Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

CHAPTER 5

COVID-19: prediction, screening, and decision-making

5.1 Background

The novel coronavirus (nCoV) outbreak, which was identified in the late 2019s, requires special attention because of its future epidemics and possible global threats. Beside clinical procedures and treatments, since artificial intelligence (AI) promises a new paradigm for healthcare, several different AI tools that are built upon machine learning (ML) algorithms are employed for analyzing data and decision-making processes. This means that AI-driven tools help identify COVID-19 outbreaks and forecast their nature of spread across the globe.

In 2003 the novel coronavirus was identified in patients with SARS, and it is not a surprising event in 2020. Beside clinical procedures and treatments, artificial intelligence (AI) has significantly contributed. Several different AI tools are employed to analyzing data and decision-making processes. Their models are varied based on their data types [1–7] Often, machine learning requires a clean set of annotated data, so classifiers can be well trained (supervised learning). Even though we have a rich state-of-the-art literature, we failed to reach the point:

> *"To model an accurate classifier, how big the size of training samples should be?"*

Deep learning (DL), as an example, requires a large amount of data to be trained. Do we still wait for collecting fairly large amount of data? If so, then how big data is big? The primary idea behind the use of DL is not only to avoid feature engineering but also to extract distinct features (e.g., pixel-level nodule in image data) [8].

In what follows, we discuss on predictive modeling and imaging tools for COVID-19. We consider a broad view of predictions (and possible pitfalls) and medical imaging tools in accordance with the dataset size.

5.2 Predictive modeling and infectious disease outbreaks

The primary idea of the predictions is to make states and citizens aware of possible threats/consequences. However, for COVID-19 outbreak, state-of-the-art prediction models are failed

Deep Learning Models for Medical Imaging
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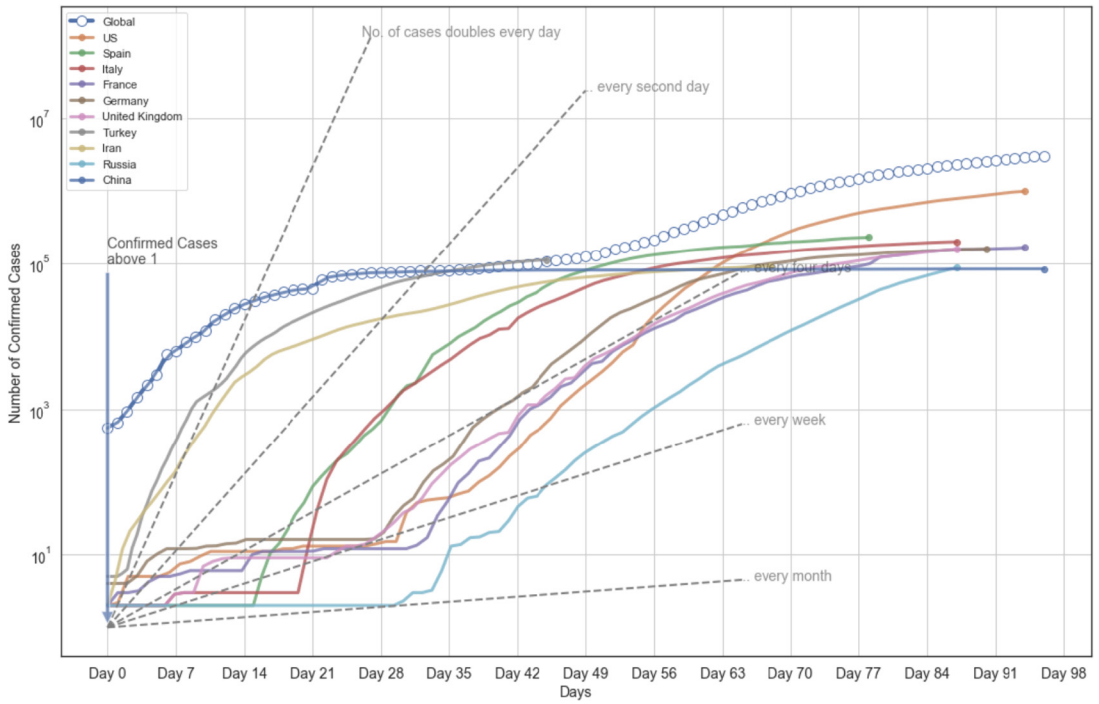

Figure 5.1: Global trend of COVID-19 confirmed cases during the first 98 days. (For interpretation of the colors in the figure(s), the reader is referred to the web version of this chapter.)

to exploit crucial and unprecedented uncertainties/factors, such as hospital settings and test rate, changes in demography, population density (including immunocompromised people), and poverty. With a high rise in deaths caused due to nCoV, immunocompromised persons (e.g., lung cancer) are at high risk. No prediction models consider immunocompromised population in terms of death cases (including recovery). Predictions can be short-term and long-term, and they rely on the aforementioned factors [4,10]. Such continuous and unprecedented factors lead us to designing complex models, rather than just relying on stochastic and/or discrete ones that are driven by randomly generated parameters. In the literature, prediction models are limited to data visualization, and they are hardly extended to simulating the data, so trends can be visualized.

To amplify/visualize COVID-19 outbreak, it requires data visualization tools. Data visualization can help estimate the trend. Figs. 5.1 and 5.2 are two examples. In Fig. 5.1, we provide an example of how we can show the COVID-19 trend for confirmed cases. Similarly, the trend of global death cases is shown in Fig. 5.2. Not to be confused, a visualization tool cannot be considered as the prediction model. Unfortunately, as mentioned earlier, in the literature, most

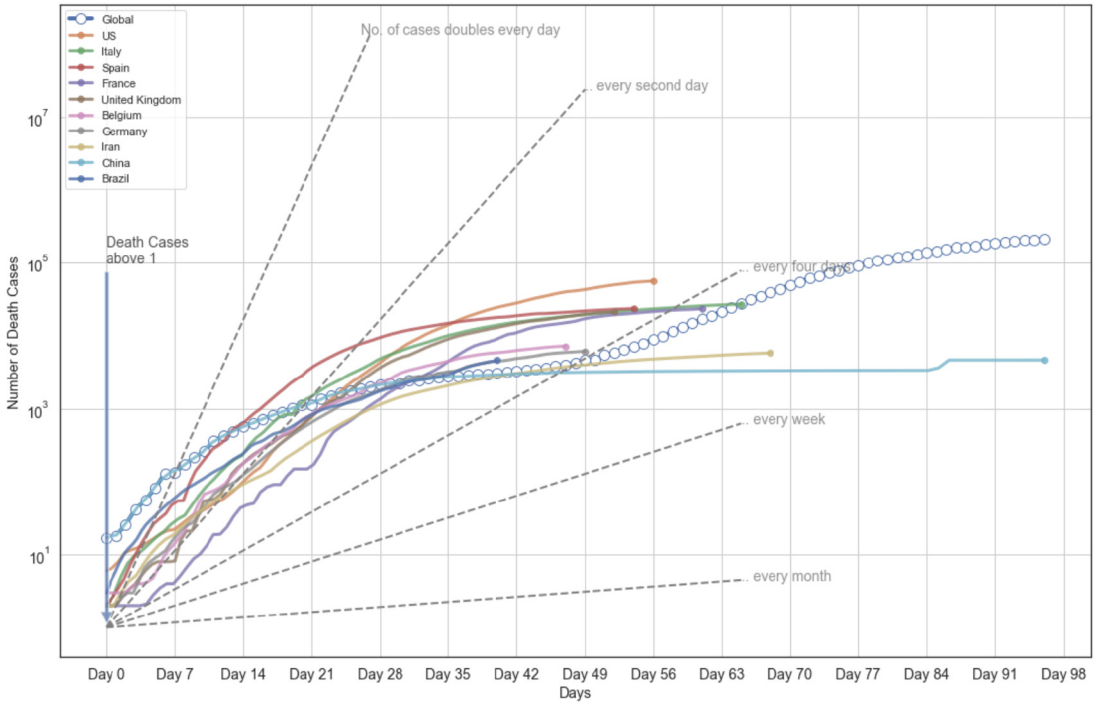

Figure 5.2: Global trend of COVID-19 death cases during the first 98 days.

of the prediction models are limited to data visualization. As an example, data simulations always help better understand the particular event(s). However, it must be limited to education/training. In simple words, simulations help us build up our intuition about how diseases work in a way that words and even static charts cannot. For visualization, distribution can be of great help (see Fig. 5.3).

Predictive analytical results hit media a lot even though tools are limited to education and training. Note that, more often, due to unprecedented nature of the situation and many uncertainties related to diseases, inaccurate information was predicted. As an example, on March 31, 2020, the White House projected 100 K to 240 K Coronavirus deaths in the next two weeks.[1] Later, on April 8, 2020, we had another media statement[2] "not every model agrees: America's most influential coronavirus model just revised its estimates downward" as previous prediction was too far from actual values (84,575 death cases in the U.S., dated May 14,

1 Fox News (Andrew O'Reilly, March 31, 2020) URL: https://www.foxnews.com/politics/trump-tells-americans-to-prepare-for-a-very-painful-two-weeks-as-white-house-releases-extended-coronavirus-guidelines.

2 The Washington Post (William Wan and Carolyn Y. Johnson, April 08, 2020) URL: https://www.washingtonpost.com/health/2020/04/06/americas-most-influential-coronavirus-model-just-revised-its-estimates-downward-not-every-model-agrees/.

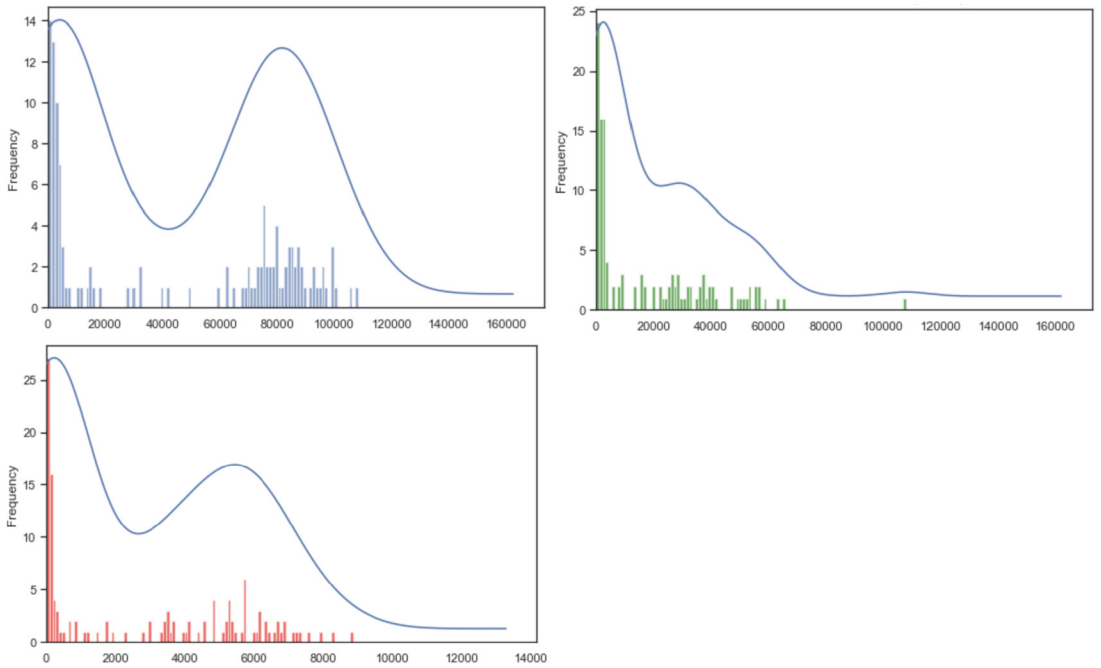

Figure 5.3: Using the first 115 days data (global): Confirmed cases (left top); Recovered cases (right top); and Death cases (left bottom).

2020). Media did not intentionally broadcast/announce inaccurate information; instead, the estimated values were based on prediction models. Not to be confused, authors are not aimed at blaming neither media nor prediction models.

Artificial and augmented intelligence (A2I) play crucial roles in understanding data by using multiple different tools/techniques. They include data analytics, machine learning, and pattern recognition, where anomaly detection is a primary element [1,9]. Predictive modeling requires exploiting comprehensive data. Missing one or two features/factors can deviate predictive values from actual ones. More often, discrete models rely on their input parameters and are application dependent. In case of continuous data (e.g., COVID-19), where there exist unavoidable uncertainties, these models behave differently. As a result, these models provide incoherent results. The primary reason behind this is lack of understanding about the particular events, that is, data sentiments and additional unavoidable uncertainties/factors, such as hospital settings/capacity, number of tests on a daily basis, demographics, and population (density) and their vulnerability in that particular region. In particular, we observed that the higher the population density, the higher the spread rate, and New York City is an example. This brings an idea that the same exact models with exact input parameters cannot be repli-

cated to other regions. Also, immunocompromised (plus old) people need to be considered in their models; Italy is an example.

In the literature, we found three different model types for COVID-19 predictions: a) SEIR/SIR models, b) agent-based models, and c) curve-fitting models [10]. Categorically, inspired by [10], let us briefly discuss them.

1) *SEIR/SIR models:*
   Medical Research Council (MRC) Centre for Global Infectious Disease Analysis used a nonpharmaceutical intervention (NPI) model, which employed SEIR approach. In a similar fashion, Columbia University used SEIR model and forecasted number of severe cases, hospitalizations, critical care, ICU use, and deaths under different social distancing scenarios for 3-week and 6-week periods starting from April 2, 2020.[3] University of Pennsylvania used CHIME, COVID-19 Hospital Impact Model, and predicted for the next three months.[4]
2) *Agent-based models:*
   A group of research centers and universities, Fogarty International Center, Fred Hutchison Cancer Center, Northeastern University, University of Florida, and more employed the agent-based COVID-19 prediction model.[5] They forecasted based on two different scenarios: a) no mitigation and b) stay-at-home. Compared to actual data, their range can be considered even though the range is really wide.
3) *Curve-fitting models:*
   Curve-fitting model can be described by considering Fig. 5.4, where polynomial regression models are studied. As COVID-19 predictions are complex by nature, linear regression (described by the linear model $\hat{y} = w_1 x + w_o$) does not fit, and therefore no estimation is possible. In such a case, considering higher-order models would be a better fit, and that would bring an idea of higher-order polynomial regression ($\hat{y} = w_k x^k + \cdots + w_2 x^2 + w_1 x^1 + w_o$). In the figure, we address a better fit by tuning a parameter k by taking an error rate for each degree of freedom (DoF) into account. In other words, we fix the value of k when we find the best fit. In Fig. 5.4, $k = 6$ is the best fit for this data, and we conclude the regression model. Let us summarize the data:

[3] Mapping tool: https://cuepi.shinyapps.io/COVID-19/. Columbia University (June 23, 2020, last accessed).
[4] CHIME v1.1.5 (2020-04-08): https://penn-chime.phl.io.COVID-19 Hospital Impact Model for Epidemics (CHIME). University of Pennsylvania (April 2020).
[5] COVID-19 Model: https://covid19.gleamproject.org/#model. Northeastern University, Fogarty International Center, Fred Hutchison Cancer Center, and University of Florida (May 15, 2020, last accessed).

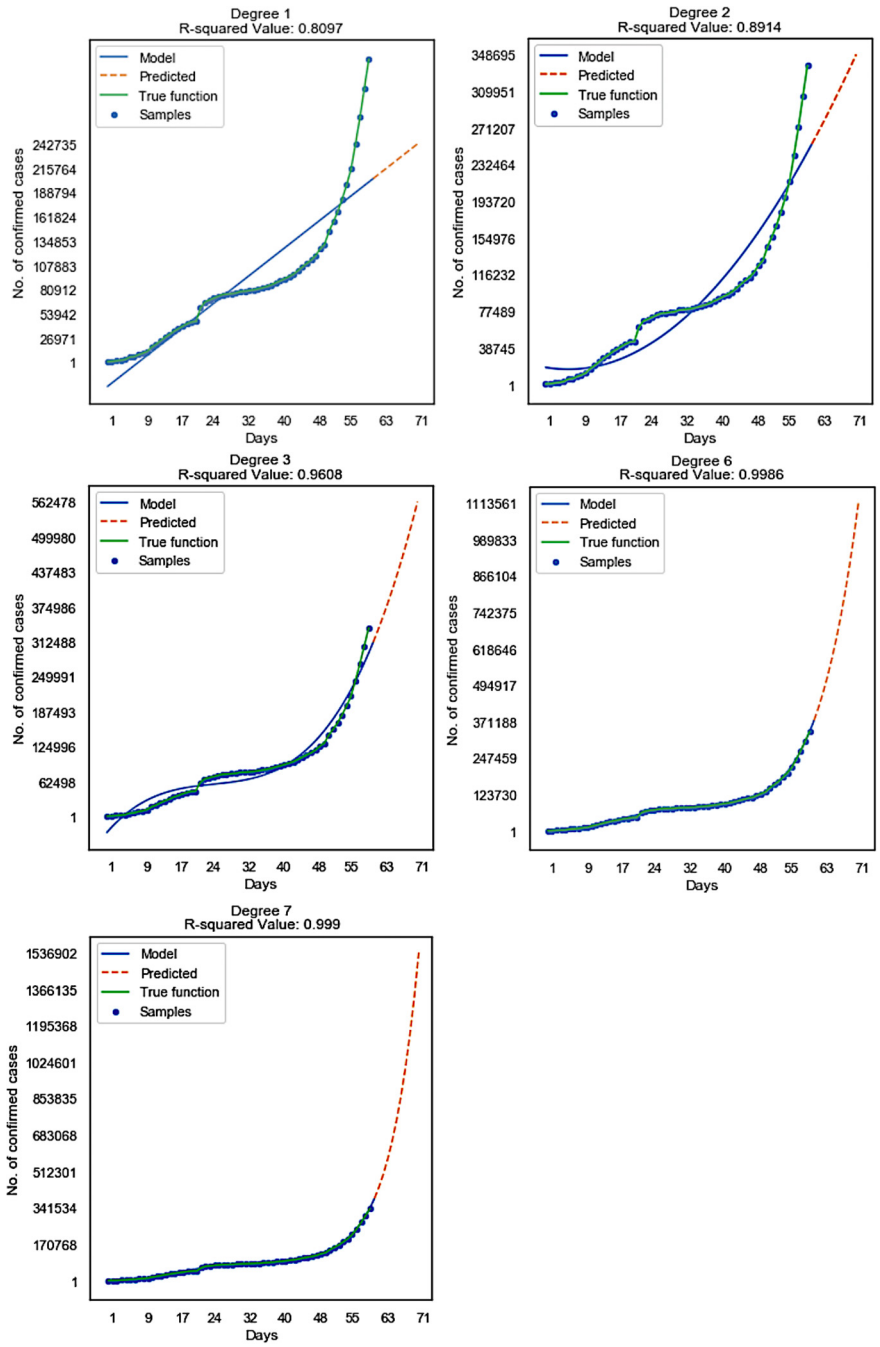

Figure 5.4: Curve fitting model using global data (the first 71 days data): polynomial regression model (predictions with different orders).

Error for each DoF (%): [32.94, 36.35, 23.08, 4.76, 4.6, 5.94, 4.27, 4.73]
DoF (selection): 6
Weights: $[4.452^{-5}, -5.31^{-3}, 3.79^{-1}, -1.91^{1}, 4.89^{2}, -1.92^{3}, 2.83^{3}]$
Model:
$\hat{y} : 4.452^{-5}x^6 - 5.31^{-3}x^5 + 3.79^{-1}x^4 - 1.91^{1}x^3 + 4.89^{2}x^2 - 1.92^{3}x^1 + 2.83^{3}$

On the whole, curve-fitting model is brittle. It does not predict the long-term behavior. In Fig. 5.4, we predict possible confirmed cases for the next five days.
Los Alamos National Laboratory (LANL) and the Institute for Health Metrics and Evaluation (IHME) employed a curve-fitting technique.[6,7] LANL's best guess was for California state as of April 08, 2020, 4,082 deaths (compared to 2,974 actual deaths, dated May 14, 2020). IHME's predictions varied over time.

In the literature, models are transparent enough in terms of how they were built. However, their predictions were far from actual values. Not to be confused, as input parameters vary, their models forecasted different results. Besides, no models integrate factors, such as social distancing and/or 100% lockdown. Other than aforementioned three different models, the authors used machine learning and/or deep learning models that are built on statistics and probabilities.

In machine learning, we call such models "garbage-in garbage-out",[8,9] as they predict values far from what they are. Stochastic models require fairly large amount of data to tune/stabilize their randomly generated parameters. Unlike the data-independent or discrete model, we are now required to employ mathematically proved data-driven models that have luxury to dynamically tune parameters over time.

It is a time to revisit how complex a model can be if we consider unprecedented events/factors (including social factors). As scientists, we do not like to limit to win over others in terms of validation; we rather focus on developing a prediction tool that is scalable and generalizable for any upcoming infectious disease outbreaks. Within the scope, it is a time to see whether deep neural networks[10]can be realized with thousands of parameters. Studying all data analytical tools is limited to education and training [5,6]. In case we consider using data science and

6 Confirmed and Forecasted Cased Data Model: https://covid-19.bsvgateway.org. Los Alamos National Laboratory (June 20, 2020, last accessed).

7 The Institute for Health Metrics and Evaluation (IHME) COVID-19 Model: https://covid19.healthdata.org/united-states-of-america (June 20, 2020, last accessed).

8 "Garbage In, Garbage Out: How Anomalies Can Wreck Your Data–Heap–Mobile and Web Analytics." heapanalytics.com (May 7, 2014).

9 Steve Goldstein. "Oops — Rick Perry says broken clock is right once a day". The New York Post (Retrieved September 19, 2019).

10 Nancy Koleva. "When and When Not to Use Deep Learning". https://www.dataiku.com (May 1, 2020).

deep learning models, their numbers of hyperparameters could potentially supersede the size of input data. In such a case, the model technically works for hyperparameters, not for input data. This is an alarming event for data science and machine learning scientists.

To sum up, the existing literature includes heavily parameterized computationally expensive tools. They neither consider unavoidable social factors nor include immunocompromised population density in that particular region. Besides, impact of immunocompromised persons (e.g., lung cancer) on mortality and/or recovery rates in COVID-19 era was not revisited [4,11]. This brings an idea of nested statistical models, where the parameters must be data-driven, and the social factors are considered as weights. The parameters are statistically adjusted based on social factors, and therefore they are dynamic in nature. Then such data-driven parameters (in terms of weights) are integrated with another statistical model for a better prediction. This, in long-term, could benefit to predict any possible infectious disease outbreaks.

5.3 Need of medical imaging tools for COVID-19 outbreak screening

Collecting large amount of data is not trivial, and we have to wait for a long time. Most of the reported AI-driven tools are limited to proof-of-concept models for coronavirus case. AI experts state that limited data may skew results away from the severity of coronavirus outbreak. The Wall Street Journal[11] reported that coronavirus reveals limits of AI health tools: some diagnostic-app makers hold off updating their tools, highlighting the shortage of data on the new coronavirus and the limitations of health services billed as AI when faced with novel, fast-spreading illnesses (Parmy Olson, February 29, 2020). In a nutshell, social medias, newspapers, and health reports, we note that conventional AI-driven tools for real-world cases (with less data) may not provide optimal performance.

Unlike other healthcare issues, for COVID-19, to detect COVID-19, AI-driven tools are expected to have AL-based cross-population train/test models that employ multitudinal and multimodal data [1]. In Fig. 5.5, we provide a better understanding of AL (in dotted red circle) with deep learning (DL) for all possible data types. In AL, expert's feedback is used in parallel with the decisions from each data type. Since DL are data dependent, separate DLs are used for different data types. The final decision is made based on multitudinal and multimodal data. For a quick understanding, two different image data are shown in Figs. 5.6 and 5.7 with clinical manifestations (for COVID-19).

[11] The Wall Street Journal, Coronavirus reveals limits of AI health tools (accessed February 29, 2020)), https://www.wsj.com/articles/coronavirus-reveals-limits-of-ai-health-tools-11582981201.

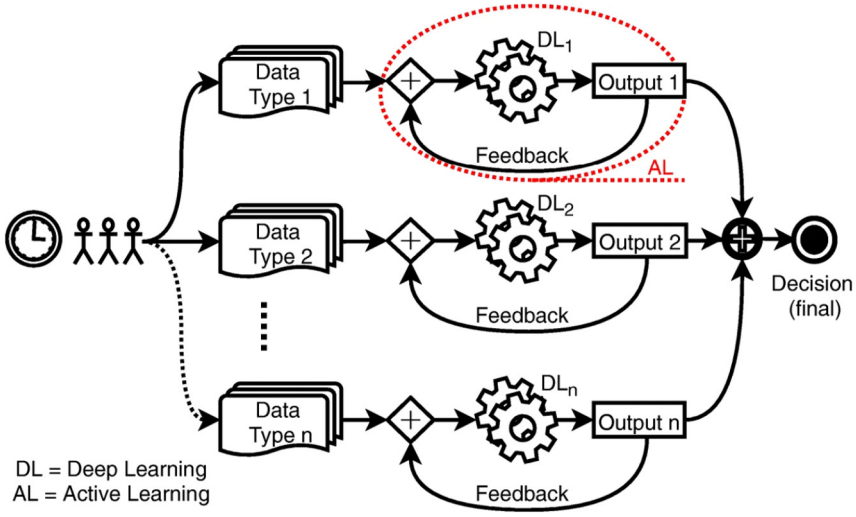

Figure 5.5: For time-series data, a schema of active learning (AL) model is provided.

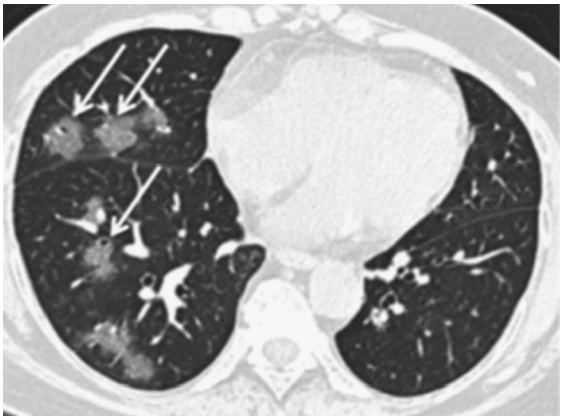

Figure 5.6: A chest CT image shows ground-glass opacities (check arrows in the right middle and lower lobes) [20].

5.4 Deep neural networks for COVID-19 screening

Following previous research papers, let us summarize deep neural networks (DNNs). As mentioned earlier, among radiological imaging data, Chest X-rays (CXRs) are of great use in observing COVID-19 manifestations. For mass screening, using CXRs, a computationally efficient AI-driven tool must detect COVID-19-positive cases from non-COVID ones (including healthy cases as well).

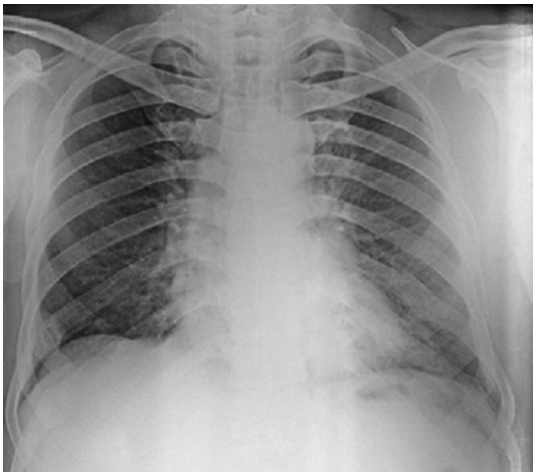

Figure 5.7: Bilateral focal consolidation, lobar consolidation, and patchy consolidation are clearly observed (check lower lung in chest X-ray).

Table 5.1: Data collection (publicly available [12–14]).

Collection	# of positive cases	# of negative cases
C1: COVID-19	162	–
C2: Pneumonia	4280	1583
C3: TB (China)	342	340
TB (USA)	58	80

5.4.1 Truncated Inception Net: COVID-19 outbreak screening using chest X-rays [7]

Motivated by the fact that X-ray imaging systems are more prevalent and cheaper than CT scan systems, we proposed a deep learning-based CNN model, which we call Truncated Inception Net (see Fig. 5.8). Our aim is to detect COVID-19 positive cases from non-COVID and/or healthy cases using chest X-rays.

To validate our proposal, we employed six different types of datasets by taking the following CXRs into account: COVID-19 positive, pneumonia positive, tuberculosis positive, and healthy cases [12–14] (see Table 5.1). For better understanding, activation maps are shown in Fig. 5.9.

The model achieved an accuracy of 99.96% (AUC of 1.0) in classifying COVID-19 positive cases from combined pneumonia and healthy cases. Similarly, an accuracy of 99.92% (AUC of 0.99) in classifying COVID-19 positive cases from combined pneumonia, tuberculosis, and healthy CXRs was reported. We proved the viability of using the proposed Truncated Inception Net as a screening tool. For more information, we refer to [7].

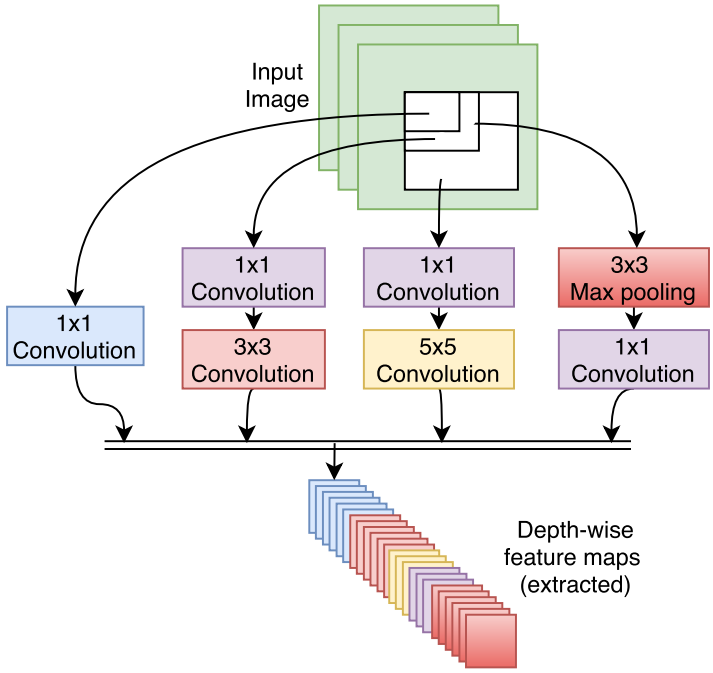

Figure 5.8: Truncated Inception network [7]. It presents the internal structure of an Inception module. Multiple-sized kernels (e.g., 3 × 3 and 5 × 5) are used to convolve with the input image, to extract features of varied spatial resolution.

Table 5.2: Generated parameters (for an image of size 25 × 25).

Layer	Parameters
Convolution	280
Dense 1	310,016
Dense 2	514
Total	310,810

5.4.2 Shallow CNN for COVID-19 outbreak screening using chest X-rays [2]

In [2], we proposed a light-weight CNN-tailored shallow architecture that can automatically detect COVID-19-positive cases using CXRs. We aimed no false negatives in our experiments. The shallow CNN-tailored architecture was designed with fewer parameters as compared to other deep learning models. For this, we refer the readers to Fig. 5.10 and Table 5.2.

The shallow CNN-tailored architecture was validated using 321 COVID-19-positive CXRs. In addition to COVID-19-positive cases, another set of non-COVID-19 5856 cases (publicly available, source: Kaggle) was taken into account, consisting of normal, viral, and bacterial

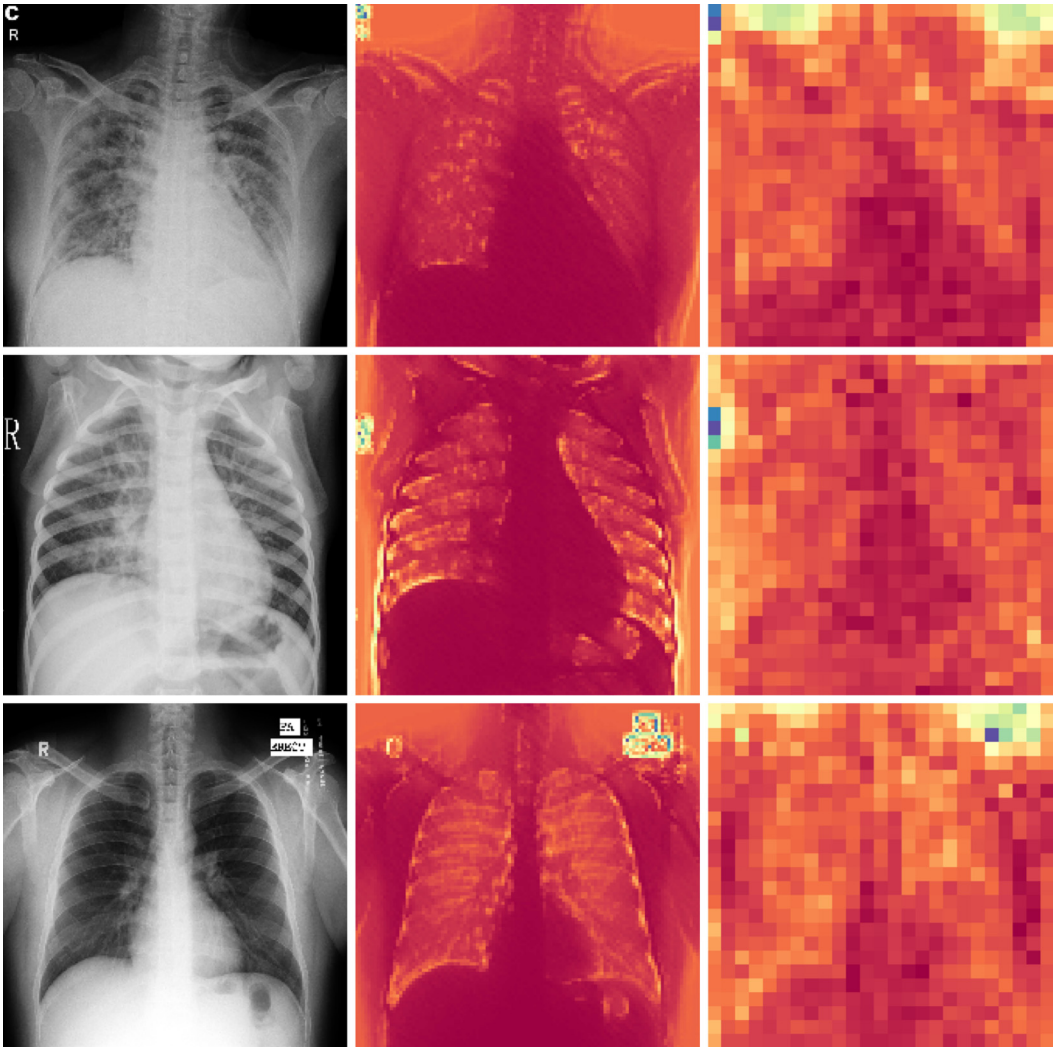

Figure 5.9: Activation maps generated by the second convolutional layer (Conv2D), the second inception module (Mixed1): COVID-19 case (top), pneumonia case (middle), and tuberculosis case (bottom).

pneumonia cases. For a better visual understanding, feature maps for COVID-19 and pneumonia cases are shown in Fig. 5.11. Using 5-fold cross-validation, we achieved the highest possible accuracy of 99.69%, sensitivity of 1.0, where AUC was 0.9995. The results were taken for a comparison with other existing deep learning models. For a comparison, the same exact set of experimental datasets was applied to other popular DL architectures, such as MobileNet [15], InceptionV3 [16], and ResNet50 [17]. The results are provided in Table 5.3.

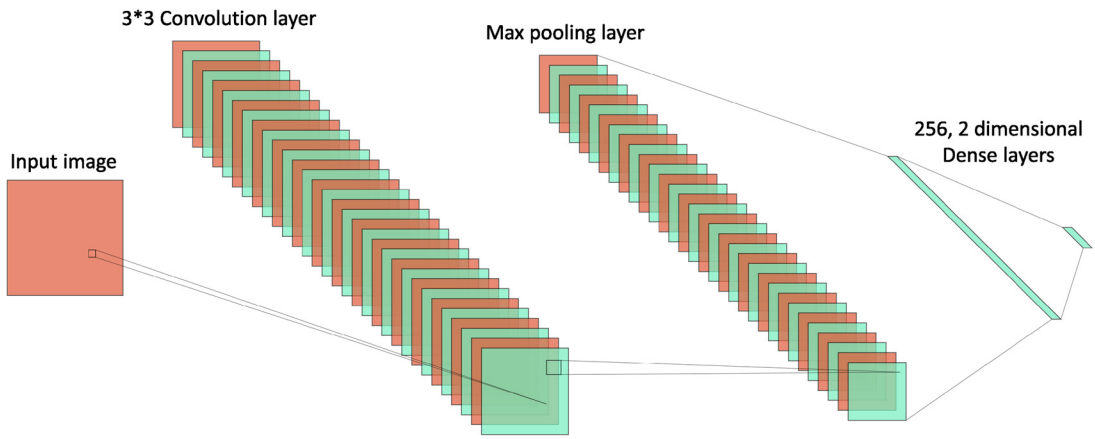

Figure 5.10: A shallow CNN architecture.

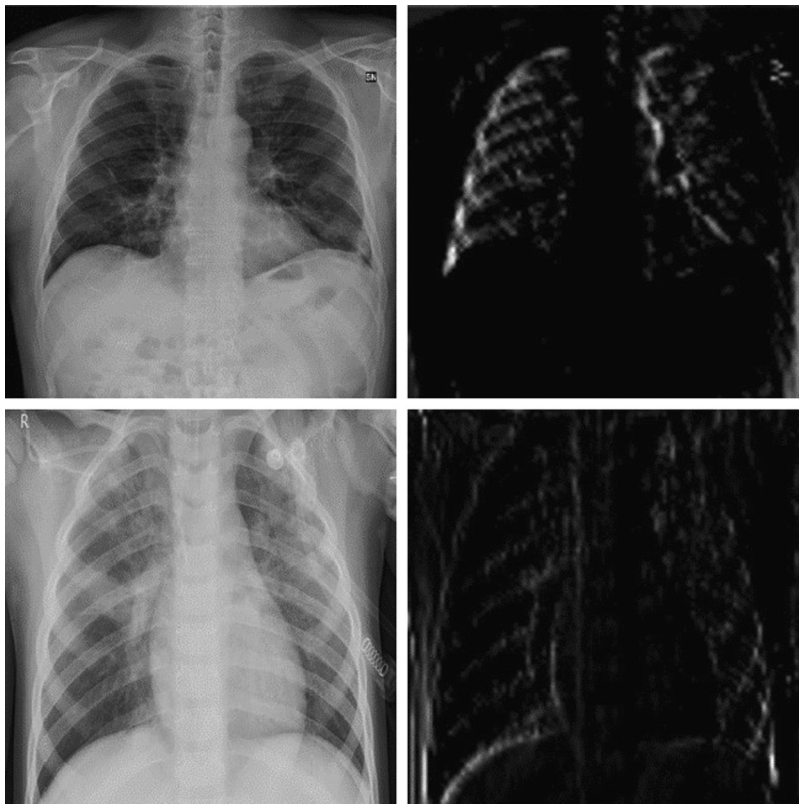

Figure 5.11: Feature maps: COVID-19 case (top), and pneumonia case (bottom).

Table 5.3: Performance comparison with other deep learning models (using balanced dataset).

Metrics	InceptionV3	MobileNet	ResNet50	Proposed CNN
Sensitivity	1.0000	1.0000	0.9252	**1.0000**
Specificity	0.9751	0.9938	0.9751	**0.9938**
Precision	0.9757	0.9938	0.9738	**0.9938**
False positive rate	0.0249	0.0062	0.0249	**0.0062**
False negative rate	0.0000	0.0000	0.0748	**0.0000**
Accuracy (%)	98.75	99.69	95.02	**99.69**
F1 score	0.9877	0.9969	0.9489	**0.9969**
AUC	0.9877	0.9969	0.9355	**0.9995**
Parameters	26,522,146	7,423,938	49,278,594	**310,810**

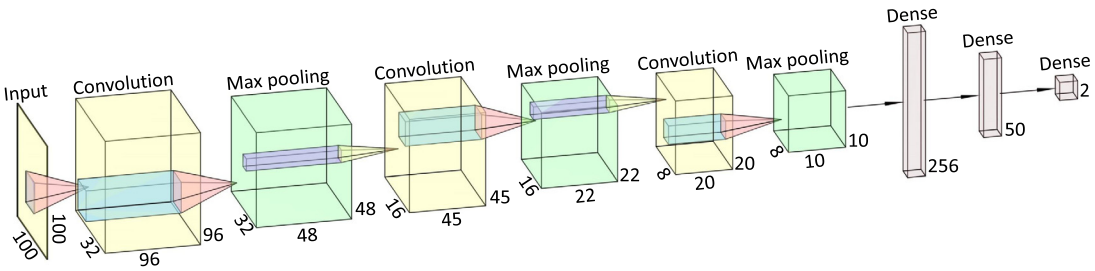

Figure 5.12: A CNN-tailored deep neural network (DNN) [3].

5.4.3 DNN to detect COVID-19: one architecture for both chest CT and X-ray images [3]

For COVID-19 screening purpose, multiple image modalities would provide higher confidence in decision-making. As chest CT and X-rays provide consistent COVID-19 manifestations [18,19], both can be considered. They can help predict, screen, and diagnose COVID-19 positive cases.

Within this scope, imaging with chest CT and X-ray images is widely used in mass triage situations. In the literature, AI-driven tools are limited to one data type, either CT scan or CXR, to detect COVID-19 positive cases. Integrating multiple data types could possibly provide more information in detecting anomaly patterns due to COVID-19. A CNN-tailored DNN that can collectively train/test both chest CT and X-rays is shown in Fig. 5.12, and its corresponding parameters are provided in Table 5.4.

Using a data collection (see Table 5.5), such a DNN architecture achieved an overall accuracy of 96.28% (AUC = 0.9808). Performance scores (using a complete dataset CXRs + CT scans) are provided in Table 5.6.

Table 5.4: Generated parameters (different layers of the CNN architecture).

Layer	Output dimension	Parameters
Convolution 1	96 × 96 × 32	2432
Convolution 2	45 × 45 × 16	8208
Convolution 3	20 × 20 × 8	1160
Dense 1	256	205,056
Dense 2	50	12,850
Dense 3 (Output layer)	2	102
Total	–	229,808

Table 5.5: Dataset collections.

Collections	COVID-19 cases	Non COVID-19 cases	Total
CXR [20,21]	168	168	336
CT [20,22]	168	168	336
CXR + CT	336	336	672

Table 5.6: Performance scores (using complete dataset CXRs + CT scans).

Metrics	Scores
Sensitivity (Recall)	0.9792
Specificity	0.9464
Precision	0.9481
False positive rate	0.0536
False negative rate	0.0208
Accuracy (%)	96.28
F1 Score	0.9634
AUC	0.9808

The uniqueness behind this work is that no existing models worked on two different modalities, chest CT and X-ray images. It opens a new window for machine learning scientists that two modalities can be used in one DNN.

5.5 Discussion: how big data is big?

In what hollows, we elaborate on the use of image data for COVID-19 screening, where the focusing point is their performance in accordance with the dataset size. As mentioned earlier, we consider both image modalities, chest CT and X-ray images. For a thorough study, we refer to [23].

1) *Chest CT imaging for COVID-19 screening:*
   For COVID-19, we elaborate on the use of chest CT imaging methods based on the performance by taking dataset size into account (see Table 5.7).
   Farid et al. [24] devised a CNN-based approach to classify COVID-19 and SARS images (51 each class). Using 10-fold cross validation, they reported an accuracy of 94.11%.

Table 5.7: Chest CT imaging tools, their datasets, and performance measured in Accuracy (ACC), Area Under the Curve (AUC), Specificity (SPEC), and Sensitivity (SEN).

Authors (2020, 2021)	Dataset size	Performance (in %) ACC, AUC, SPEC, SEN
Farid et al. 2020 [24]	Dataset (Kaggle): 102 images COVID-19 +ve (51) + SARS (51)	94.11, 99.4, –, –
Hasan et al. 2020 [25]	Dataset: COVID-19 and SPIE-AAPM-NCI: 321 images COVID-19 +ve (118) + pneumonia (96) + normal (107)	99.68, –, –, –
Loey et al. 2020 [26]	Dataset: 742 images COVID-19 +ve (345) + COVID-19 -ve (397)	82.91, –, 87.62, 77.66
Li et al. 2020 [27]	Dataset: 3, 322 images COVID-19 +ve (468) + CAP (1, 551) + non-pneumonia (1, 303)	–, 0.96, 96, 90
Ardakani et al. 2020 [28]	Dataset: 1, 020 images COVID-19 +ve (510) + COVID-19 -ve (510)	99.51, 99.4, 99.02, 100
Alshazly et al. 2021 [29]	Dataset: 2, 482 images COVID-19 (1, 252) + other (1, 230)	99.4, –, 99.8, 99.6
Ni et al. 2020 [30]	Dataset: 14, 435 images COVID-19 +ve (2, 154) + pneumonia (5, 874)	82, 86.54, 63, 96
Chen et al. 2020 [31]	Dataset: 30, 764 images COVID-19 +ve (13, 734) + normal (17, 030)	96, –, 94, 98

A notable study was conducted by Hasan et al. [25], who used handcrafted features from Q-deformed entropy to distinguish between lung scans, pneumonia, and COVID-19 CT slides. They achieved 99.68% accuracy on 321 subjects. Loey et al. [26] used five different DNN architectures, namely AlexNet, VGG16, VGG19, GoogleNet, and ResNet50. On dataset of 742 images, they achieved an accuracy of 82.91%, sensitivity of 77.66%, and specificity of 87.62% with ResNet50 classifier (best performance). Li et al. [27] used CT dataset of size 3, 322 subjects (468 COVI-19 cases) and achieved an AUC score of 0.96. Ardakani et al. [28] utilized 1, 020 CT COVID-19 cases and achieved the best accuracy of 99.51% (with AUC = 0.994 and sensitivity = 100%) from ResNet101 model. Alshazly et al. [29] experimented on two different CT datasets and used seven different DNNs. They used a $k(= 5)$-fold cross-validation and achieved accuracies of 99.4% and 92.9% in the two separate datasets, respectively. They also implemented a Grad-CAM to localize COVID-19 infected regions. In Table 5.7, we only show the distribution of one of the datasets, which is the largest and with the best performance. Ni et al. [30] implemented a deep learning model to train and validate with CT data acquired from 14,435 subjects. The method detects lesions, with segmentation and location with sensitivity and F1-score of 100% and 97% per-patient basis. The model also achieved a median volume of 40.10 cm^3, considering per-lung lobe basis. Chen et al. [31] developed a COVID-19 CT screening tool validated on 46,096 images and achieved the maximum accuracy of 96%.

2) *Chest X-ray imaging for COVID-19 screening:*
As before, in Table 5.8, we summarize different imaging methods and their performance in accordance with the dataset size. Let us briefly summarize them. Alqudah et al. [32] used 79 images, and the performance was 95.2% (accuracy). Horry et al. [33] used 400 images, and the achieved best performance was 83% (precision). Mukherjee et al. [2] used 260 X-ray images (130 of them were COVID-19 cases), and an accuracy of 96.92 was reported. Rahimzadeh and Attar [34] used 180 COVID-19 cases and obtained an overall accuracy of 99.5. Nour et al. [35] used a dataset of size 2,033 images (219 of them were COVID-19 cases), and their performance was 96.72% (accuracy). Brunese et al. [36] used a dataset of size 6,523 images, where 250 of them were COVID-19 cases. An accuracy of 97% was reported. Khan et al. [37] used 1251 images (COVID-19 cases = 284), and they achieved an accuracy of 89.6%. Marques et al. [38] used 1,508 images (COVID-19 cases = 504), and they achieved an accuracy of 96.70% (multiclass). Needless to mention that the aforementioned research papers (see Tables 5.7 and 5.8) have used different feature extractors, decision-making processes, and experimental setups. More importantly, for COVID-19, their dataset sizes are varied over time, and so the sources are. For a fair analysis, let us not discuss on their methodologies and/or techniqut rather focus on the dataset size. We then elaborate on the strength of machine learning and deep learning algorithms by taking the following factors into account, such as fitting, transfer learning in the era of deep learning, and data augmentation.

Table 5.8: Chest X-ray imaging tools, their datasets, and performance measured in Accuracy (ACC), Area Under the Curve (AUC), Specificity (SPEC), and Sensitivity (SEN).

Authors	Dataset size	Performance (in %) ACC, AUC, SPEC, and SEN
Alqudah et al. (2020) [32]	COVID-19 dataset: 71 images COVID-19 +ve (48) + COVID-19 -ve (23)	95.2, –, 100, 93, 3
Horry et al. (2020) [33]	COVID-19 dataset: 400 images COVID-19 +ve (100) + normal (100) + pneumonia (100)	–, –, –, 80
Mukherjee et al. (2020) [2]	COVID-19 dataset (Kaggle): 260 images COVID-19 +ve (130), COVID-19 -ve (130)	96.92, 99.22, 100, 94.20
Rahimzadeh and Attar [34]	COVID-19 dataset: 15, 085 images COVID-19 (180) + pneumonia (6, 054) + normal (8, 851)	99.50, –, 99.56, 80.53
Nour et al. (2020) [35]	COVID-19 dataset: 2, 905 images COVID-19 (219) + pneumonia (1, 345) + normal (1, 341)	98.97, 99.42, 99.75, 89.39
Brunese et al. (2020) [36]	2 COVID-19 X-ray datasets, NIH Chest X-ray: 6, 523 images COVID-19 (250) + pulmonary (2, 753) + normal (3, 520)	97, –, 98, 96
Khan et al. (2020) [37]	Dataset (Kaggle): 1, 251 images COVID-19 (284) + bac (330) + viral (327) + normal (310)	89.5, –, –, 100
Marques et al. [38]	A chest (pneumonia) and a COVID-19 dataset: 1, 508 images COVID-19 +ve (504) + pneumonia (504) + normal (500)	99.63, 97, –, 99.63

For easy understanding, we organize research papers, in both Tables 5.7 and 5.8, in accordance with the dataset size. In machine learning, we state that the bigger the data, the better the performance. This is true as we are looking at collecting all possible COVID-19 manifestations, rather than just increasing number of images. We have not observed better results from bigger datasets. If so, then how big data is big? Machine learning tools require to learn all possible manifestations related to particular diseases (COVID-19 in our case) not just the size of the dataset. However, the dataset size opens the possibility of having new cases (i.e., manifestations), which is always not the case.

Underfitting and overfitting situations are not explicitly discussed/analyzed in all these aforementioned COVID-19 screening tools (see Tables 5.7 and 5.8). They rather engaged in producing better performance scores by tuning (hyper)parameters, due to which biased results are possible.

In general, transfer learning works relatively greatly in computer vision. It may not work as expected for COVID-19 screening when we consider both image data types, chest CT and X-rays.

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