CXR image data collection, currently totalling 679 frontal chest X-ray images from 412 people from 26 countries and growing. The dataset contains clinical attributes about survival, ICU stay, intubation events, blood tests, location, and freeform clinical notes for each image/case. In contrast to other works, we focus on prospective metadata for the development of prognostic and management tools from CXR. Images collected have already been made public and are presented in an ML-ready dataset with toolchains that are easily used in many testable settings.
- We also present and discuss clinical use-cases and propose ML tasks that may address these clinical use cases such as predicting pneumonia severity, survival outcome, and need for the intensive care unit (ICU). Benchmark results using transfer learning with neural networks are included.
- We also discuss how to use the location information in this dataset for a Leave-One-Country/Continent-Out (LOCO) evaluation to simulate domain shift and provide a more robust evaluation.

Currently, all images and data are released under the following GitHub URL¹. We hope that this dataset and tasks will allow for quick uptake of COVID-related prediction problems in the machine learning community.

1. <https://github.com/ieee8023/covid-chestxray-dataset>

2. Background and Related Work

2.1 Learning in Medical Imaging

In recent years, ML applications on CXR data have seen rising interest, such as lung segmentation [Gordienko et al., 2018; Islam and Zhang, 2018], tuberculosis and cancer analysis [Gordienko et al., 2018; Stirenko et al., 2018; Lakhani and Sundaram, 2017], abnormality detection [Islam et al., 2017], explanation [Singla et al., 2020], and multi-modality predictions Rubin et al. [2018]; Hashir et al. [2020]. With the availability of large-scale public CXR datasets created with ML in mind (e.g. CheXpert [Irvin et al., 2019], Chest-xray8 [Wang et al., 2017], PadChest [Bustos et al., 2019] or MIMIC-CXR [Johnson et al., 2019]), neural networks have even reported being able to achieve performance near radiologist levels [Rajpurkar et al., 2018, 2017; Irvin et al., 2019; Putha et al., 2018a; Majkowska et al., 2019; Putha et al., 2018b]. However, the adoption has its own challenges [Couzin-Frankel, 2019].

2.2 Use of Imaging for COVID-19

In this section we will give a high level overview of the recommendations for the clinical use of imaging in COVID-19 patient management. It should be noted that this list is only meant to help guide algorithm development and is not medically comprehensive.

Ever since the dawn of the outbreak, imaging has stood out as a promising avenue of research and care [Zu et al., 2020; Poggiali et al., 2020]. Particularly in the beginning of the outbreak, computed tomography (CT) scans captured the attention of both the medical [Ng et al., 2020; Kanne et al., 2020] and the ML [McCall, 2020] communities.

From March to May 2020, the Fleischner Society [Rubin et al., 2020], American College of Radiology (ACR) [ACR, 2020], Canadian Association of Radiologists (CAR) [Dennie et al., 2020a], Canadian Society of Thoracic Radiology (CSTR) [Dennie et al., 2020b], and British Society of Thoracic Imaging (BSTI) [Nair et al., 2020] released the following recommendations:

1. Imaging tests (CXR and chest CT scans) should not be used alone to diagnose COVID-19 nor used systematically on all patients with suspected COVID-19;
2. Findings on CT scans and CXR are non-specific and these imaging techniques should not be used to inform decisions on whether to test a patient for COVID-19 (in other words, normal chest imaging results do not exclude the possibility of COVID-19 infection and abnormal chest imaging findings are not specific for diagnosis);
3. CXR and chest CT scans can be used for patients at risk of disease progression and with worsening respiratory status as well as in resource-constrained environments for triage of patients with suspected COVID-19.

However, CXRs remain the first choice in terms of the initial imaging test when caring for patients with suspected COVID-19. CXRs are the preferred initial imaging modality when pneumonia is suspected [ACR, 2018] and the radiation dose of CXR (0.02 mSv for a PA film) is lower than the radiation dose of chest CT scans (7 mSv), putting the patients less at risk of radiation-related diseases such as cancer [FDA, 2017].

In addition, CXR are cheaper than CT scans, making them more viable financially for healthcare systems and patients. [Beek, 2015; Ball et al., 2017]. Finally, portable CXR units

can be wheeled into ICU as well as emergency rooms (ER) and are easily cleaned afterwards, reducing impact on patient flow and risks of infection [Dennie et al., 2020a; ACR, 2020].

A recent hypothesis that is increasingly confirmed by research suggesting that COVID-19 is not a pulmonary but rather a vascular disease [Varga et al., 2020] [Ackermann et al., 2020]. This could explain the variety of symptoms which do not necessarily include pneumonia but can still lead to ICU hospitalization [Wadman et al., 2020].

2.3 COVID-19 Prediction from CXR

While many works have attempted to predict COVID-19 through medical imaging, the results have been on small or private data. Many of these methods use the dataset presented here. For example, while promising results were achieved by Raj [2020] (90% AUC), these were reported over a large private dataset and are not reproducible. Additionally, much research is presented without appropriate evaluations, potentially leading to overfitting and performance overestimation [Maguolo and Nanni, 2020; Tartaglione et al., 2020; DeGrave et al., 2020]. Many prediction models are not viable for use in clinical practice, as they are inadequately reported, particularly with regard to their performance, and at strong risk of bias Wynants et al. [2020]. A study by Murphy et al. [2020] found that an AI system achieved an AUC of 0.81 and was comparable with that of six independent readers.

Most ML work using this dataset has focused on COVID-19 Prediction similar to our task definition in §5.1. Many have used a transfer learning approach, similar to what we use for baselines in this work, where a model that is pretrained on existing CXR datasets is used to construct features from the images in this dataset which are lower dimensional and are less prone to overfitting [Apostolopoulos and Mpesiana, 2020] [Minaee et al., 2020]. Another similar approach taken is utilizing a multi-task network which predicts both standard CXR tasks as well as a COVID-19 task to assign a likelihood to samples and perform anomaly detection [Zhang et al., 2020]. Another work has utilized the pathology hierarchy we provide to improve predictions by using the Clus-HMC method [Pereira et al., 2020].

Many groups have also used this dataset to make severity and survival outcome predictions similar to our task definition in §5.2 and 5.3. Such work like Signoroni et al. [2020] focused on predicting a Brixia Score which has been clinically studied against severity and outcomes [Borghesi and Maroldi, 2020b]. It is laborious to create these annotations so an approach by Amer et al. [2020] predicts a lung segmentation, generates a prediction saliency, and then calculates the ratio of coverage which acts as a proxy for the Brixia and geographic extent scores we discuss later.

3. Cohort Details

The current statistics as of September 18th 2020 are shown in Table 1, which presents the distribution of frontal CXR by diagnosis, types of pneumonia and responsible microorganisms when applicable. For each image, attributes shown in Table 2 are collected. Statistics are presented by sub-region in Table 3 and by projection/view in Table 4. Figures 1 and 2 present demographics for patients and frontal CXR images. In terms of unique patients the M/F ratio is 230/139. In total, 761 images were collected, of which 679 are frontal and 82 are lateral view. Of the frontal views 518 are standard frontal PA/AP (Posteroanterior/Anteroposterior) views and 161 are AP Supine (Anteroposterior laying down). The images originate from various hospitals across 26 different countries.

Table 2: Descriptions of each attribute of the metadata

Attribute	Description
patientid	Internal identifier
offset	Number of days since the start of symptoms or hospitalization for each image. If a report indicates "after a few days", then 5 days is assumed.
sex	Male (M), Female (F), or blank
age	Age of the patient in years
finding	Type of pneumonia
RT_PCR_positive	Yes (Y) or no (N) or blank if not reported/taken
survival	If the patient survived the disease. Yes (Y) or no (N)
intubated	Yes (Y) if the patient was intubated (or ventilated) at any point during this illness or No (N) or blank if unknown.
went_icu	Yes (Y) if the patient was in the ICU (intensive care unit) or CCU (critical care unit) at any point during this illness or No (N) or blank if unknown.
needed_supplemental_O2	Yes (Y) if the patient required supplemental oxygen at any point during this illness or No (N) or blank if unknown.
extubated	Yes (Y) if the patient was successfully extubated or No (N) or blank if unknown.
temperature	Temperature of the patient in Celsius at the time of the image.
view	Posteroanterior (PA), Anteroposterior (AP), AP Supine (APS), or Lateral (L) for X-rays; Axial or Coronal for CT scans
modality	CT, X-ray, or something else
date	Date on which the image was acquired
location	Hospital name, city, state, country
filename	Name with extension
doi	Digital object identifier (DOI) of the research article
url	URL of the paper or website where the image came from
license	License of the image such as CC BY-NC-SA. Blank if unknown
clinical_notes	Clinical notes about the image and/or the patient
other_notes	e.g. credit

Table 3: Statistics with respect to sub-regions. Y/N counts represent only the subset of images which are labelled.

Region	Sub-region	Frontal		Age Mean	Survival Y/N	Went		COVID-19 Count	RT-PCR	
		Patient Count	CXR Count			ICU Y/N	Intubation Y/N		Positive Count	Male Ratio
Africa	Northern Africa	5	13	40.00	0/1	0/0	0/0	0	0	0.00
Americas	Latin Amer./Caribbean	5	5	42.80	1/0	1/1	0/1	3	1	0.80
	Northern America	27	46	53.12	6/5	11/2	11/4	17	15	0.56
Asia	Eastern Asia	54	90	55.14	16/6	6/5	8/6	50	40	0.35
	South-eastern Asia	9	17	46.67	4/1	1/3	1/3	8	8	0.56
	Southern Asia	15	24	48.27	4/0	3/0	3/0	14	14	0.73
	Western Asia	13	20	46.92	2/0	3/0	2/0	6	4	0.54
Europe	Eastern Europe	4	7	67.50	1/0	0/0	0/0	1	1	0.50
	Northern Europe	31	60	58.78	3/3	7/0	7/1	22	18	0.55
	Southern Europe	123	195	59.30	31/4	25/9	13/22	91	74	0.63
	Western Europe	53	92	52.83	19/2	19/29	1/1	49	5	0.60
Oceania	Australia/New Zealand	42	60	50.48	4/0	1/1	1/1	1	2	0.57
Unknown	Unknown	31	50	53.64	3/3	6/0	7/2	19	0	0.55
Totals		412	679	55.1	119	133	95	281	182	0.55

Table 1: Counts of each pneumonia frontal CXR by type and genus or species when applicable. The hierarchy structure is shown in the table from left to right. Information is collected by manually reading clinical notes for a mention of a confirmed test.

Type	Genus or Species	Image Count
Viral	COVID-19 (SARSr-CoV-2)	468
	SARS (SARSr-CoV-1)	16
	MERS-CoV	10
	Varicella	5
	Influenza	4
	Herpes	3
Bacterial	<i>Streptococcus</i> spp.	13
	<i>Klebsiella</i> spp.	9
	<i>Escherichia coli</i>	4
	<i>Nocardia</i> spp.	4
	<i>Mycoplasma</i> spp.	5
	<i>Legionella</i> spp.	7
	Unknown	2
	<i>Chlamydophila</i> spp.	1
	<i>Staphylococcus</i> spp.	1
Fungal	<i>Pneumocystis</i> spp.	24
	<i>Aspergillosis</i> spp.	2
Lipoid	Not applicable	8
Aspiration	Not applicable	1
Unknown	Unknown	59

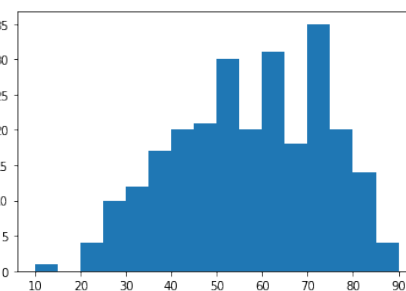


Figure 1: Age per patient

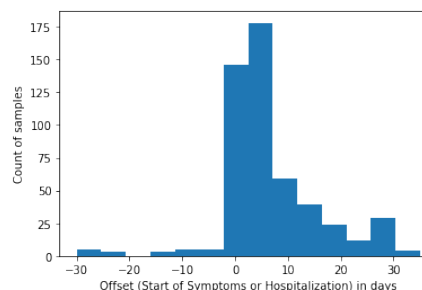


Figure 2: Offset per image

Table 4: Statistics with respect to the projection/view of the CXR. Y/N counts represent only the subset of images which are labelled.

View/Projection	Patient Count	Age Mean	Survival Y/N	ICU Y/N	Intubation Y/N	COVID-19 Count	RT-PCR Positive	Male Ratio
PosteroAnterior (PA)	326	52.21	104/19	53/67	33/55	191	112	0.54
AnteroPosterior (AP)	192	57.93	36/13	58/6	51/15	141	109	0.54
AP Supine	161	57.84	51/20	89/11	42/6	136	64	0.64
Lateral (L)	82	49.78	25/2	5/11	2/16	25	20	0.73

3.1 Data Collection

As mentioned earlier, data was largely compiled from public databases on websites such as Radiopaedia.org, the Italian Society of Medical and Interventional Radiology², Figure1.com³, and the Hannover Medical School [Winther et al., 2020b], both manually and using scrapers. A full list of publications is included in Appendix §C.1.

2. <https://www.sirm.org/category/senza-categoria/covid-19/>

3. <https://www.figure1.com/covid-19-clinical-cases>

Images were extracted from online publications, websites, or directly from the PDF using the tool `pdfimages`⁴. Throughout data collection, we aimed to maintain the quality of the images. Many articles were found using the list of literature provided by Peng et al. [2020]. A limitation of this approach is that we have no control over the processing between the PAC system and the PDF or website. However, we believe that information about the radiological finding was maintained otherwise the image in publication would not be useful. We also believe the images from PDFs and other image sources provide useful information when compared to raw data and expect studies to show this.

A challenge in extracting metadata is the alignment with images. To belong in the same row as an image, a clinical measurement must have been taken on the same day. It can be difficult to automatically determine when the measurement was taken if the metadata appears outside of image captions. For details on scraper design, see §Appendix C. All scripts are made publicly available.

4. Experimental Setup

Using this dataset as a benchmark is very challenging because, by the nature of its construction, it is very biased and unbalanced (recall geographically unbalanced labels in Table 3). This can lead to many negative outcomes if treated as a typical benchmark dataset [Maguolo and Nanni, 2020; Cohen et al., 2020b; Seyyed-Kalantari et al., 2020; Kelly et al., 2019]. Unless otherwise specified only AP and PA views are used to avoid confounding image artifacts of the AP Supine view.

4.1 Leave-One-Country/Continent-Out (LOCO) Evaluation:

In order to deal with issues of bias, we perform a “leave one country/continent out” (LOCO) evaluation. This approach is motivated from training bias common in small, unbalanced datasets. For our evaluation the test set will be composed of data from a single continent. Ideally, we would separate by countries, but this is not possible given the current distribution of data. We also note that not every sample is labelled, so models may be trained and evaluated on data from the same continent, but we ensured that samples in training and evaluation did not originate from the same research group/image source.

This approach should give us a distributional shift that will allow us to correctly evaluate the model. For each task, a subset of the samples will have enough representation to be included. Continents which do not have at least one representative for each class are filtered out and not used.

4.2 Models and Features

In place of images, features are extracted using a pre-trained DenseNet model [Huang et al., 2017] from the TorchXRyVison library [Cohen et al., 2020d] which is trained on 7 large CXR datasets as described in Cohen et al. [2020b]. These datasets were manually aligned with each other on 18 common radiological finding tasks in order to train a model using all datasets at once (atelectasis, consolidation, infiltration, pneumothorax, edema, emphysema, fibrosis, fibrosis, effusion, pneumonia, pleural thickening, cardiomegaly, nodule, mass, hernia,

4. <https://poppler.freedesktop.org/>

lung lesion, fracture, lung opacity, and enlarged cardiomeastinum). For example “pleural effusion” from one dataset is considered the same as “effusion” from another dataset in order to consider these labels equal. In total, 88,079 non-COVID-19 images were used to train the model on these tasks. We will use the term pre-sigmoid which refers to the output of the last layer of the network multiplied by a weight vector corresponding to each task which would normally then be passed through a sigmoid function. Features will be used in the following constructions (as in Cohen et al. [2020a]):

- **Intermediate features** - the result of the convolutional layers and global averaging (1024 dim vector);
- **18 outputs** - each image was represented by the 18 outputs (pre-sigmoid) here: Atelectasis, Consolidation, Infiltration, Pneumothorax, Edema, Emphysema, Fibrosis, Effusion, Pneumonia, Pleural Thickening, Cardiomegaly, Nodule, Mass, Hernia, Lung Lesion, Fracture, Lung Opacity, Enlarged Cardiomeastinum;
- **4 outputs** - a hand picked subset of the above mentioned outputs (pre-sigmoid) were used containing radiological findings more frequent in pneumonia: Lung Opacity, Pneumonia, Infiltration, and Consolidation;
- **Lung Opacity output** - the single output (pre-sigmoid) for lung opacity was used because it was very related to this task. This feature was different from the opacity score that we would like to predict;
- **Image pixels** - the image itself as a vector of pixels ($224 \times 224 = 50176$).
- **Baseline prevalence** - to compare against a model which predicted based on the prevalence of the labels only.

Model training is done using linear or logistic regression with default parameters from Sci-kit learn [Pedregosa et al., 2011]. An L2 penalty was used with an LBFGS solver. In the case of “image pixels” an MLP is used with 100 hidden units and ReLU activations Glorot et al. [2011]. It is trained with full batch gradient descent using an Adam optimizer Kingma and Ba [2014] (with $\beta_1 = 0.9$, $\beta_2 = 0.999$, $\epsilon = 1e^{-8}$, a learning rate of 0.001, and 10% of the data used for early stopping).

5. Task Ideas with Baseline Evaluations

We present multiple clinical use cases and potential tools which could be built using this dataset and present a baseline task which is evaluated. We describe the scenarios in detail to both convey what our group has learned while interacting with clinicians as well as solidify what the value is of such a model to avoid misguided efforts solving a problem that doesn’t exist. For the results presented in Tables 6 and 5 a full listing over all data splits is presented in Appendix §C.2.

Table 5: Classification tasks. Evaluation is performed using LOCO evaluation. The metrics here are the average over each hold out countries test set. AUROC is the area under the TPR-FRP (ROC) curve, and AUPRC is the area under the precision-recall curve. The scores are averages over the held out test countries.

Task	Test Regions	Features	# params	AUROC	AUPRC
COVID-19 0<offset<8 days True=128 False=27	Americas, Asia, Europe, Oceania	18 outputs	18+1	0.58±0.12	0.78±0.16
		Intermediate features	1024+1	0.57±0.12	0.77±0.15
		4 outputs	4+1	0.50±0.01	0.73±0.22
		Baseline prevalence	1+1	0.50±0.00	0.73±0.22
		lung opacity output	1+1	0.50±0.01	0.73±0.22
		Image pixels (MLP)	5017801	0.48±0.06	0.72±0.20
Viral or Bacterial 0<offset<8 days True=140 False=10	Europe, Oceania	18 outputs	18+1	0.82±0.26	0.97±0.04
		Intermediate features	1024+1	0.70±0.19	0.84±0.13
		lung opacity output	1+1	0.56±0.08	0.72±0.31
		4 outputs	4+1	0.52±0.03	0.71±0.30
		Baseline prevalence	1+1	0.50±0.00	0.71±0.30
		Image pixels (MLP)	5017801	0.50±0.01	0.71±0.23
Survival prediction 0<offset<8 days True=46 False=7	Americas, Asia, Europe	lung opacity output	1+1	0.55±0.08	0.86±0.05
		4 outputs	4+1	0.54±0.07	0.85±0.05
		Baseline prevalence	1+1	0.50±0.00	0.84±0.04
		Image pixels (MLP)	5017801	0.50±0.00	0.84±0.03
		Intermediate features	1024+1	0.50±0.00	0.84±0.04
		18 outputs	18+1	0.47±0.03	0.84±0.03
ICU stay 0<offset<8 days True=17 False=27	Asia, Europe	18 outputs	18+1	0.81±0.10	0.50±0.24
		Intermediate features	1024+1	0.71±0.18	0.40±0.21
		4 outputs	4+1	0.55±0.15	0.35±0.36
		Baseline prevalence	1+1	0.50±0.00	0.28±0.26
		lung opacity output	1+1	0.42±0.12	0.28±0.26
		Image pixels (MLP)	5017801	0.40±0.13	0.28±0.20
Intubated 0<offset<8 days True=12 False=23	Asia, Europe	Intermediate features	1024+1	0.61±0.06	0.40±0.21
		Baseline prevalence	1+1	0.50±0.00	0.32±0.21
		Image pixels (MLP)	5017801	0.50±0.07	0.32±0.17
		lung opacity output	1+1	0.50±0.00	0.32±0.21
		18 outputs	18+1	0.45±0.22	0.35±0.26
		4 outputs	4+1	0.45±0.00	0.31±0.20

5.1 Complement to COVID-19 Pneumonia Diagnosis and Management

Motivation: While reverse transcriptase polymerase chain reaction (RT-PCR) assay remains the gold standard for diagnosis, CXR plays a major role as the top initial imaging test for patients with suspected COVID-19 pneumonia [Dennie et al., 2020b]. Because of their relative lack of sensitivity (69%, although this was computed with a small sample size) [Wong et al., 2019] and the fact that they are often normal early in the disease [Dennie et al., 2020b; Wong et al., 2019], a negative CXR should not be used to rule out COVID-19 infection [Dennie et al., 2020b]. Instead, features of COVID-19 pneumonia in CXR, although nonspecific, raise the pretest probability of infection. For example, distinguishing between

viral and bacterial pneumonia could influence management in addition to other clinical clues [Heneghan et al., 2020]. According to the CSTR and CAR, a CXR is “most useful when an alternative diagnosis is found that completely explains the patient’s presenting symptoms such as, but not limited, to pneumothorax, pulmonary edema, large pleural effusions, lung mass or lung collapse [Dennie et al., 2020b].”

Task Specification: The hierarchy of labels (Table 1) allows us to perform multiple different classification tasks. A first task is to classify COVID-19 from other causal agents of pneumonia such as bacteria or other viruses. A second task is to distinguish viral from bacterial pneumonia.

Results: When classifying between COVID/non-COVID most recent works using this dataset have taken other datasets and treated them as non-COVID-19 [Wang and Wong, 2020; Apostolopoulos and Mpesiana, 2020] while results with balanced datasets from Tartaglione et al. [2020] report much lower performance. Our LOCO evaluation aims to avoid these issues and in Table 5 we find that the best performance is only slightly higher than random guessing which would yield a 0.5 AUROC. We specifically note that the “4 outputs” which are commonly associated with Pneumonia are not predictive, possibly implying something about the disease that should be explored more. We find that predicting between bacterial and viral yields reasonably good performance using intermediate features or the 18 specific outputs. This is not surprising as previous work has reported high accuracy when predicting bacterial and viral from pediatric CXR [Kermany et al., 2018].

5.2 Severity Prediction, Including Intensive Care Unit (ICU) Stay

Motivation: The ICU is reserved for patients who require life support such as mechanical ventilation. In this invasive intervention reserved for patients unable to breathe on their own, an endotracheal tube is inserted into the windpipe (intubation) and the lungs are mechanically inflated and deflated [Tobin and Manthous, 2017]. Predicting the need for mechanical ventilation in advance could help plan management or prepare the patient. Another challenge is knowing when to remove mechanical ventilation (extubation), which falls in a specific window of time [Thille et al., 2013].

Assessing the severity of a patient’s condition using a well adopted scoring system is a key aspect of patient management [Wong et al., 2019; Cohen et al., 2020a; Borghesi and Maroldi, 2020b; Signoroni et al., 2020]. A model which predicts the severity of COVID-19 pneumonia, and pneumonia in general, based on CXR could be used as an assistive tool when managing patient care for escalation or de-escalation of care, especially in the ICU.

Non-ML work by Allenbach et al. [2020] combines information from CT scans and CXR with other clinical information to create a score-based predictive model for transfer to the ICU.

This task is further motivated by papers published after a preprint of this work which employed siamese networks to represent severity [Li et al., 2020] as well as predicted deterioration risk scores and time estimates [Shamout et al., 2020].

It is important to note with this task that predicting these events could be confounded by the presence of an endotracheal tube in the CXR of a mechanically ventilated patient; when available, this is annotated in our dataset.

Table 6: Regression Tasks. Evaluation is performed using LOCO evaluation. The metrics here are the average over each held-out-continent test set. R^2 : coefficient of determination; MAE: mean absolute error. "4 outputs" refers to Lung Opacity, Pneumonia, Infiltration, and Consolidation.

Task	Test Regions	Features	# of parameters	Pearson Correlation	R^2	MAE
Geographic Extent Score (0-8) N=94	Asia, Europe	4 outputs	4+1	0.82±0.05	0.62±0.05	1.11±0.08
		18 outputs	18+1	0.80±0.09	0.59±0.17	1.15±0.15
		lung opacity output	1+1	0.80±0.05	0.58±0.02	1.15±0.01
		Intermediate features	1024+1	0.77±0.06	0.41±0.17	1.41±0.08
		Baseline prevalence	1+1	0.00±0.00	-0.33±0.25	2.14±0.31
Opacity Score (0-6) N=94	Asia, Europe	4 outputs	4+1	0.79±0.07	0.61±0.11	0.73±0.10
		lung opacity output	1+1	0.79±0.07	0.60±0.09	0.76±0.10
		18 outputs	18+1	0.66±0.13	0.29±0.26	0.90±0.16
		Intermediate features	1024+1	0.68±0.11	-0.09±0.45	1.20±0.26
		Baseline prevalence	1+1	0.00±0.00	-0.26±0.20	1.30±0.00

Due to the reduced mobility of ICU patients, CXR are often obtained with the patient lying down in a view referred to as "AP supine" [Khan et al., 2009], which includes but is not limited to patients who are intubated or soon to be. Because this position drastically modifies the appearance of the CXR, a naive approach could confound such changes with the need to be intubated.

Task Specification: The first thing that is required for this task is a well defined scoring system that defines patient severity. The mRALE (modified Radiographic Assessment of Lung Edema) score [Wong et al., 2019; Cohen et al., 2020a] was developed specifically with in context of assessing COVID-19 severity from CXR and was used to score 94 images in this dataset in Cohen et al. [2020a] by two chest radiologists and a radiology resident. Also, the Brixia score [Borghesi and Maroldi, 2020b; Signoroni et al., 2020] was used by another group to score 192 of these images by "two expert radiologists, a board-certified staff member and a trainee with 22 and 2 years of experience respectively" [Signoroni et al., 2020].

Our task and evaluation will use the severity scores created by Cohen et al. [2020a]. This work provides two scores: Geographic Extent (0-8), how much opacity covers the lungs, and Opacity (0-6), how opaque the lungs are.

Also, an ICU stay and the patient being intubated are both predicted given patients between 0 and 8 days from symptoms/presentation. Images marked as intubation present are excluded from the evaluation as this would be a visible confounder in the image. For ICU stay prediction images marked as already in the ICU are excluded.

Results: Table 6 shows performance similar to that reported by Cohen et al. [2020a]. The evaluation used in that work is not LOCO.

Table 5 shows ICU stay is predicted reasonably well at 0.81 AUROC using all 18 outputs. The improvement over the "4 outputs" which are associated with Pneumonia may imply that ICU stay is predictive by features not related to pneumonia. Intubation is predicted poorly.

5.3 Survival outcome

Motivation: Not too dissimilar to severity prediction, determining at what point survival can be predicted could be useful for patient management. Given a series of patient chest X-rays over time, it could be possible to determine the probability of survival.

Non-ML models are able to predict in-hospital mortality for patients with COVID-19 using an original severity score for CXR (Brixia score) combined with two predictive factors, which are patient age and immunosuppressive conditions [Borghesi et al., 2020a]. ML models are able to predict survival based on clinical features (lactate dehydrogenase, lymphocyte count, and high-sensitivity C-reactive protein) with high accuracy [Yan et al., 2020].

Task Specification: In order to make predictions which are relevant to the clinical context, it is important to control for the time period when the patient is observed. Our evaluation is on data between 0 and 8 days since symptoms or admission in order to simulate predicting at the beginning of management. Predictions will be made on non-intubated patients to avoid this confounder of severity.

Results: In Table 5, almost random performance of 0.55 AUROC is obtained using lung opacity and the 4 hand picked features of Pneumonia. In general, no method works well.

5.4 Trajectory Prediction

Motivation: The ability to gauge severity of COVID-19 lung infections could be used to complement other severity tools for escalation or de-escalation of care, especially in the ICU. Following diagnosis, patients' CXR could be scored periodically to objectively and quantitatively track pulmonary disease progression and treatment response. Eventually, physicians could track patients' response to various drugs and treatments using CXR and uploading the images to the dataset, allowing researchers to create predictive tools to measure recuperation. Such a model could also be used as an objective tool to compare response to different management algorithms and inspire better management strategies.

If the representation is expressive enough, patients can be plotted as shown in Figure 3a. A conceptual figure and our current realization are shown using a pre-trained CXR model showing the available trajectories and patient outcomes. This approach could serve as a way to iterate quickly with a medical team (to simply explore the learned representation instead of building complete tools) to make sense of the complexities of these models and patients.

Task Specification: Using this dataset, we could visualize a model's representation of CXRs and plot the trajectory of patients according to a color scheme representing their state/image (good or bad). The representation is based off of the 18 pre-sigmoid outputs of the DenseNet discussed. A good state is defined as non-intubated, not in the ICU, or the last state before discharge. A bad state is defined as intubated, in the ICU, or any state which is the last in the series and the patient is determined to have died. A kernel density estimation is taken of the 2d embeddings of all bad states to illustrate severity. Here PA, AP, and AP Supine images are used to maximize the data visualized as we did not observe any shift in the representation.

Results: Figure 3b shows proximity of image embeddings which represent patients in a good or bad state, demonstrating the potential insight already contained in these pre-trained

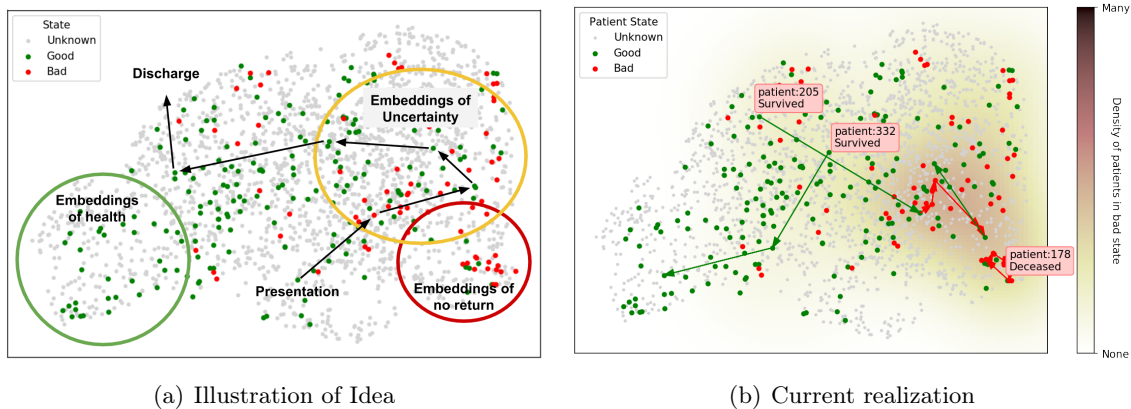


Figure 3: A UMAP [McInnes et al., 2018] visualization of each CXR from this dataset together with the Kaggle RSNA pneumonia images. CXRs with a trajectory are shown with an arrow between timepoints. If survival outcome is known the arrows and/or points are colored. The background is colored based on the density of points in the ICU or that are intubated.

models. The three patients display trajectories as we would imagine. Patient 178⁵ spirals in an area which appears bad. Patient 205⁶ progresses into bad states but manages to pull themselves out. Patient 332 [Sivakorn et al., 2020] seems to recover quickly to a region which is only populated by good states.

6. Future Task Ideas

There are many potential tasks that we were not able to explore in this work, primarily the use of saliency maps and the utility of out-of-distribution models.

Evaluating saliency maps can be challenging, but it is a useful evaluation for methods which aim to explain model predictions [Taghanaki et al., 2019; Singla et al., 2020]. Our dataset contains lung bounding boxes, which were contributed by Andrew Gough at General Blockchain Inc. for 167 images annotated for the left and right lung. Also, 209 generated lung segmentations were added to the dataset by Selvan et al. [2020]; the team trained a model on an external dataset and applied it to our dataset. As there are no “ground truth” segmentations, these can be used to examine if saliency maps are located reasonably within lung regions to detect overfitting. This can be seen by checking if the predictive regions of the image lie outside of the region of interest [Ross et al., 2017; Badgeley et al., 2019; Viviano et al., 2019].

General anomaly detection could be a useful model when trying to identify what is new about an illness such as COVID-19. Out-of-distribution (OoD) tools [Shafaei et al., 2018] or unpaired distribution matching models [Zhu et al., 2017; Kim et al., 2017] could capture the shift in distributions and present them as changes to images Cohen et al. [2018]. Identifying what about the COVID-19 distribution is different from other viral or bacterial pneumonias could aid in studying both the disease as well as the models representations for

5. <https://www.eurorad.org/case/16660>

6. <https://radiopaedia.org/cases/covid-19-pneumonia-progression-and-regression>

overfitting [Singla et al., 2020]. Transfer learning methods actively under development in the ML community such as few/zero-shot [Wang et al., 2019; Tian et al., 2020b; Larochelle et al., 2008; Ren et al., 2019], meta-learning [Andrychowicz et al., 2016; Snell et al., 2017], deep metric learning [Roth et al., 2020], and domain adaptation [Motiian et al., 2017] will likely be useful in this setting.

7. Conclusion

This paper presents a dataset of COVID-19 images together with clinical metadata which can be used for a variety of tasks. This dataset puts existing ML algorithms to the test. Given the number of existing large CXR datasets, novel tasks related to COVID-19 present a relevant challenge to overcome. We note that a major limitation of this work is the selection bias when gathering publicly available images which are likely made public for educational reasons because they are clear examples or interesting cases. Therefore, they do not represent the real world distribution of cases. Furthermore, another selection bias is that the information given on public platforms such as Figure 1 or Radiopaedia might not be complete for all patients and/or omit normal values (e.g., presence or absence of transfer to the ICU, lymphocyte count). Lastly, we do not yet have variables such as ethnic background, pre-existing conditions, and immunosuppression status. Any clinical claims made from models must therefore be backed by rigorous evaluation and take into account these limitations. Nevertheless, we believe that this dataset and the discussion of clinical context will contribute towards the machine learning community developing solutions with potential use in healthcare.

Broader Impact

This project aims to make a dataset of patients with a novel life-threatening disease accessible to researchers so that tools can be created to aid in the care of future patients. The manner in which we collect existing public data ensures that patients are not put at risk.

Data impact: Image data linked with clinically relevant attributes in a public dataset that is designed for ML will enable parallel development of diagnosis and management tools and rapid local validation of models. Furthermore, this data can be used for a variety of different tasks.

Tool impact: Tools developed using this data and with the ideas presented can give physicians an edge and allow them to act with more confidence while they wait for the analysis of a radiologist by having a digital second opinion confirm their assessment of a patient’s condition. In addition, these tools can provide quantitative scores which can enable large scale analysis of CXR without the need for costly/time consuming manual annotations.

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Ethical Standards

The work follows appropriate ethical standards in conducting research and writing the manuscript, following all applicable laws and regulations regarding treatment of animals or human subjects. This project is approved by the University of Montreal's Ethics Committee #CERSES-20-058-D

Conflicts of Interest

We declare we don't have conflicts of interest.

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Appendix

Appendix A. Extra dataset statistics

Just considering PA, AP, and AP Supine views there are 367 JPEG files and 171 PNGs. All images are 8-bit except for 1 which is 16-bit.

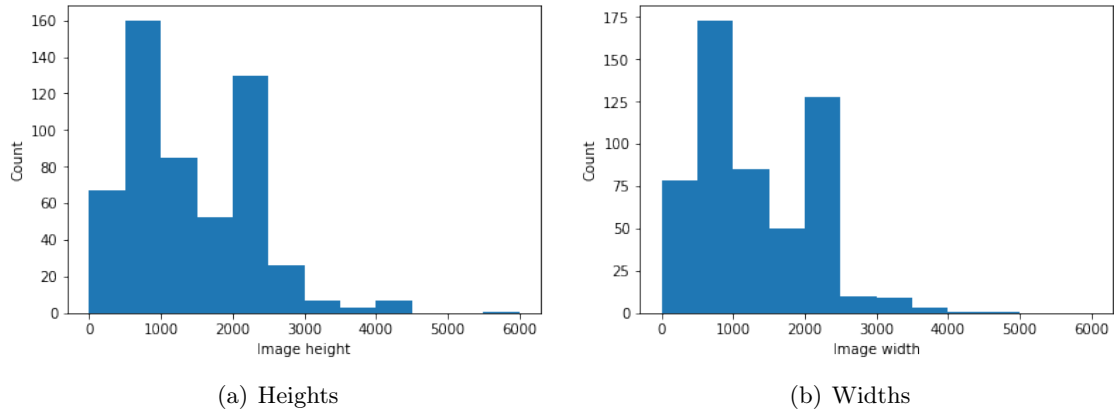


Figure 4: Histograms of image sizes in pixels.

Appendix B. Example images

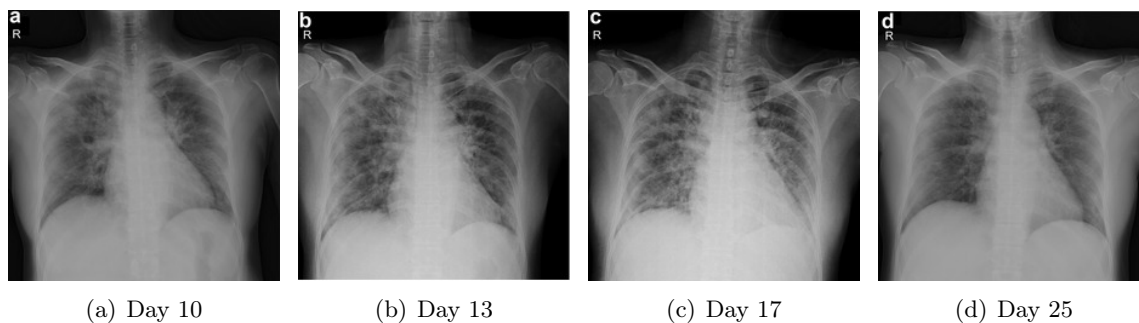


Figure 5: Example images from the same patient (#19) extracted from Cheng et al. [2020]. This 55 year old female survived a COVID-19 infection.

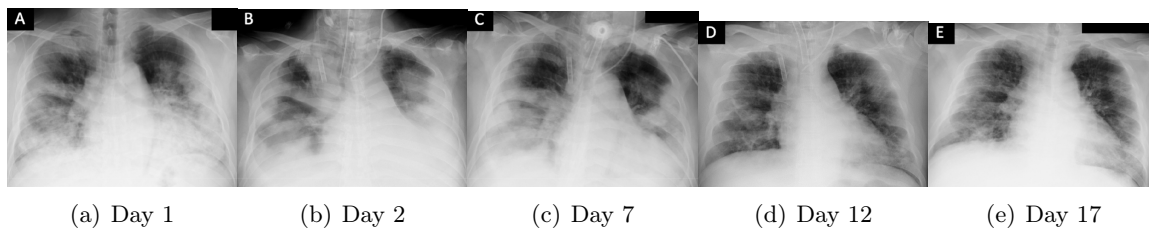


Figure 6: Example images from the same patient (#318) extracted from Nakamura et al. [2020]. This patient was intubated in the ICU for days 2, 7 and 12.

Appendix C. Scraper details

Each scraper identifies relevant radiographs using the "search" feature of the site being scraped, and saves the images together with a csv file of the corresponding metadata. Internally, the scraper uses Selenium to visit each page of the search results, saving metadata and images from any new cases. Images are downloaded at the highest resolution available. Data from each case is converted to a single, interoperable JSON format. Finally, the needed metadata is exported as a csv file.

Currently, the scrapers only retrieve metadata from structured fields that can be easily detected on webpages, such as "Age", "Sex", "Imaging Notes", and "Clinical Notes." Other clinically important information (such as whether the patient went to the ICU or was intubated) is extracted by human annotators.

Care has been taken to use these websites' resources conservatively and avoid creating a burden on their servers. Crawling is done in a lazy manner, so that no pages are requested until they can be used. Also, within each scraping session, each web page is kept open in an individual browser instance as long as it is needed to reduce re-requested resources .

C.1 Papers where images and clinical data are sourced

Table 7: Papers and counts on specific views

Citation	PA/AP	AP Supine	L
Winther et al. [2020a]	48	44	0
Paul et al. [2004]	11	0	0
Wong et al. [2019]	9	0	0
Wong et al. [2003]	5	0	0
Cheng et al. [2020]	4	0	0
Hsieh et al. [2020]	4	0	0
Woznitza et al. [2020]	4	0	0
Holshue et al. [2020]	4	0	3
Phan et al. [2020]	4	0	0
Ng et al. [2020]	4	0	0
Coimbra et al. [2020]	3	0	0
Song et al. [2020b]	3	0	0
Hiramatsu et al. [2020]	3	0	0
Ong et al. [2020]	3	0	0
Azekawa et al. [2020]	3	0	0
Sánchez-Oro et al. [2020]	3	0	0
Wu et al. [2020]	3	0	0
Qian et al. [2020]	3	0	0
Lim et al. [2020]	3	0	0
Yoon et al. [2020]	3	0	0
Sivakorn et al. [2020]	3	0	0
Borghesi and Maroldi [2020a]	2	3	0
jin Zhang et al. [2020]	2	3	0
Rodriguez et al. [2020]	2	1	0
Chen et al. [2020]	2	0	0
Cuong et al. [2020]	2	0	0
SINGH et al. [2020]	2	0	0
Hare et al. [2020]	2	0	0
Huang et al. [2020]	2	0	0
Lee et al. [2020]	2	0	0
Banerjee et al. [2020]	2	0	0
Vollono et al. [2020]	2	0	0
Tian et al. [2020a]	2	0	0
Thevarajan et al. [2020]	2	0	0
Liu et al. [2020a]	2	0	0
Cai et al. [2020]	2	0	0
Ahmed et al. [2020]	2	0	0
Fichera et al. [2020]	1	7	0
Ebrille et al. [2020]	1	3	0
Xu et al. [2020]	1	2	0
Dastan et al. [2020]	1	2	0
Monfardini et al. [2020]	1	1	0
Borghesi et al. [2020b]	1	1	0
Mastaglio et al. [2020]	1	1	0
Silverstein et al. [2020]	1	0	0
Aigner et al. [2020]	1	0	0
Wong et al. [2020]	1	0	0
Tay and Harwood [2020]	1	0	0
Liu et al. [2020b]	1	0	0
Wanshu Zhang and Heshui Shi [2020]	1	0	0
WANG et al. [2020]	1	0	0
Vu and Vu [2020]	1	0	0
Shi et al. [2020]	1	0	0
Song et al. [2020a]	1	0	0
Zu et al. [2020]	1	0	0
Kong and Agarwal [2020]	1	0	0
Millán-Oñate et al. [2020]	1	0	0
Jin et al. [2020]	1	0	0

Citation	PA/AP	AP Supine	L
Wei et al. [2020]	1	0	0
Allen et al. [2010]	1	0	0
An et al. [2020]	1	0	0
Yu et al. [2020]	1	0	0
Mukherjee et al. [2020]	1	0	0
Nakamura et al. [2020]	0	5	0
Zhu et al. [2020]	0	2	0
Bhatraju et al. [2020]	0	2	0
Siddamreddy et al. [2020]	0	2	0
Zanin et al. [2020]	0	1	0
Prince and Sergel [2020]	0	1	0
Fidan [2020]	0	1	0
Avula et al. [2020]	0	1	0
Radbel et al. [2020]	0	1	0
Tonelli et al. [2020]	0	1	0
Salehi et al. [2020]	0	1	0
Salehi et al. [2020]	0	1	0
Filatov et al. [2020]	0	1	0

C.2 Output of models on each split

Table 8: Geographic Extent

# params	# test samples	Correlation	MAE	R ²	method	name	test_region
1024+1	36.0	0.73	1.46	0.30	linear	Intermediate features	Asia
1024+1	41.0	0.82	1.35	0.53	linear	Intermediate features	Europe
1+1	36.0	0.00	1.92	-0.15	linear	Baseline prevalence	Asia
1+1	41.0	0.00	2.36	-0.51	linear	Baseline prevalence	Europe
18+1	36.0	0.73	1.25	0.47	linear	18 outputs	Asia
18+1	41.0	0.86	1.04	0.71	linear	18 outputs	Europe
4+1	36.0	0.78	1.17	0.58	linear	4 outputs	Asia
4+1	41.0	0.86	1.06	0.66	linear	4 outputs	Europe
1+1	36.0	0.77	1.15	0.57	linear	lung opacity output	Asia
1+1	41.0	0.83	1.16	0.60	linear	lung opacity output	Europe

Table 9: Opacity

# params	# test samples	Correlation	MAE	R ²	method	name	test_region
1024+1	36.0	0.60	1.39	-0.41	linear	Intermediate features	Asia
1024+1	41.0	0.76	1.02	0.22	linear	Intermediate features	Europe
1+1	36.0	0.00	1.30	-0.12	linear	Baseline prevalence	Asia
1+1	41.0	0.00	1.30	-0.40	linear	Baseline prevalence	Europe
18+1	36.0	0.57	1.02	0.11	linear	18 outputs	Asia
18+1	41.0	0.76	0.79	0.48	linear	18 outputs	Europe
4+1	36.0	0.75	0.80	0.54	linear	4 outputs	Asia
4+1	41.0	0.84	0.66	0.69	linear	4 outputs	Europe
1+1	36.0	0.74	0.83	0.53	linear	lung opacity output	Asia
1+1	41.0	0.84	0.69	0.67	linear	lung opacity output	Europe

Table 10: COVID-19

# params	# test samples	AUPRC	AUROC	method	name	test_region
1024+1	{True: 39, False: 2}	0.95	0.50	logistic	Intermediate features	Asia
1024+1	{False: 3, True: 7}	0.70	0.50	logistic	Intermediate features	Americas
1024+1	{False: 4, True: 3}	0.60	0.75	logistic	Intermediate features	Oceania
1024+1	{True: 68, False: 14}	0.84	0.55	logistic	Intermediate features	Europe
1+1	{True: 39, False: 2}	0.95	0.50	logistic	Baseline prevalence	Asia
1+1	{False: 3, True: 7}	0.70	0.50	logistic	Baseline prevalence	Americas
1+1	{False: 4, True: 3}	0.43	0.50	logistic	Baseline prevalence	Oceania
1+1	{True: 68, False: 14}	0.83	0.50	logistic	Baseline prevalence	Europe
18+1	{True: 39, False: 2}	0.95	0.49	logistic	18 outputs	Asia
18+1	{False: 3, True: 7}	0.70	0.50	logistic	18 outputs	Americas
18+1	{False: 4, True: 3}	0.60	0.75	logistic	18 outputs	Oceania
18+1	{True: 68, False: 14}	0.86	0.59	logistic	18 outputs	Europe
4+1	{True: 39, False: 2}	0.95	0.50	logistic	4 outputs	Asia
4+1	{False: 3, True: 7}	0.70	0.50	logistic	4 outputs	Americas
4+1	{False: 4, True: 3}	0.43	0.50	logistic	4 outputs	Oceania
4+1	{True: 68, False: 14}	0.83	0.52	logistic	4 outputs	Europe
1+1	{True: 39, False: 2}	0.95	0.50	logistic	lung opacity output	Asia
1+1	{False: 3, True: 7}	0.70	0.50	logistic	lung opacity output	Americas
1+1	{False: 4, True: 3}	0.43	0.50	logistic	lung opacity output	Oceania
1+1	{True: 68, False: 14}	0.83	0.51	logistic	lung opacity output	Europe
5017801	{True: 39, False: 2}	0.94	0.42	MLP	Image pixels (MLP)	Asia
5017801	{True: 39, False: 2}	0.95	0.50	MLP	Image pixels (MLP)	Asia
5017801	{True: 39, False: 2}	0.95	0.50	MLP	Image pixels (MLP)	Asia
5017801	{False: 3, True: 7}	0.67	0.43	MLP	Image pixels (MLP)	Americas
5017801	{False: 3, True: 7}	0.65	0.36	MLP	Image pixels (MLP)	Americas
5017801	{False: 3, True: 7}	0.70	0.50	MLP	Image pixels (MLP)	Americas
5017801	{False: 4, True: 3}	0.43	0.50	MLP	Image pixels (MLP)	Oceania
5017801	{False: 4, True: 3}	0.43	0.50	MLP	Image pixels (MLP)	Oceania
5017801	{False: 4, True: 3}	0.43	0.50	MLP	Image pixels (MLP)	Oceania
5017801	{True: 68, False: 14}	0.83	0.49	MLP	Image pixels (MLP)	Europe
5017801	{True: 68, False: 14}	0.86	0.60	MLP	Image pixels (MLP)	Europe
5017801	{True: 68, False: 14}	0.83	0.49	MLP	Image pixels (MLP)	Europe

Table 11: Viral or Bacterial

# params	# test samples	AUPRC	AUROC	method	Features	test_region
1024+1	{False: 3, True: 3}	0.75	0.83	logistic	Intermediate features	Oceania
1024+1	{True: 72, False: 6}	0.93	0.57	logistic	Intermediate features	Europe
1+1	{False: 3, True: 3}	0.50	0.50	logistic	Baseline prevalence	Oceania
1+1	{True: 72, False: 6}	0.92	0.50	logistic	Baseline prevalence	Europe
18+1	{False: 3, True: 3}	1.00	1.00	logistic	18 outputs	Oceania
18+1	{True: 72, False: 6}	0.94	0.64	logistic	18 outputs	Europe
4+1	{False: 3, True: 3}	0.50	0.50	logistic	4 outputs	Oceania
4+1	{True: 72, False: 6}	0.93	0.54	logistic	4 outputs	Europe
1+1	{False: 3, True: 3}	0.50	0.50	logistic	lung opacity output	Oceania
1+1	{True: 72, False: 6}	0.94	0.61	logistic	lung opacity output	Europe
5017801	{False: 3, True: 3}	0.50	0.50	MLP	Image pixels (MLP)	Oceania
5017801	{False: 3, True: 3}	0.50	0.50	MLP	Image pixels (MLP)	Oceania
5017801	{False: 3, True: 3}	0.50	0.50	MLP	Image pixels (MLP)	Oceania
5017801	{True: 72, False: 6}	0.92	0.50	MLP	Image pixels (MLP)	Europe
5017801	{True: 72, False: 6}	0.92	0.50	MLP	Image pixels (MLP)	Europe
5017801	{True: 72, False: 6}	0.92	0.48	MLP	Image pixels (MLP)	Europe

Table 12: Survival prediction

# params	# test samples	AUPRC	AUROC	method	Features	test_region
1024+1	{True: 20, False: 3}	0.87	0.50	logistic	Intermediate features	Asia
1024+1	{False: 1, True: 4}	0.80	0.50	logistic	Intermediate features	Americas
1024+1	{True: 19, False: 3}	0.86	0.50	logistic	Intermediate features	Europe
1+1	{True: 20, False: 3}	0.87	0.50	logistic	Baseline prevalence	Asia
1+1	{False: 1, True: 4}	0.80	0.50	logistic	Baseline prevalence	Americas
1+1	{True: 19, False: 3}	0.86	0.50	logistic	Baseline prevalence	Europe
18+1	{True: 20, False: 3}	0.86	0.45	logistic	18 outputs	Asia
18+1	{False: 1, True: 4}	0.80	0.50	logistic	18 outputs	Americas
18+1	{True: 19, False: 3}	0.85	0.45	logistic	18 outputs	Europe
4+1	{True: 20, False: 3}	0.87	0.50	logistic	4 outputs	Asia
4+1	{False: 1, True: 4}	0.80	0.50	logistic	4 outputs	Americas
4+1	{True: 19, False: 3}	0.89	0.61	logistic	4 outputs	Europe
1+1	{True: 20, False: 3}	0.87	0.50	logistic	lung opacity output	Asia
1+1	{False: 1, True: 4}	0.80	0.50	logistic	lung opacity output	Americas
1+1	{True: 19, False: 3}	0.90	0.64	logistic	lung opacity output	Europe
5017801	{True: 20, False: 3}	0.87	0.50	MLP	Image pixels (MLP)	Asia
5017801	{True: 20, False: 3}	0.87	0.50	MLP	Image pixels (MLP)	Asia
5017801	{True: 20, False: 3}	0.87	0.50	MLP	Image pixels (MLP)	Asia
5017801	{False: 1, True: 4}	0.80	0.50	MLP	Image pixels (MLP)	Americas
5017801	{False: 1, True: 4}	0.80	0.50	MLP	Image pixels (MLP)	Americas
5017801	{False: 1, True: 4}	0.80	0.50	MLP	Image pixels (MLP)	Americas
5017801	{True: 19, False: 3}	0.86	0.50	MLP	Image pixels (MLP)	Europe
5017801	{True: 19, False: 3}	0.86	0.50	MLP	Image pixels (MLP)	Europe
5017801	{True: 19, False: 3}	0.86	0.50	MLP	Image pixels (MLP)	Europe

Table 13: ICU Stay

# params	# test samples	AUPRC	AUROC	method	Features	test_region
1024+1	{False: 9, True: 1}	0.25	0.83	logistic	Intermediate features	Asia
1024+1	{False: 15, True: 13}	0.55	0.58	logistic	Intermediate features	Europe
1+1	{False: 9, True: 1}	0.10	0.50	logistic	Baseline prevalence	Asia
1+1	{False: 15, True: 13}	0.46	0.50	logistic	Baseline prevalence	Europe
18+1	{False: 9, True: 1}	0.33	0.89	logistic	18 outputs	Asia
18+1	{False: 15, True: 13}	0.67	0.74	logistic	18 outputs	Europe
4+1	{False: 9, True: 1}	0.10	0.44	logistic	4 outputs	Asia
4+1	{False: 15, True: 13}	0.61	0.66	logistic	4 outputs	Europe
1+1	{False: 9, True: 1}	0.10	0.33	logistic	lung opacity output	Asia
1+1	{False: 15, True: 13}	0.46	0.50	logistic	lung opacity output	Europe
5017801	{False: 9, True: 1}	0.11	0.56	MLP	Image pixels (MLP)	Asia
5017801	{False: 9, True: 1}	0.10	0.50	MLP	Image pixels (MLP)	Asia
5017801	{False: 9, True: 1}	0.10	0.50	MLP	Image pixels (MLP)	Asia
5017801	{False: 15, True: 13}	0.46	0.30	MLP	Image pixels (MLP)	Europe
5017801	{False: 15, True: 13}	0.46	0.27	MLP	Image pixels (MLP)	Europe
5017801	{False: 15, True: 13}	0.46	0.27	MLP	Image pixels (MLP)	Europe

Table 14: Intubated

# params	# test samples	AUPRC	AUROC	method	Features	test_region
1024+1	{False: 10, True: 2}	0.25	0.65	logistic	Intermediate features	Asia
1024+1	{False: 8, True: 7}	0.54	0.57	logistic	Intermediate features	Europe
1+1	{False: 10, True: 2}	0.17	0.50	logistic	Baseline prevalence	Asia
1+1	{False: 8, True: 7}	0.47	0.50	logistic	Baseline prevalence	Europe
18+1	{False: 10, True: 2}	0.17	0.30	logistic	18 outputs	Asia
18+1	{False: 8, True: 7}	0.53	0.61	logistic	18 outputs	Europe
4+1	{False: 10, True: 2}	0.17	0.45	logistic	4 outputs	Asia
4+1	{False: 8, True: 7}	0.45	0.45	logistic	4 outputs	Europe
1+1	{False: 10, True: 2}	0.17	0.50	logistic	lung opacity output	Asia
1+1	{False: 8, True: 7}	0.47	0.50	logistic	lung opacity output	Europe
5017801	{False: 10, True: 2}	0.17	0.50	MLP	Image pixels (MLP)	Asia
5017801	{False: 10, True: 2}	0.17	0.50	MLP	Image pixels (MLP)	Asia
5017801	{False: 10, True: 2}	0.18	0.55	MLP	Image pixels (MLP)	Asia
5017801	{False: 8, True: 7}	0.50	0.56	MLP	Image pixels (MLP)	Europe
5017801	{False: 8, True: 7}	0.47	0.38	MLP	Image pixels (MLP)	Europe
5017801	{False: 8, True: 7}	0.47	0.50	MLP	Image pixels (MLP)	Europe



Figure 7: A montage of all frontal view (PA, AP, AP Supine) images.