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# MAPPING THE LANDSCAPE OF ARTIFICIAL INTELLIGENCE APPLICATIONS AGAINST COVID-19

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## ABSTRACT

COVID-19, the disease caused by the SARS-CoV-2 virus, has been declared a pandemic by the World Health Organization, with over 294,000 cases as of March 22, 2020 (WHO, 2020). In this review, we present an overview of recent studies using Machine Learning and, more broadly, Artificial Intelligence, to tackle many aspects of the COVID-19 crisis at different scales including molecular, medical and epidemiological applications. We finish with a discussion of promising future directions of research and the tools and resources needed to facilitate AI research.

### Executive Summary

- There is a broad range of potential applications of AI covering medical and societal challenges created by the COVID-19 pandemic; however, few of them are currently mature enough to show operational impact.
- AI can support COVID-19 diagnosis from medical imaging, provide alternative ways to track disease evolution using non-invasive devices, and generate predictions on patient outcomes based on multiple data inputs including electronic health records (EHR).
- From a molecular perspective, AI can be used to estimate the structure of SARS-CoV-2-related proteins, to identify existing drugs that may be repurposed to treat the virus, and to propose new compounds that may be promising for drug development.
- AI modelling has been applied in several areas of epidemiological research, including forecasting the number of new confirmed case given different public policy choices and modelling the rate of asymptomatic cases.
- In light of the vast amounts of information being generated and shared, AI can help investigate the scale and spread of the “infodemic”, as well as specifically address the propagation of misinformation.
- Sharing and hosting data and models, whether they be medical, molecular, or scientific, is critical to accelerate the development and operationalization of AI to support the response to the COVID-19 pandemic.
- International cooperation based on multidisciplinary AI research and open science can help to prepare the regions of the world which have not yet experienced widespread outbreaks.

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## 1 INTRODUCTION

With the continued growth of the COVID-19 pandemic, researchers worldwide are working to better understand, mitigate and suppress its spread. Key areas of research include studying COVID-19 transmission, facilitating its detection, developing possible vaccines and treatments, and understanding the socio-economic impacts of the pandemic. In this article, we discuss how Artificial Intelligence can contribute to these goals by enhancing all of these different activities, improving the efficiency and speed of existing approaches as well as proposing original lines of research. We have conducted an extensive review of the rapidly emerging literature and identified specific applications of AI at three different scales: the molecular scale, including drug discovery-related research; the medical scale, including individual patient diagnosis and treatment; and the societal scale, including epidemiological and infodemic research. We also review open-source datasets and resources that are available to facilitate the development of AI solutions.

The purpose of this review is not to evaluate the impact of the described techniques, nor to recommend their use, but to show the reader the extent of existing applications and to provide an initial picture and road map of how AI could help the global response to the COVID-19 pandemic. We note that the scope of this review is restricted to applications of Machine Learning (ML) and Artificial Intelligence (AI), and that we have therefore made judgement calls regarding whether certain methodologies fall into this category. For example, we have included applications where authors have explicitly described the use of models such as neural networks and decision trees, while excluding applications based on regression. Furthermore, we note that many of the articles cited are still pre-prints at the time of writing this review; given the fast-moving nature of the crisis we strove to be comprehensive in our coverage, but their full scientific rigour should still be assessed by the scientific community through peer-reviewed evaluation and other quality control mechanisms. For specificity, we signify all preprints with <sup>†</sup>.

## 2 PATIENT SCALE: FROM DIAGNOSIS TO OUTCOME PREDICTIONS

To date, most clinical applications of AI to the COVID-19 response have focused on diagnosis based on medical imaging. In recent literature, we have found several works that use AI to support diagnosis from computational tomography (CT) scans, in addition to others that use patient medical data to predict the evolution of the disease, as well as original non-invasive measurements which can be used for monitoring purposes.

### 2.1 MEDICAL IMAGING FOR DIAGNOSIS

Reverse Transcription Polymerase Chain Reaction (RT-PCR) tests are the key approach used for diagnosing COVID-19, however they have limitations in terms of specimen collection, time required for the analysis, and performance (Ai et al., 2020). As such, there is growing interest in other diagnostics methodologies which use medical imaging for the screening and diagnosis of COVID-19 cases (Kanne et al., 2020). It has been found that COVID-19 has particular radiological signatures and image patterns which can be observed in CT scans (Ai et al., 2020). The identification of these patterns is time-consuming even for expert radiologists. This makes diagnosis of COVID-19 from lung CT scans of patients a good candidate for ML-based approaches, which could help accelerate the analysis of these scans supporting specialists.

Several studies have addressed diagnosis as a binary classification problem, i.e. healthy vs. COVID-19 positive. For example, Wang et al. (2020a)<sup>†</sup> use a modified Inception neural network architecture (Szegedy et al., 2015) trained on regions of interest identified by radiologists to carry out binary classification between healthy patients and those infected with COVID-19. Based on a dataset of roughly 1,000 image slices from 259 patients, they were able to train a model capable of identifying potential COVID-19 cases that could later be passed on to radiologists for further validation. Similarly, Chen et al. (2020b)<sup>†</sup> found that by training a UNet++ neural network (Zhou et al., 2018) on over 6,000 CT image slices of both healthy and infected patients labeled by expert radiologists, it was possible to achieve performance comparable to that of an expert radiologist. The trained model from this study was subsequently deployed at the Renmin Hospital of Wuhan University to help radiologists accelerate the analysis of new cases, and open-sourced on the Internet to enable rapid review of new images.

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Other ML approaches have framed the diagnosis problem as a 3-category classification task: distinguishing healthy patients from those with other types of pneumonia and those with COVID-19. In both Xu et al. (2020)<sup>†</sup> and Song et al. (2020)<sup>†</sup>, classical ResNet architectures (He et al., 2016) are used for feature extraction. Xu et al. (2020)<sup>†</sup> add several fully-connected layers for classification, while Song et al. (2020)<sup>†</sup> add a Feature Pyramid Network (Lin et al., 2017) and attention module, making the network more complex but also able to represent more fine-grained aspects of the images. Both of these studies show that even in cases where there are several competing potential diagnoses, ML approaches have the potential to distinguish COVID-19 from other diseases with similar symptoms.

Finally, some studies adopt a hybrid approach, combining off-the-shelf software with bespoke ML approaches in order to achieve higher accuracy. For example, in Gozes et al. (2020)<sup>†</sup> a commercial medical imaging program is used for initial image processing and then combined with an ML pipeline. The two step ML approach consists of a U-Net architecture (Ronneberger et al., 2015) trained on medical images of lung abnormalities in order to pinpoint lung regions of interest and a Resnet-50 (He et al., 2016) trained on ImageNet (Deng et al., 2009) and fine-tuned on COVID-19 cases in order to classify the images as Coronavirus or healthy.

Studies which report operational deployment, such as Shan et al. (2020)<sup>†</sup>, have adopted human-in-the-loop approaches to reduce the labeling time required while utilizing ML architectures. The authors use small manually-labelled batches of data for training an initial model based on the V-Net architecture (Milletari et al., 2016). This model proposes segmentations of new CT scans, which can then be corrected by radiologists and fed back into the model, in an iterative process. This approach enabled the development of a Deep Learning-based system for both automatic segmentation and counting of infection regions, as well as assessing the severity of COVID-19, e.g., the percentage of infection in the whole lung. The authors show not only that the model improved its own performance incrementally, but also that the human time required for analysis of new images dropped from over 30 minutes initially to under 5 minutes after 200 annotated examples were used to train the model, reducing the effort required by radiologists to review a new scan. This is a promising direction which harnesses the power of ML alongside human annotation and expertise, which can be complementary and mutually beneficial.

## 2.2 NON-INVASIVE MEASUREMENTS FOR DISEASE TRACKING

Another original approach that does not require specialized medical imaging equipment uses footage from Kinect depth cameras to identify respiratory patterns of patients (Wang et al., 2020b)<sup>†</sup>. This is based on recent findings suggesting that COVID-19 has respiratory patterns which are distinct from those of the flu and common cold, notably that they exhibit tachypnea (rapid respiration) (Casella et al., 2020). Based on this information, the researchers developed a GRU neural network (Cho et al., 2014) with bidirectional and attentional mechanisms to classify abnormal respiratory patterns, trained on both real world data from 20 participants and more abundant simulated data generated based on the real recordings. While these abnormal respiratory patterns are not necessarily correlated with real-world diagnosis of COVID-19, prediction of tachypnea could be a relevant first-order diagnostic feature that may contribute to large-scale screening of potential patients. Other proposals have also been made to utilize mobile phones in COVID-19 detection, either using embedded sensors to identify COVID-19 symptoms (Maghdid et al., 2020)<sup>†</sup> or phone-based surveys to filter high-risk patients based on responses to key questions (Rao & Vazquez, 2020); while these are important efforts given the accessibility of mobile phone technology, the existing studies are not sufficiently advanced to evaluate their feasibility and performance.

## 2.3 PATIENT OUTCOME PREDICTION

Yan et al. (2020)<sup>†</sup> propose a novel approach based on features contained in patients medical data and blood tests to help clinicians identify high-risk patients as early as possible, thereby hopefully improving the prognosis of all patients and reducing the mortality of those that are critically ill. Within the scope of this study, a prediction model based on the XGBoost algorithm (Chen & Guestrin, 2016) was built to predict mortality risk and identify key measurable features which can be tested for in hospitals. Based on data from 375 patients, the authors identified three key clinical indicators (lactic dehydrogenase, lymphocyte and high-sensitivity C-reactive protein) from more than 300 in-

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put features and thereby provide a clinical heuristic for estimating patient mortality. An advantage of this approach is its interpretability, since the three indicators identified by the approach correspond to the most important factors in the pathophysiological progress of COVID-19, namely: cell injury, cellular immunity, and inflammation. A complementary study aimed to predict whether existing COVID-19 patients would require long-term hospitalization or not based on a U-Net derivative trained on CT imaging data labeled semi-automatically (Qi et al., 2020)<sup>†</sup>. This means that once initial diagnosis is established, it could also be possible to use ML to predict to what extent patients conditions are liable to deteriorate and require long-term hospitalization. These two approaches can help identify the patients that might require intensive and long-term care, helping hospitals manage their resources more effectively. Finally, while both of these studies were limited in scope and data, they constitute important avenues of research that can be complemented and extended with clinical data from incoming cases around the world.

### 3 MOLECULAR SCALE: FROM PROTEINS TO DRUG DEVELOPMENT

Biochemistry applications of AI have also been used to better understand the proteins involved in SARS-Cov-2 infection and to inform the search for potential treatments. With respect to the virus itself, five types of structural proteins are of interest: nucleocapsid proteins (N), envelope proteins (E), membrane proteins (M), and spike proteins (S) (Zhavoronkov et al., 2020b)<sup>†</sup>, (Liu et al., 2020) and those not included in virion but that are translated in host cell and are crucial for viral replication (the nonstructural proteins, or nsp). Research has focused on one of these nsps (nsp5), the 3-chymotrypsin-like (3C-like) protease, an enzyme that assists in processing of viral proteins and the replication of the virus. On the human side, research has focused on the angiotensin-converting enzyme 2 (ACE2) protein, a receptor that facilitates the virus' entry into host cells (Hoffmann et al., 2020). Potential applications of AI include predicting the structure of these associated proteins, identifying existing drugs which may be effective in targeting these proteins, and proposing new chemical compounds for further testing as potential treatments (Zhavoronkov, 2018).

#### 3.1 PROTEIN STRUCTURE PREDICTION

Proteins have a 3D structure, which is determined by their genetically encoded amino acid sequence, and this structure influences the role and function of the protein (Senior et al., 2020a). Protein structure is traditionally determined through experimental approaches such as X-ray crystallography, but these can be costly and time-consuming. More recently, computational models have been used to predict protein structure. There are two primary approaches to the prediction task: *template modeling*, which predicts structure using similar proteins as a template sequence, and *template-free modeling*, which predicts structure for proteins that have no known related structure.

Senior et al. (2020b) have developed a system called AlphaFold which focuses on the latter challenge. The AlphaFold model is based on a dilated ResNet architecture (He et al., 2016; Yu & Koltun, 2016) and uses amino acid sequences, as well as features extracted from similar amino acid sequences using multiple sequence alignment, to predict the distance and the distribution of angles between amino acid residues. These predictions are used to construct a "potential of mean force" which can be used to characterize the protein's shape (Senior et al., 2019). This system has been applied to predict the structures of six proteins related to SARS-CoV-2 (SARS-CoV-2 membrane protein, protein 3a, Nsp2, Nsp4, Nsp6, and papain-like proteinase) (Jumper et al., 2020).

#### 3.2 IMPROVING VIRAL DNA TESTING

There are also efforts to use Machine Learning and novel genome technologies to improve the current RT-PCR test. Metsky et al. (2020)<sup>†</sup> use CRISPR (a tool which uses an enzyme to edit genomes by cleaving specific strands of genetic code) to develop assay designs for detecting 67 respiratory viruses, including SARS-CoV-2. The authors note that this technology can speed up the processing of test samples in order to assist overburdened diagnostic facilities, and help address the challenge of false positives which occur as a result of sequence similarity between SARS-Cov-2 and other coronaviruses. ML models have been built to rapidly design assays which are predicted to be sensitive and specific, and cover a diverse range of genomes. The authors state that they are aiming to build a Cas13-based point-of-care assay for SARS-CoV-2 in the future.

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### 3.3 DRUG REPURPOSING

One approach to discovering existing drugs which could be repurposed to treat COVID-19 is the use of biomedical knowledge graphs. Biomedical knowledge graphs are networks capturing the relationships between different entities – such as proteins and drugs – in order to facilitate higher-level exploration of how they connect to each other. Richardson et al. (2020) use this technique to identify Baricitinib, a drug which is commonly used to treat arthritis via inhibition of JAK1/2 kinases, as a promising therapy for COVID-19 because it inhibits the AP2-associated protein kinase 1 (AAK1) enzyme and may therefore make it harder for the virus to enter host cells. Related work has described two approaches which potentially inform the graph construction. First, Segler et al. (2018) describe an approach to mining a structured database of chemical reactions (Reaxys) using a three-part neural network pipeline combined with a Monte Carlo Tree Search approach (3N-MCTS), in order to understand how various compounds are formed hierarchically from reactions between simpler component compounds. Second, Fauqueur et al. (2019) describe a strategy for mining an unstructured scientific article database (PubMed) to identify stylized relationships between gene-disease pairs expressed in individual sentences (e.g. “GENE promotes DISEASE”).

Ge et al. (2020)<sup>†</sup> describe a similar approach to constructing a knowledge graph connecting human proteins, viral proteins, and drugs using databases which capture the relationships between these entities. The graph is used to predict potentially effective candidate drugs. This list is further refined using a Natural Language Processing (NLP) model (a Biomedical Entity Relation Extraction (BERE) approach (Hong et al., 2019)<sup>†</sup>) applied to the PubMed database, filtered for mentions of the candidate drug compounds, coronaviruses, or their associated proteins. The authors identify a Poly (ADP-Ribose) Polymerase 1 (PARP1) inhibitor, CVL218, as a promising candidate, and it is currently undergoing clinical testing.

Other studies use models developed to predict protein-ligand binding affinities in order to tackle the drug repurposing problem. Ligands are small molecules which bind with a protein to trigger a signal, which can be activation or inhibition. Hu et al. (2020a)<sup>†</sup> use a multi-task neural network for the general prediction of these affinities. The authors identify a list of SARS-CoV-2 related proteins (RNA-dependent RNA polymerase, 3C-like protease, papain-like protease, helicase, spike glycoprotein, exonuclease, endoRNase, 2'-O-ribose methyltransferase, and envelope protein), which they attempt to target using a database of 4,895 drugs. They suggest 10 promising drugs, along with their target proteins and binding affinity scores (which indicate the likelihood that the drug will act as an inhibitor). In an attempt to increase model interpretability, they also estimate the precise regions of each target protein where binding is likely to occur. In a similar vein, Beck et al. (2020)<sup>†</sup> use their own Molecule Transformer-Drug Target Interaction (MT-DTI) model (Shin et al., 2019) of binding affinities to identify US Food and Drug Administration (FDA) approved antivirals which may be effective in targeting six coronavirus-related proteins (3C-like protease, RNA-dependent RNA polymerase, helicase, 3'-to-5' exonuclease, endoRNase, and 2'-O-ribose methyltransferase). The MT-DTI model ingests string data in the form of simplified molecular-input line-entry system (SMILES) data and amino acid sequences, and applies a text-modeling approach that leverages ideas from the BERT algorithm (Devlin et al., 2018). The model identifies drugs that are expected to be effective in targeting each protein studied. Finally, Zhang et al. (2020)<sup>†</sup> use a dense fully connected neural network, trained to predict binding affinities on the PDDBind database, in order to identify potential inhibitors of the 3C-like protease. They develop a homology (template) model of the target protein using its SARS variant, and explore databases of existing compounds (e.g. ChemDiv and TargetMol) as well as tripeptides to find treatments which may be effective at targeting this protein.

### 3.4 DRUG DISCOVERY

There is also some research that attempts to discover novel compounds for use in targeting SARS-Cov-2. Zhavoronkov et al. (2020a)<sup>†</sup> use a proprietary pipeline to find inhibitors for the 3C-like protease. Their models use three types of input: the crystal structure of the protein, the co-crystallized ligands, and the homology model of the protein. For each input type, the authors fit 28 different models including Generative Autoencoders (Makhzani et al., 2015) and Generative Adversarial Networks (Goodfellow et al., 2014). The authors explore potential candidates using a reinforcement learning approach with a reward function that incorporates factors such as measures of drug-likeness, novelty, and diversity. Moreover, they confirm that the identified candidate molecules are dissimilar to existing compounds, suggesting that they have indeed found novel candidate drugs.

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Tang et al. (2020)<sup>†</sup> also apply a reinforcement learning approach to the discovery of compounds that inhibit the 3C-like protease. Specifically, the authors create a list of 284 molecules known to act as inhibitors in the context of SARS. They break these proteins into a series of 316 fragments, which can then be combined using an advanced deep Q-learning network with fragment-based drug design (ADQN-FBDD) which rewards three aspects of discovered molecules: a drug-likeness score, the inclusion of pre-determined “favorable” fragments, and the presence of known pharmacophores (which are essentially abstract design patterns believed to be correlated with a compound’s effectiveness (Qing et al., 2014)). The 4,922 results are heuristically filtered and the 47 top compounds assessed with molecular docking simulations, from which the researchers then select the top most promising compound and manually tailor it to produce suggested variants for testing.

## 4 SOCIETAL SCALE: EPIDEMIOLOGY AND INFODEMIOLOGY

### 4.1 EPIDEMIOLOGY

The spread of SARS-CoV-2 across the globe has received much policy attention, with advice at the national and local level changing daily in many locations as new information and model forecasts become available. Understanding how the virus is transmitted, and its likely effect on different demographics and geographic locations, is crucial for public policy healthcare interventions.

The field of epidemiological research is incredibly vast, and the relevance and scale of the pandemic, in addition to new data becoming available, has resulted in multiple modelling efforts. While most of the modeling endeavours develop on well-established classical models such as susceptible-infected-recovered (SIR) models and fine-tune them to the COVID-19 situation, we focus here on cases specifically employing Machine Learning techniques for epidemiological modeling tasks.

Given the rapid progression of infections, real-time short-term forecasting can be a vital source of information. In particular, models must be flexible in order to adapt to changing protocols and procedures. Hu et al. (2020b)<sup>†</sup> have compiled data collected by World Health Organization (WHO) and other actors across the period from January 11 - February 27, 2020 to develop a dataset of accumulated and new confirmed cases in 31 provinces and cities of China. This information is used to train a modified auto-encoder (MAE) for real-time forecasting of new cases, and may be used to estimate the extent and duration of the epidemic. Models can be trained at the city, provincial, or national level. Furthermore, the authors extract information from the auto-encoder’s latent variable layers to determine the model’s most important features for each analysed region. These features are then fed into a k-means clustering algorithm that groups similar regions for further analysis. The hope is that this final step will enable more efficient investigation in the regions showing infected/recovered characteristics of interest.

Similarly, Al-qaness et al. (2020) propose a new forecasting model for predicting the total number of confirmed cases ten days in advance, using historical data. The authors base their model on an adaptive neuro-fuzzy inference system (ANFIS) (Jang, 1993), along with an enhanced flower pollination algorithm (FPA) (Yang, 2012) and salp swarm algorithm (SSA) (Mirjalili et al., 2017) to optimize the parameters of the model. The resulting ANFIS-FPASSA model is optimised according to the mean-squared error on data collected from the WHO’s published daily confirmed cases in China. Given the short-term nature of the WHO data, the authors also test the robustness of their approach by training and testing on weekly confirmed influenza cases as collected by the US Centre for Disease Control and the WHO over two different four-year periods. In all three cases the authors found their model to outperform similar ANFIS models trained using other methods for parameter setting.

A more specific use of ML methods is employed by Mizumoto et al. (2020) who seek to understand the rate of asymptomatic cases using data collected from the COVID-19 outbreak on-board the *Diamond Princess* cruise ship. Here, asymptomatic is defined as a patient who has tested positive for the virus but is not displaying any symptoms at the time of testing. In this work, the authors use time-series data collected at different test times up until two days after the scheduled quarantine ended on February 21, 2020. In total, the dataset contained 634 confirmed cases and the proportion of asymptomatic patients at different time stamps. Using this data the authors modelled the time-series using a Bayesian analysis technique, with Hamiltonian Monte Carlo (HMC) and a No-U-Turn-Sampler (Homan & Gelman, 2014) used for model parameter estimation, to estimate the probability

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of a given patient being asymptomatic given infection, along with the duration an individual is infected for. Using point estimates from the posterior, the authors estimated that asymptomatic proportion of individuals was 17.9% at the level of the 95% credible interval. Whether this study can be extrapolated to the wider population has yet to be seen, although analysis from contained environments such as this one could be of great importance.

## 4.2 INFODEMOLOGY

While not specifically an application of AI, we feel it prudent to discuss the current impact of the recent “infodemic” being experienced around the world. In this section we highlight work being carried out to quantify the spread of information surrounding the pandemic, and understand its dynamics. Moreover, dealing with this vast amount of information requires the development and adoption of new tools, particularly surrounding the dissemination of misinformation. While this is already an area in which much AI and, more specifically ML, research has been carried out, there is still a need for greater understanding of the underlying social dynamics. This is of particular importance in times such as these, in which vital information needs to be able to cut through the noise to prevent loss of life.

Social media and online platforms have become key distribution channels for information surrounding the virus. Although national and international organizations have used these platforms to constructively communicate with the public, we are also seeing an infodemic in which populations can become overwhelmed with information, and the propagation of misinformation or mis-informed information is increasingly prevalent. Zarocostas (2020) highlight the WHO’s response to combating this infodemic through the use of its Information Network for Epidemics (EPI-WIN) platform for sharing information with key stakeholders. Additionally, the WHO is also working with social media and search companies to track the spread of specific rumors and to ensure that WHO content is displayed at the top of searches for terms related to the virus.

In a broad-ranging study, Cinelli et al. (2020)<sup>†</sup> analyze interaction and engagement with COVID-19-related social media content. The authors collected eight million comments and posts, selected using COVID-19 related keywords, posted between January 1 and February 14, 2020 from Twitter, Instagram, YouTube, Reddit and Gab. The authors estimate engagement and interest in COVID-19 and comparatively assess the evolution of discourse on each platform. Interaction and engagement are measured using the cumulative number of posts, and the number of reactions (e.g. comments, likes etc.) to these posts across the 45-day period. The authors then employed phenomenological (Fisman et al., 2013) and classical SIR models to characterize the reproduction numbers. Specifically, they examine the average number of secondary cases (users that start posting about COVID-19) created by an “infectious” individual (already posting) on each of the social media platforms. As in epidemiological models, the authors simulate the likelihood of an infodemic in which discussion of COVID-19 will grow exponentially, at least in its initial stages. Moreover, the authors examine the spread of misinformation (which they identify using external fact-checking organizations). The authors find that information from both reliable and unreliable sources propagate in similar patterns, but that user engagement with posts from less-reliable sources is lower than engagement with content from reliable sources on major social media streams.

Similarly, Mejova & Kalimeri (2020)<sup>†</sup> have examined the use of Facebook advertisements with content related to the virus. The authors used the [Facebook Ad Library](#) to search for all advertisements using the keywords “coronavirus” and “covid-19” and collected 923 results across 34 countries, with most in the US (39%) and the EU (Italy made up 25% of the advertisement markets). While the majority of adverts were found to be paid for by non-profits to disseminate information and solicit donations, the authors found that around 5% of advertisements contained possible erroneous or misinformation.

Finally, efforts are underway to curate specific news content related to the virus and perform both manual and automated fact-checking and relevance analysis. Pandey et al. (2020)<sup>†</sup> have developed a pipeline for assessing the similarity between daily news headlines and WHO recommendations. The pipeline uses word embedding and similarity metrics, such as cosine similarity, to assess the relevance level of WHO recommendations to news article titles and content. If the similarity is above a certain threshold then the new article displays on the user’s timeline with the associated relevant WHO recommendation. The setting of the similarity threshold is determined by human reviewers

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prior to release and then can be updated through user feedback. In the face of conflicting information, such methods could help identify accurate and trustworthy news articles which highlight important guidelines and promote official recommendations.

## 5 DATASETS AND RESOURCES

The success of the global effort to use AI techniques to address the COVID-19 pandemic hinges upon sufficient access to data. Machine Learning, and Deep Learning in particular, requires notoriously large amounts of data and computing power in order to develop and train new algorithms and neural network architectures. In this section, we describe some of the datasets and data collection efforts that exist at the present time.

### 5.1 CASE DATA

The current number and location of cases is essential for tracking the progress of the COVID-19 pandemic in different locations, calculating the growth factor of new infections, and observing the impact of preventative measures. Several datasets from organizations such as the [WHO](#) and national centers for disease control (CDCs) exist for this purpose, and they have been aggregated into public repositories hosted by institutions such as [Johns Hopkins CSSE](#) and crowd-sourced efforts on platforms like [Github](#), in order provide day-level information on COVID-19 affected cases gathered from a variety of reliable sources. There are also other complementary data sources including regional data as school closures, bank interest rates, and even community perceptions of the virus, many of which are continuously being added to a data portal hosted by the [Humanitarian Data Exchange](#). There are a multitude of AI algorithms that can be applied on this kind of data, ranging from time series forecasting approaches such as Auto Regressive Integrated Moving Average (ARIMA) to other regression approaches. Given a sufficient quantity of data and features, neural network architectures such as Long-Short Term Memory (LSTM) networks (Hochreiter & Schmidhuber, 1997) could also be applied to predict the evolution of cases on a global and regional scale.

There are also some tools and resources that are being developed specifically for medical professionals and institutions. For instance, [CHIME](#) is an open-source COVID-19 Hospital Impact Model for Epidemics based on SIR modeling, which uses the number of susceptible, infectious, and recovered individuals to compute the theoretical number of people infected over time and to predict outcomes in specific circumstances. While this project is currently not using any ML techniques, it could certainly benefit from these techniques in order to be able to incorporate more features and data points, and therefore to improve prediction quality. There are also efforts being made to use de-identified, large-scale data assess mobility changes and their impact on the local unfolding of the epidemic, for instance by the [COVID19 MM working group](#) in Italy.

### 5.2 TEXTUAL DATA

NLP approaches in particular can be extremely useful, given the vast quantity of textual information that exists regarding COVID-19 and other coronaviruses. These can be used to answer key research questions such as:

1. What is known about the virus' transmission, incubation, and environmental stability?
2. What do we know about COVID-19 risk factors?
3. What do we know about non-pharmaceutical interventions?
4. What do we know about vaccines and therapeutics?
5. What has been published about ethical and social science considerations?
6. What has been published about medical care?

These questions can be analyzed using different sources, such as articles from the [WHO Global Research Database on COVID-19](#), a curated literature hub for COVID-19 scientific information, and the [COVID-19 Open Research Dataset \(CORD-19\)](#), the current largest open



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dataset available with over 29,000 research articles about COVID-19, SARS-CoV-2, and other coronaviruses. There are already several ongoing [Kaggle challenges](#) involving this data, with dozens of questions submitted daily and many teams involved. There are also several other scientific research datasets that can be exploited, including [LitCOVID](#) and the [Dimensions AI COVID-19 dataset](#), which contain supplementary information regarding datasets and clinical trial data when available. The textual data from scientific articles can also be completed with data from other sources, such as social media. For instance, several public Twitter datasets (such as [COVID-19 TweetIDs](#) and [Covid19 Tweets](#)) have recently been released, which are maintained based on coronavirus-related tweets.

Using any of the sources mentioned above, NLP techniques can be applied to develop text mining tools that can help the medical community find answers to key scientific questions regarding the nature and progress of COVID-19. Different NLP and Information Retrieval (IR) methods could be utilized to glean relevant information from these rich sources of data, including out-of-the-box toolkits like [SciSpacy](#), a text processing toolkit optimized for scientific text, and [SciBERT](#), a powerful universal NLP model that can be used to represent scientific texts and to carry out tasks like summarization, question answering, and the retrieval of relevant passages. Social media sources could also be used to enhance scientific literature-based approaches, to help track misinformation and unverified rumors, or to enable the monitoring of population reactions to the virus on social media (Chen et al., 2020a).

### 5.3 BIOMEDICAL DATA

At the current moment, there are not many open-source datasets and models for diagnostic purposes. Some of the CT scan detection approaches described in Section 2 are available online and accessible to the public, for instance those of [Wang et al.](#) and [Song et al.](#) However, the data used to train the various models described is not systematically shared, which would be of great value to the ML research community. Initiatives like the [Covid Chest X-Ray Dataset](#) are aiming to build such a dataset with a crowdsourced approach, but are slow to put together and maintain manually. Also, while data collection and ML model training can be carried out by computer scientists, data labelling and annotation often need to be done by medical professionals such as radiologists or clinicians. This is why projects such as [Data Against Covid](#) are particularly important – they aim to bring together the medical community, who have data regarding the COVID-19 crisis, with data scientists and ML experts who can help them extract insights and actionable information from this data. These kinds of initiatives are promising given their potential to bridge the gap between those with medical and biological knowledge and experience and those with data skills.

In terms of genomic sequencing and drug discovery, there are several datasets based on pre-existing initiatives or created from scratch for COVID-19 specifically. In fact, tracking the genome sequence of SARS-CoV-2 is crucial to design and evaluate diagnostic tests, to track and trace the pandemic, and to identify the most promising intervention options. Notably, the [GISAID Initiative](#), founded over a decade ago for the specific purpose of promoting the international sharing of influenza virus sequences and related clinical and epidemiological data, is tracking the genomic epidemiology of SARS-CoV-2. Furthermore, other well-established initiatives such as the [RCSB Protein Data Bank](#) and the [Global Health Drug Discovery Institute](#) also have centralized portals with data and resources for different aspects of understanding COVID-19 and for carrying out structure-guided drug discovery. [Nextstrain](#) is an open-source project looking at genetic diversity of coronaviruses to characterize the geographic spread of COVID-19 by inferring the lineage tree of hundreds of publicly shared genomes of SARS-CoV-2. Another interesting resource is the citizen science game [Fold.it](#) which leverages collective intelligence against COVID-19 by proposing to design an antiviral protein.

## 6 DISCUSSION

As seen in this research mapping exercise, ML and AI can support the response against COVID-19 in a broad set of domains. In particular, we have highlighted emerging applications in diagnosis, clinical outcome prediction, drug discovery and development, epidemiology, and infodemiology. However, we note that very few of the reviewed systems have operational maturity at this stage. In order to operationalize this research, it is important to define a research road map and a funnel for AI applications to understand how this technology can immediately assist with the response, how it

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might help later on in the evolution of the current pandemic, and how it can be used to combat future pandemics. As members of a global community of researchers and data scientists, we identify three key calls for action.

First, we believe that scalable approaches to data sharing using open repositories will drastically accelerate the development of new models and unlock data for the public interest. Image-based medical diagnosis, in particular, is a domain in which training data is currently scarce but the value of AI models may be high. In order to facilitate the sharing of such data, clinical protocols and data sharing mechanisms will need to be designed and data governance frameworks will need to be put in place. It is important to reinforce that research with medical data must be subject to strong regulatory requirements and privacy protecting mechanisms. Overall, any AI application developed should undergo an assessment to ensure that complies with ethical principles and above all respects human rights.

Second, the multidisciplinary nature of the research required to deploy AI systems in this context calls for the creation of extremely diverse, complementary teams and long-term partnerships. Beyond the examples shown in this review, other promising domains in which AI could be used to fight against COVID-19 include robotics (e.g. cleaning or disinfecting robots) and logistics (e.g. the allocation and distribution of personal protective equipment). Funding opportunities which encourage such collaborations and define key research directions may help accelerate the success of such partnerships.

Third, we believe that open science and international cooperation can play an important role in this pandemic – in particular to prepare the regions which have not yet experienced widespread outbreaks, as well as to improve the resilience of health systems, which are currently under tremendous stress across all dimensions. In the face of healthcare capacity being overstretched, we must strengthen our health systems to sustain services beyond the control and management of COVID-19 to truly protect the vulnerable, such as people living with noncommunicable diseases (NCDs). AI systems, methods, and models can act as a compact form of knowledge sharing which can be used to train other specialists, or shared directly if they are designed to be widely deployable. In particular, given that many private sector companies and AI partnerships operate across international borders, they may be in position to facilitate the knowledge dissemination and capacity building of national health systems.

We acknowledge the difficulty of adding value through AI in the current situation. Nevertheless, we hope that this review is a first step towards helping the AI community understand where it can be of value, which are the promising domains for collaboration, and how research agendas can be best directed towards action against this or the next pandemic.

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