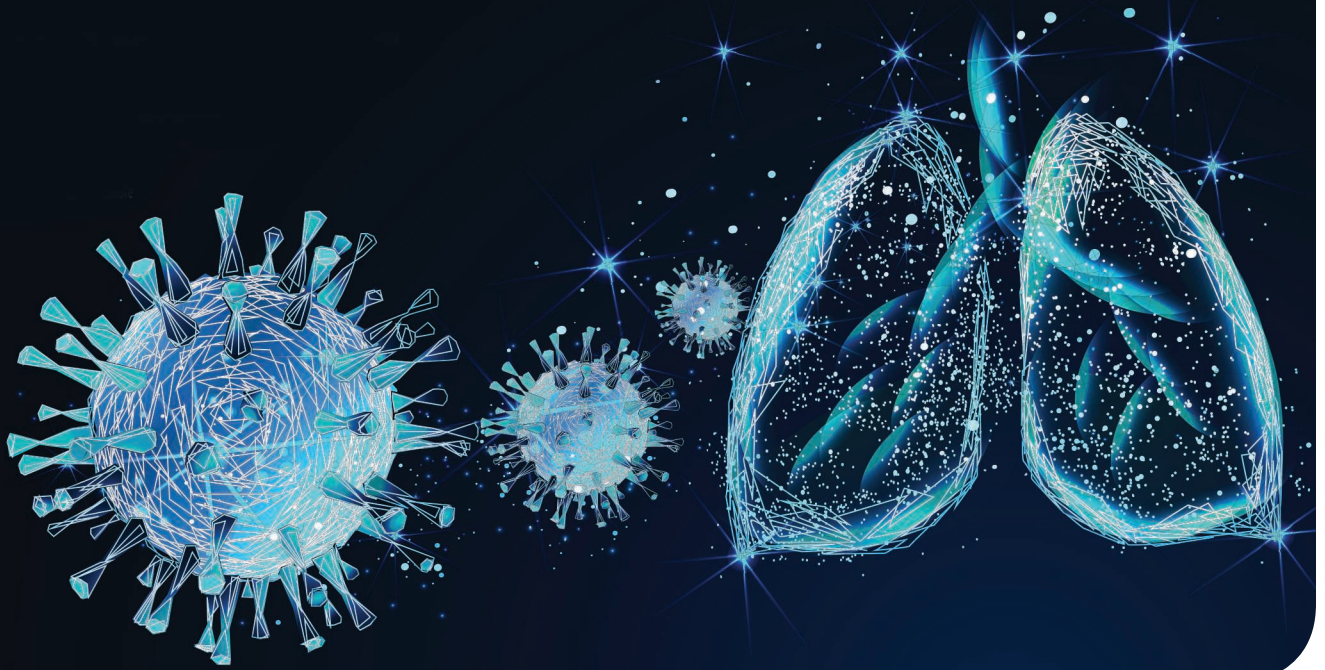# Computational Intelligence Techniques for Combating COVID-19: A Survey

©SHUTTERSTOCK/IRINA SHI

Vincent S. Tseng
National Chiao Tung University, TAIWAN.

Josh Jia-Ching Ying
National Chung Hsing University, TAIWAN.

Stephen T. C. Wong
Houston Methodist Cancer Center, USA.

Diane J. Cook
Washington State University, USA.

Jiming Liu
Hong Kong Baptist University, CHINA.

Abstract—Computational intelligence has been used in many applications in the fields of health sciences and epidemiology. In particular, owing to the sudden and massive spread of COVID-19, many researchers around the globe have devoted intensive efforts into the development of computational intelligence methods and systems for combating the pandemic. Although there have been more than 200,000 scholarly articles on COVID-19, SARS-CoV-2, and other related coronaviruses, these articles did not specifically address in-depth the key issues for applying computational intelligence to combat COVID-19. Hence, it would be exhausting to filter and summarize those studies conducted in the field of computational intelligence from such a large number of articles. Such inconvenience has hindered the development of effective computational intelligence technologies for fighting COVID-19. To fill this gap, this survey focuses on categorizing and reviewing the current progress of computational intelligence for fighting this serious

Corresponding Author: Vincent S. Tseng (vtseng@cs.nctu.edu.tw).

disease. In this survey, we aim to assemble and summarize the latest developments and insights in transforming computational intelligence approaches, such as machine learning, evolutionary computation, soft computing, and big data analytics, into practical applications for fighting COVID-19. We also explore some potential research issues on computational intelligence for defeating the pandemic.

I. Introduction

COVID-19 is an infectious disease caused by a novel coronavirus and has been declared by the World Health Organization (WHO) as a pandemic in March 2020. Since this disease was first identified in December 2019, it has become a global pandemic and has caused infections in millions of people. The coronavirus death toll surpassed 687,000 worldwide as of the end of July 2020, and the number of infections and deaths continues to rise. Such an extremely serious situation has led to high threat in healthcare systems worldwide and severe damage in the global economy being. To combat COVID-19, many countries are working to develop novel and effective mechanisms to overcome this disaster. Governments, industry leaders, and academics alike are devoting substantial resources and effort into mitigating the effects of the pandemic. Over the past few months, various emerging solutions and systems for combating COVID-19 have been developed and deployed. For example, fast screening methods utilizing different types of clinical data, including X-rays, computed tomography (CT) scans, and vital signs, have enabled timely diagnosis and disease monitoring. Computer systems are also being designed for risk profiling, patient surveillance, contact tracing, or propagation modeling by using social media data.

Owing to the advancement of computational intelligence, numerous integrations of computational intelligence mechanisms with various devices and systems have already achieved considerable success in dealing with the underlying challenges of epidemic diseases such as new influenzas [1], SARS [2], and MERS [3]. As a result, many systems and solutions for combating COVID-19 have adopted computational intelligence, and the design of proper computational intelligence mechanisms plays a crucial role in building such solutions. Since the integration of computational intelligence mechanisms with various devices and systems under different application conditions would require different types of computational intelligence techniques, including data analytics, computational modeling, high-performance computing, artificial intelligence, and in particular its subfield of machine learning, many researchers have devoted their efforts to developing systems of computational intelligence specifically for the fight against COVID-19.

By the end of July 2020, more than 200,000 scholarly articles were published regarding COVID-19, SARS-CoV-2, and other related coronaviruses [4]. However, these articles did not address in-depth the key issues in applying computational intelligence to combating the COVID-19 pandemic. Thus, it would be exhausting to filter and summarize studies related to computational intelligence from such a large number of articles. In light of the above observations, now is the time to systematically categorize and review the current progress of research on computational intelligence. Accordingly, this survey aims to assemble and summarize the highlights of the latest developments and insights in applying computational intelligence approaches, such as machine learning, evolutionary computation, soft computing, and big data analytics, to practical applications used to combat COVID-19.

The remainder of this paper is organized as follows. In Section II, we briefly survey the history of computational intelligence. In Sections III through VII, we categorize computational intelligence into its five principles and determine the urgent issues concerning COVID-19, which have been, or can be, resolved using computational intelligence approaches. We then review the current computational intelligence studies that have attempted to address these urgent issues based on these five principles. Then, in Section VIII, we review some current systems or applications for combating COVID-19 that have employed principles of computational intelligence. Finally, in Section IX, we conclude the article and discuss recommendations for future studies.

II. Overview

Computational intelligence techniques have already been successfully integrated into various systems for dealing with the underlying challenges of epidemic diseases. Before we introduce the specific issues which computational intelligence can be used to solve to fight COVID-19, we should first understand the history and various categories of this method. Based on the principles of computational intelligence, we can further clarify what types of issues can be dealt with when battling COVID-19 with computational intelligence.

A. Brief Introduction to Computational Intelligence

Computational intelligence was formally defined by Bezdek in 1994 [5] [6] such that a system is called "computationally intelligent" if the system deals with data on a basic level (such as pixels of an image), contains a module of pattern recognition, and does not utilize prior knowledge in the sense of artificial intelligence. According to Bezdek's definition, computational intelligence is one branch of artificial intelligence. Actually, the goals of both artificial intelligence and computational intelligence are the same, which is to realize general intelligence. Marks [7] clarified the difference between artificial intelligence and computational intelligence by claiming that the former is made from hard computing technologies, whereas the latter is made from soft computing technologies.

Therefore, we can presume that two types of machine intelligence exist: 1) artificial intelligence, which is developed by the concept of hard-computing and 2) computational intelligence, which is developed by the concept of soft-computing.

Based on our observations, there are several urgent issues related to COVID-19 that must be combatted. These issues can be categorized into five topics: tracking and predicting virus propagation (TPVP), characterization of symptoms of virus infections (CSVI), treatment design (TrD), precaution development (PD), and public health policy making (PHPM).

Compared to the hard-computing-based artificial intelligence, computational intelligence can adapt to many different conditions via the benefits of the concept of soft-computing. Hard computing techniques are designed using a Boolean logic based only on true or false values that information engineering relies on. One critical issue in Boolean logic is that Boolean values are unable to interpret natural language easily. However, based on fuzzy logic, soft computing techniques can deal with uncertain cases. This type of logic is one proprietary aspect of computational intelligence, and by aggregating data into partial facts, it is approximated to the manner in which the human brain acts [7].

B. Categorization of Computational Intelligence

As mentioned above, the notion of computational intelligence has been around for 30 years. During this period, new concepts have been constantly added to the field, thereby reinforcing the discipline. Today, we can broadly divide computational intelligence techniques into five categories: neural networks, fuzzy logic, evolutionary computation, computational learning theory, and probabilistic methods.

1) Neural Networks

Based on biological neural networks, an artificial neural network (called "neural network" for short) is designed as a network of artificial neurons or nodes. Artificial neural networks can be used for regression or classification modeling for prediction and automatic control. A large number of simulation data using limited data sets. This structure is the foundation of deep learning, which is good at representation learning. Accordingly, artificial neural networks process and learn information from data via the systems of distributed information processing [8]. By doing so, one of the crucial properties of artificial neural networks is fault tolerance, which is approximately modeled on the manner in which the human brain operates [6]. Based on these characteristics, neural networks have been widely applied to data analytics, clustering, classification, and automatic control engineering. In real-world applications, such methods aim to analyze and classify medical data, recognize human faces, detect computer fraud, and deal with the nonlinearity of a system for better process control [9]. Furthermore, neural network techniques can incorporate fuzzy logic concepts.

2) Fuzzy Logic

Fuzzy logic [10] can be seen as a formulation defined by multi-valued logic. Meanwhile, the true value of a variable's formulation can be any real number between, but not limited to, 0 and 1. It is often utilized to solve the problem of uncertainty, where the truth value may not be all true or all false. As a result, fuzzy logic has been successfully applied in the field of clinical realms, including a continuous blood glucose prediction system and a tuberculosis diagnosis platform based on chest X-ray, among other devices. We can also see this in use of a video camera to help stabilize an image endoscope. Other areas such as household appliances, business decision making, and financial analysis are also examples of applications of this principle [6]. A main application of fuzzy logic is approximate reasoning. However, the methods of fuzzy logic reasoning usually lack learning abilities, which are necessary for a multitude of tasks.

3) Evolutionary Computation

Evolutionary computation (EC) is global optimization method inspired by biological evolution [6]. It is a family of algorithms and is a branch of computational intelligence and natural computing. EC systems solve problems via populations, error and success, meta-heuristics, or stochastic optimization. An initial set of candidate solutions is generated and updated iteratively, such as the removal of less-desired solutions and the insertion of noise. A population of solutions is subject to natural selection or artificial selection and mutation, and therefore evolves and adapts—i.e., increases fitness (function quantizes how adapted/desired the solution is). EC is popular in computational intelligence because it results in near-optimal solutions in a wide spectrum of contexts [11] where there are many variants and extensions for specific data structures and problems.

4) Computational Learning Theory

Computational learning theory (referred to as learning theory for short) is a sub-field of artificial intelligence mainly for the research and development of learning strategies for machine learning. Computational learning theory is one of the principal methods in computational intelligence, which seeks for a way to achieve reasoning that recapitulates human rezoning humans. In psychology, learning is the process of enhancing or changing knowledge, skills, values, and world views through cognition and experience [6]. Inspired by psychology, computational learning theory is utilized to actualize the process of experience and decision making according to previous experiences.

5) Probabilistic Methods

A probabilistic method is a nonconstructive approach used to prove the existence of specified types of mathematical objects. It operates by showing that if one randomly selects an object from a specified category, the probability that the result will

become the specified type is strictly greater than zero. Although probabilistic methods are designed based on the probability theories, the results are determined with certainty and without any possible errors. Probabilistic methods were first introduced as the main foundation of fuzzy logic by Erdos and Spencer [6]. To evaluate the outcomes of a system based on computational intelligence, probabilistic methods are mostly defined by randomness [12]. Accordingly, probabilistic methods can provide proper solutions to problems based on prior knowledge.

C. Issues on Fighting COVID-19
Based on our observations, there are several urgent issues related to COVID-19 that must be combatted. These issues can be categorized into five topics: tracking and predicting virus propagation (TPVP), characterization of symptoms of virus infections (CSVI), treatment design (TrD), precaution development (PD), and public health policy making (PHPM). The issues of each topic are listed below:
1) *Tracking and Predicting Virus Propagation (TPVP)*
   - Surveillance and tracking of COVID-19-infected patients.
   - Modeling and predicting virus propagation and pathways.
   - Visual analytics techniques and applications for propagation modeling and monitoring.
2) *Characterization of Symptoms of Virus Infections (CSVI)*
   - Discovery of early markers/symptoms of viral infections.
   - Personalized and group-based risk profiling and prediction.
   - Real-time and early alerting systems for hazardous and forefront outbreaks.
   - Fast and accurate diagnosis of COVID-19 through analytics and modeling using various biomedical data, e.g., images, vital signs, genome, etc.
3) *Treatment Design (TrD)*
   - Treatment optimization and care planning for the best care of patients.
   - Prognosis and outcome prediction for patients for effective resource allocation.
   - Drug discovery and repurposing through big data analytics approaches.
4) *Precaution Development (PD)*
   - Vaccine design through machine learning approaches.
   - Intelligent analysis of social media and networks for contact tracing and safety control.
   - Integrations of intelligent computing mechanisms with information technology systems and the internet of things (IoT) for smart care in COVID-19.
5) *Public Health Policy Making (PHPM)*
   - Secure and privacy-preserving analysis of data in public health emergencies.
   - Public health policy making through big data analytics and model simulations.

To overcome these issues, researchers are actively conducting research to obtain various outcomes, and many have adopted computational intelligence. Since there are so many studies that address the issues associated with COVID-19, this survey focuses on studies designed using computational intelligence were selected for discussion in the following sections.

III. Neural Networks for Combating COVID-19
As mentioned earlier, an artificial neural network applies the principle of deep learning and achieves a high level of representation learning. Representation learning is a learning method that can automatically learn representations from data. Learning algorithms do not require humans to help them extract features. Accordingly, neural networks can be easily utilized for extracting important representations of virus propagation and the characteristic symptoms of a viral infection, among other factors. However, deep neural networks can extract useful knowledge mostly if the amount of data is sufficient, which means they can hardly deal effectively with incompleteness or, most importantly, data with missing values in the processing model. Fortunately, many countries have established a series of COVID-19 data collection mechanisms. As a result, building an effective deep neural network to fight COVID-19 is possible. For example, many researchers have built deep neural network models for characterizing viral infections by using CT chest images, as shown in Fig. 1, or X-ray images [23], [24]. Table I summarizes the issues that have been addressed by existing neural network methods. Owing to their excellent ability to extract important representations, most applications involving neural networks have addressed the issue of CSVI, as shown in Table I.

Roy *et al.* [14] proposed the application of artificial neural networks for analyzing lung ultrasonography (LUS) images.
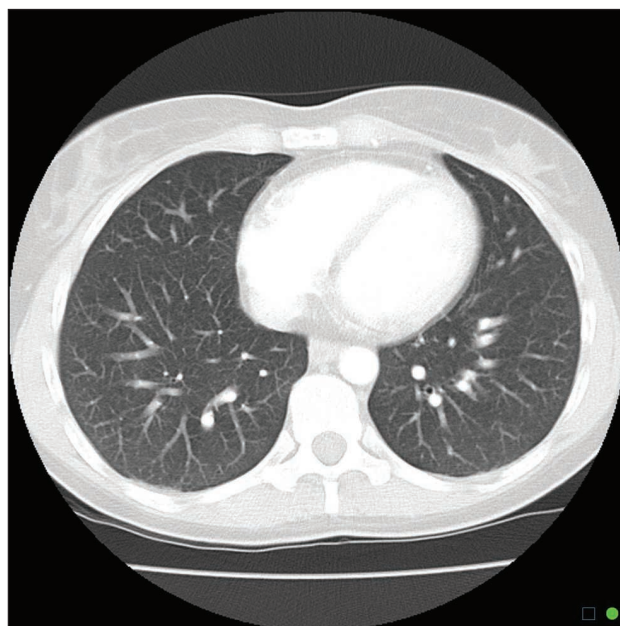

FIGURE 1 Example of computed tomography (CT) image [13].

They collected a new fully-annotated LUS image dataset from several hospitals in Italy, and the labels indicate the severity of the disease at the frame, video, and pixel levels (segmentation masks). Using these data, several artificial neural network models have been developed to solve the tasks related to the automatic analysis of LUS images. To predict the severity of the disease associated with an input frame, an extension of spatial transformer networks was proposed, which can provide localization of the diseased area in a weakly supervised manner. To conduct scoring at the video level, an effective frame score aggregation function was proposed, and three artificial neural networks, vanilla U–Net [25], U–Net++ [26], and Deeplabv3+ [27], have been adopted for the segmentation of COVID-19 imaging biomarkers at the pixel level.

Wang et al. [15] proposed a CNN-based model, COVID-Net, for detecting COVID-19 infected patients from a dataset of chest radiography images. The dataset is an open dataset consisting of 13,800 images collected from 13,725 patients. COVID-Net utilizes a novel lightweight residual block, the projection-expansion-projection-extension (PEPX), to improve representational capacity while maintaining reduced computational complexity. Furthermore, COVID-Net is designed to make predictions using a qualitative analysis method called GSInquire, to obtain deeper insight into crucial features related to COVID-19 infected patients, which can assist clinicians in efficient and precise diagnosis.

Han et al. [16] presented an attention scheme involving deep 3D multiple instance learning called AD3D-MIL to learn a detection model from 3D chest CTs. With the attention scheme AD3D-MIL, not only can it accurately predict an individual category of disease such as COVID-19, common pneumonia, or no pneumonia, but it also produces interpretability of results. During the learning process, users will not receive a set of labeled instances, but each bag contains many instances,

and each bag has a label rather than separately labeled sets of instances. The idea behind AD3D-MIL is to treat all CT images of an individual patient as the instances of a labeled bag. Meanwhile, a fully 3D convolutional neural network is used to produce the feature map of each instance, and an attention-based MIL pooling is designed to select and combine the feature maps into a bag representation. Finally, the bag representation is fed into a typical fully-connected neural network to make the final predictions.

Panwar et al. [17] developed a deep learning-based COVID-19 detection model that can detect a COVID-19 positive patient within 5 seconds using X-ray images. The proposed model extends VGG-16 by adding five custom layers as the head layers, of which the first layer is an average pooling 2D layer. Unlike max pooling, this average pooling layer uses the average value of all the pixels with a pool size of (4, 4) to down-sample the images. The second layer is a flattened layer that transforms a two-dimensional tensor into a vector as an input of a fully dense connected layer (i.e., the third layer). Meanwhile, the activation function of the fully dense connected layer is ReLU. The fourth layer is a dropout layer that ignores half of the units of the fully dense connected layer. The fifth layer is the output layer, which uses two units to produce the confidence values for the infected and uninfected, respectively. Based on a pre-trained VGG-16 with the five layers added, the proposed model was able to achieve a 97.62% true-positive rate with a limited amount of data, consisting of 142 images of uninfected and 192 images of infected people.

The training of neural networks with limited training sample sizes is key to applying deep learning to address the issues regarding COVID-19. To deal with the limited data size, Oh et al. [18] developed a neural network for COVID-19 diagnosis that is suitable for training with limited X-ray images. An extended fully convolutional neural network called (FC)-DenseNet103 [28] was adopted for lung image segmentation. The results of the lung image segmentation from the segmentation networks are utilized for masking the pre-processed images. To classify the masked images, ResNet–18 [29] was adopted to build a classification model. Meanwhile, the classification model was implemented with two different contexts: global appearance and zooming in a partial area. To consider the view of global appearance, each masked image is resized to 224×224 so that each input is a complete X-ray image. Oh et al. utilized this approach as a baseline network for experimental evaluation. To consider zooming in a partial area of an X-ray image, each masked image is cropped randomly to produce several 224×224 images so that a masked image may produce several input images. Although the overall accuracy of this approach is 91.9%, slightly lower than that of COVID-Net [15] (92.4%), the model size of this approach (11.6 M parameters) is much smaller than that of COVID-Net (116.6 M parameters). In other words, this approach requires much less data to train the model.

Apostolopoulos et al. [19] examined the significance of the extracted features and utilized MobileNet V2 [30] to train a

TABLE I Issues addressed by existing neural network methods.

	TPVP	CSVI	TRD	PD	PHPM
ROY ET AL.'S STUDY [14]		✓			
COVID-NET [15]		✓			
HAN ET AL.'S STUDY [16]		✓			
PANWAR ET AL.'S STUDY [17]		✓			
OH ET AL.'S STUDY [18]		✓			
APOSTOLOPOULOS ET AL.'S STUDY [19]		✓			
WANG ET AL.'S STUDY [20]		✓			
AYYOUBZADEH ET AL.'S STUDY [21]	✓		✓		
VAID ET AL.'S STUDY [22]		✓			

classification model using 3,905 X-ray images for classification of six similar diseases, including COVID-19. As the symptoms shown in the X-ray images of the five diseases are very similar to those of COVID-19, the idea behind the training scheme is to use similar cases to extract reliable features. The proposed model, trained based on MobileNet V2, achieved 99.18% accuracy in detection of COVID-19, but the overall accuracy of the seven classes, including six diseases and one normal group, was about 88%. This phenomenon may suggest that vital biomarkers of COVID-19 can be brought to light by using the proposed model trained on MobileNet V2.

In addition to building a deep neural network model for characterizing viral infections using CT or X-ray images, Wang *et al.* [20] developed a deep learning system to fully automatically diagnose and prognose COVID-19. This system consists of three parts: 1) automatic lung segmentation, 2) non-lung area suppression, and 3) COVID-19 diagnostic and prognostic analysis. For automatic lung segmentation, DenseNet121 [31] was developed and combined with feature pyramid networks (FPN) [32] to produce a lung-ROI, which contains the whole lung and all inflammatory tissues and eliminates most areas outside the lung. Therefore, the lung-ROI would contain some non-lung tissues. A non-lung area suppression operation was proposed to decrease the luminance of non-lung areas inside the lung-ROI. Finally, a novel neural network called COVID-19-Net was proposed for diagnostic and prognostic analyses.

Google Trends has previously been used to accurately predict the outbreak of a new flu. Ayyoubzadeh *et al.* [21] imitated Google Trend's method of analysis for the prediction of incidence of COVID-19 in Iran. Two types of machine learning methods, i.e., linear regression and a recurrent neural network with long short-term memory (LSTM), were adopted to build the prediction model. The effectiveness of the linear regression model achieved 7.562 ± 6.492 in terms of RMSE, while the model utilizes factors such as previous day incidence, hand sanitizer, antiseptic topics, and the frequency of searches for handwashing. The effectiveness of the LSTM model only reached only 28.487 ± 20.705 in terms of RMSE. In addition, the LSTM model showed a fluctuating performance and a low training loss, which might have been caused by overfitting. The reason why a linear regression outperforms an LSTM might be that the data size of the daily incidence of COVID-19 in Iran is quite small, whereas the capacity of the deep learning model, such as the LSTM, is too high for such limited data. Therefore, the LSTM model overfits the limited number of training data easily.

To overcome the problem of a limited amount of training data, Vaid *et al.* [22] developed a transfer learning approach to build a deep learning model by transferring pre-trained CNNs. Structural abnormalities are key to uncover hidden patterns. Based on the transfer learning approach, a pre-trained detection model from anterior-posterior radiographs of the chest of patients was transferred to detect structural abnormalities and disease categorization. Publicly available datasets consisting of patient information from multiple countries were used to refine the pre-trained model and improve the accuracy. The experimental results showed an extremely high accuracy, of 96.3%, and a low loss, of 0.151, in terms of binary cross-entropy. Meanwhile, the proposed model was able to accurately identify 74 true negatives and 32 true positives while incorrectly identifying three false-positives and one false-negative.

According to the papers we surveyed in this section, several insightful findings can be gleaned:

1) Most existing studies on neural networks have focused on dealing with the problem of characterization of symptoms of virus infections. The primary reason for this might be that many LUS images have been produced and collected, and many pre-trained CNNs can be retrieved from open sources. Accordingly, many works straightforwardly utilized pre-trained CNNs to extract vital biomarkers of COVID-19 from LUS images. The variants of neural networks are numerous and varied, which can be utilized for addressing various issues. For example, recurrent neural network (RNN) and its variants are suitable for time series analysis. As more and more patients are cured, many treatment records will be produced. Such treatment records could be viewed as a set of time series data. Therefore, we believe a hybrid model that combines the aforementioned CNN-based works with RNN-based mechanisms is a promising research direction to address the issues on treatment design (TrD).

2) Since datasets are very limited, using a pretrained model is a promising way to quickly produce accurate results. Panwar *et al.* [17] achieved the highest performance using this approach (97.62% true-positive rate). However, using pretrained CNNs for the extraction of vital biomarkers of COVID-19 usually requires labeled LUS images, and this motivates [18], [19] to consider building a lightweight model from small datasets. However, the design for a lightweight model may limit the applicability of these existing works: they may be effective for only a small group of patients who have the same symptoms as shown in the training images.

3) More and more countries have been utilizing the IoT technologies for smart care in COVID-19. Massive data collected from the IoT devices may benefit the effectiveness and applicability of the artificial neural network model. Based on the data collected from IoT devices, integrations of intelligent computing mechanisms with these existing works, such as Ayyoubzadeh *et al.*'s study [21], may be applied to address the issue on precaution development (PD) and the prediction of virus propagation.

IV. Fuzzy Logic for Combating COVID-19

Fuzzy logic is one of the main principles of computational intelligence and enables measurements and process modeling for complex processes in real life. Unlike artificial intelligence, which requires precise knowledge, fuzzy logic may be used with incomplete and even incorrect data applied in a process model. That is, fuzzy logic can easily be used for an

uncertainty-based analysis of limited data. Most of the issues in the fight against COVID-19 can be inherently dealt with using fuzzy logic. For example, when characterizing viral infections, we can find that different patients may have different symptoms, which makes COVID-19 difficult to be diagnosed without virus testing. Table II shows the issues addressed by existing fuzzy logic methods.

Dhiman and Sharma [33] utilized six input factors to build a fuzzy inference system to diagnose COVID-19. By using the proposed fuzzy inference system, the severity level of the infected patients can be presented with three linguistic categories: low, medium, and high. Through a series of training and optimizations, the model learned the following three fuzzy rules:

1) When the atmospheric temperature is medium, if a patient takes a high volume of ethanol and has a slight body temperature, the patient may have a medium severity level.
2) When the atmospheric temperature is low, if a patient takes a low volume of ethanol, has a medium body temperature and suffers from a cough, then the patient may have a low severity level.
3) If a patient takes a low volume of ethanol and has high breath shortness and a sneezing problem, then the patient may have high severity level.

We can see that these rules are reasonable, and thus the proposed inference system can be utilized to accelerate the preliminary diagnosis of COVID-19-infected patients.

The transfusion of blood plasma of recovered COVID-19 patients has been recognized as one possible treatment method. The development of a donation system that can distinguish whether donors have undergone COVID-19 infection is extremely important. However, some infected people have no symptoms, and performing mass testing on all donors is unrealistic. Nazarov [34] used statistical data to construct a fuzzy model to evaluate the quality of blood from donor systems in the Sverdlovsk region in Russia. The evaluation of factors reflects not only the number of donors who have experienced COVID-19 but also the general statistics of donation based on region, age, gender, regularity of blood donation, and the number of donors per 1000 people. The system uses 12 input variables to estimate three output variables according to three rule

blocks. By doing so, the problem of evaluating the quality of blood from donor systems in each region can be solved.

Tinh [35] utilized a fuzzy time series model combined with particle swarm optimization to forecast the trend in the number of confirmed cases of COVID-19 in Vietnam. Unlike a conventional fuzzy logic model, the proposed fuzzy model uses fuzzy relationship groups, instead of a fuzzy relationship matrix, in the building of the fuzzy forecasting model. To learn the fuzzy rules for constructing fuzzy logical relationship groups, a particle swarm optimization algorithm was designed to determine the proper number of intervals and to refine the length of each interval. The basic idea behind fuzzy logical relationship groups is that the fuzzy logical relationships, which have the same precedence, can be grouped together into a fuzzy logical relationship group. This approach can deal with the problem of time-series forecasting based on limited data. Accordingly, the best performance achieved 2.85% MAPE based on setting a fifth-order fuzzy time series with an interval number of 16.

Yang et al. [36] defined the new form of a spherical normal fuzzy set (SpNoFS) that could be used to generate operational rules. Based on the operational rules, a decision support algorithm was designed for optimization of antivirus mask selection. Owing to the complementary use of the Bonferroni mean operator, the new information aggregation operators that can evaluate the utility of antivirus mask selection were formed via the operational rules of SpNoFS. Since the Bonferroni mean operator has two types (Bonferroni mean and weighted Bonferroni mean), there are two kinds of aggregating operators. One is the operator formed by the spherical normal fuzzy rules using the Bonferroni mean (SpNoFBM), and the other is the operator formed by the spherical normal fuzzy rules made using the weighted Bonferroni mean (SpNoFGBM). Based on the SpNoFBM and SpNoFGBM operators, a multi-criteria decision-making method can be realized to reasonably select suitable antivirus masks during the COVID-19 pandemic.

Ren et al. [37] adopted the Dempster–Shafer theory to design a multi-criterion decision-making method and the concept of generalized Z-numbers to select medicine for patients with mild symptoms of COVID-19. Meanwhile, the idea behind the medicine selection based on generalized Z-numbers was extended with the expression of human habits, inspired by the concept of a hesitant fuzzy linguistic term set. To avoid ambiguity in the expression form of the generalized Z-numbers, the identification framework in the Dempster–Shafer theory was employed to describe the expression form of generalized Z-numbers. For medicine selection, the basic probability assignment of the evidence could be derived by the expression form of the generalized Z-numbers, and all evaluations of each delivered medicine could be integrated by using the synthetic rules in the Dempster–Shafer theory.

Several insightful findings have been gleaned from the papers surveyed in this section:

1) Fuzzy logic is good at reasoning by analyzing uncertainty from limited data. Therefore, we can see that most kinds of issues we mentioned have been addressed by the fuzzy

TABLE II Issues addressed by existing fuzzy logic methods.

	TPVP	CSVI	TRD	PD	PHPM
DHIMAN AND SHARMA'S STUDY [33]		✓			
NAZAROV'S STUDY [34]	✓		✓		
TINH'S STUDY [35]	✓				
YANG ET AL.'S STUDY [36]					✓
REN ET AL.'S STUDY [37]			✓		

logic models we surveyed. This may imply that we can combine fuzzy logic and neural networks so that the hybrid system can be applied for almost all issues relevant to COVID-19.

2) Since the main advantage of the fuzzy logic methods is to produce fuzzy rules that can deal with the uncertainty from limited data, the findings from fuzzy rules are expected to be shown in the literature. However, most relevant existing works [35]–[37] did not provide such discussions. One relevant work [34] only briefly introduced the fuzzy rules without deep discussion. This has led to the low applicability of these works. This is noteworthy for future studies on fuzzy logic.

V. Evolutionary Computation for Combating COVID-19

Evolutionary computation initially creates a set of candidate solutions and refines the set iteratively. The set of candidate solutions at each iteration is called the population. By stochastically removing the less-desired solutions and putting small random changes in the current generation, the next generation is produced. In biological terms, a set of solutions undergoes natural selection (or manual selection) and mutation. As a result, the population incrementally increases in fitness. The fitness function of the algorithm determines the goal of learning. Evolutionary computation techniques can produce highly optimized solutions for various problems. Many variants and extensions have been designed for group-based risk profiling, and they are suitable for analysis of the possible impacts of COVID-19 and forecasting how COVID-19 will behave in the future. Table III shows the issues addressed by existing evolutionary computation methods.

Yousefpour *et al.* [38] combined Susceptible, Exposed, Infectious, and Recovered (SEIR) [43] with a multi-objective genetic algorithm that focuses on epidemic prevention and economic concerns to estimate the early transmission dynamics of COVID-19. Besides, Yousefpour *et al.* utilized the estimation results to find the best decision rules. Two cost functions were designed and involved in the multi-objective genetic algorithm. The first cost function represents epidemic prevention:

$$J_1 = \sum E(t) + A(t), \tag{1}$$

where $E(t)$ indicates the number of exposed people at time t, and $A(t)$ indicates the number of asymptomatic infected people at time t. The second cost function represents economic concerns:

$$J_2 = -\eta_1(c_0 + c_f) + \eta_2 q, \tag{2}$$

where c_0 denotes the contact rate at the initial time, c_f denotes the minimum contact rate under the current control strategies, and q denotes the quarantined rate of exposed individuals. Based on [38], the optimal policies were designed and showed that treating infection control as an optimization

problem can protect countries against both disease outbreaks and economic breakdown.

Niazkar *et al.* [39] adopted the multi-gene genetic programming (MGGP) to predict COVID-19 outbreaks. Since the numbers of daily confirmed cases fluctuate, predicting a COVID-19 outbreak is a challenging task. MGGP was originally designed for behavioral modeling, which is suitable for modeling series with high fluctuations. The proposed method based on MGGP showed very promising results. More specifically, the predicted number of confirmed cases of COVID-19 approximated the observations in the seven countries considered in their study. Therefore, the MGGP-based approach has been suggested to be appropriate for the estimation of COVID-19 outbreaks.

Salgotra *et al.* [40] proposed a prediction model by developing genetic programming (GP) which analyzes the possible impact of COVID-19 in India and predicts the future behavior. The developed GP predicted the number of confirmed cases and numbers of death cases in the three most affected states in India. The fitness function was designed with respect to the mean squared error. To validate the evolved models, statistical parameters and metrics were used to evaluate the fitness. Furthermore, the proposed GP-based models were lined with each other by using simple linkage functions for gene size greater than 1. The experimental results showed that the proposed GP-based models are significantly reliable for predicting the numbers of confirmed and death cases in India.

To expand the contributions of GP for predicting the possible impact of COVID-19 in India, Salgotra *et al.* [41] further applied their GP to build a prediction model for forecasting the potential effects of COVID-19 in the 15 most affected countries in the world. The prediction model estimated that the daily confirmed cases and daily death count would result in a negative value in China. Besides the results in China, the overall prediction results are listed in Table IV. We can find that Brazil had the highest daily increase in the COVID-19 reproduction rate. This prediction was made at the end of May, and Brazil's situation did fall into its worst in June. This indirectly proves the applicability of Salgotra *et al.*'s study.

TABLE III Issues addressed by existing evolutionary computation methods.

	TPVP	CSVI	TRD	PD	PHPM
YOUSEFPOUR *ET AL.'*S STUDY [38]	✓				✓
NIAZKAR *ET AL.'*S STUDY [39]	✓			✓	
SALGOTRA *ET AL.'*S STUDY [40]	✓			✓	
SALGOTRA *ET AL.'*S STUDY [41] (EXTENSION OF [40])	✓			✓	
DILBAG *ET AL.'*S STUDY [42]		✓			

Dilbag *et al.* [42] proposed a multi-objective differential evolution algorithm to optimize the hyperparameters of the regular CNN that was trained from CT images for classification of COVID-19-infected patients. A multi-objective fitness function was designed according to both the sensitivity and specificity of classifications of COVID-19-infected patients. According to Dilbag *et al.*'s experiments, the proposed model slightly outperformed state-of-the-art models, such as a regular CNNs, an adaptive neuro-fuzzy inference system, and an artificial neural network. The overall improvement in terms of accuracy was 1.9789%.

According to the papers we surveyed in this section, several insightful observations can be made:

1) Since evolutionary computation was designed for the optimization of parameters, we can see that most works, like [38]–[40], utilize evolutionary computation to predict virus propagation. Meanwhile, some of these works [38], [39] adopted the concept of multi-objective genetic algorithm to estimate the number of confirmed cases and tackle other properties such as economic concerns. The prediction results can also address other issues such as precaution development.

2) Although multi-objective genetic algorithm could be utilized for solving multi-objective problems, the works [37], [38] only adopted them straightforwardly without any modifications. Since the application scenarios of the works of [37], [38] are different from that of multi-objective genetic algorithms, their effectiveness is not significant in supporting their reliability and applicability. We believe these works could be further improved. For example, the interaction among the multiple fitness functions could be included to adjust for the process of optimization.

VI. Computational Learning Theory for Combating COVID-19

Computational learning theory has many implementations. Based on different assumptions, various inference principles can be deduced. As a result, the deduced inference principles are utilized to design different computational learning theory approaches. These approaches can usually be categorized into six types: 1) exact learning; 2) probably approximately correct learning, which is a machine learning framework based on mathematical analysis; 3) Vapnik–Chervonenkis theory, which is a learning process explained by a statistical point of view; 4) Bayesian inference, which is a statistical inference based on Bayes' theorem; 5) algorithmic learning theory, which is a machine learning theory explained by an algorithmic point of view; and 6) online machine learning, which is a sort of machine learning method for continuously updating data. Although its primary goal is to understand learning in an abstract manner, through the development of learning theory, we can design various practical learning algorithms. For example, Bayesian inference is the foundation of the concept of belief networks. Because the concept of belief networks is the foundation of the deep neural networks introduced in the previous section, we will introduce the remaining approaches in this section, which are designed based on belief networks except deep neural networks. Table V shows the issues that have been addressed by existing computational learning theory methods.

Duffey and Zio [44] proposed a computational learning theory that can learn a prediction model from the prediction errors in the recovery time from the outbreak of the COVID-19 pandemic. This approach uses the exponential Universal Learning Curve to estimate the trend in the infection rates of the COVID-19 pandemic. The key to the proposed approach is to treat the infection rate as a measure of false prediction results and time as a measure of experience/knowledge or risk exposure to allow learning. The results of Universal Learning Curve, which was learned from China, South Korea, and other nations, show a decreasing trajectory after a peak. The reason might be that countermeasures are effective for controlling the spread of the virus.

Wang *et al.* [45] proposed a novel noise-robust learning framework called COPLE-Net based on the self-ensemble of convolutional neural networks [50], [51], a sort of semi-supervised learning mechanism. Unlike conventional semi-supervised learning mechanisms that use the exponential moving average of a model to adjust standard model, Wang *et al.* [45] developed two designs to address the issue on noisy labels. The first design is a dynamic adjustment that can reduce the impact of the exponential moving average of a model while the training loss is decreased. The second is an adaptive learner that enables the standard model to learn from the exponential moving average of a model. The proposed COPLE-Net outperforms state-of-the-art models in terms of the average Dice similarity (80.29%) and the average 95-th percentile of Hausdroff distance (18.72 mm).

Barstugan *et al.* [46] presented an early phase detection method for COVID-19 using a support vector machine classifier. The classifier was trained from four extensive datasets, which were produced by fetching patches with sizes of 16 × 16, 32 × 32, 48 × 48,

TABLE IV Prediction results of Salgotra *et al.*'s study [41].

COUNTRY	DAILY CONFIRMED CASES	DAILY DEATH COUNT	COUNTRY	DAILY CONFIRMED CASES	DAILY DEATH COUNT
USA	20,972	1358	TURKEY	1,071	17
BRAZIL	28,822	1076	CANADA	717	103
RUSSIA	6,928	270	SPAIN	321	148
MEXICO	4,121	466	GERMANY	271	23
UK	3,759	204	ITALY	247	178
IRAN	1,652	57	FRANCE	191	50
SOUTH AFRICA	1,895	60	SINGAPORE	68	0.05

and 64 × 64 from 150 CT images. To increase the classification performance, the feature extraction process was performed on each patch. Five computational learning theory algorithms were adopted and utilized as feature extraction methods: a gray level co–occurrence matrix (GLCM), a gray level run length matrix (GLRLM), a local directional pattern (LDP), a discrete wavelet transform (DWT), and a gray-level size zone matrix (GLSZM). To avoid an overfitting problem, k-fold cross validation was performed during training. With GLSZM and 10-fold cross-validation, the classifier achieved the best accuracy (99.68%).

Randhawa *et al.* [47] proposed a method of using computational learning theory for genome analyses. This method combines decision trees with digital signal processing to construct a model for classification of the COVID-19 virus sequences and can identify intrinsic viral genomic signatures. To validate the results of identifications, Spearman's rank correlation coefficient analysis was adopted. The proposed method can be used to analyze large datasets containing more than 5,000 unique viral genomic sequences. In this dataset, there are 29 COVID-19 viral sequences, implying an imbalanced data issue (29: 5000). The proposed method achieved a 100% accuracy. Furthermore, the proposed method uses only raw DNA sequence data to discover the most relevant relationships between more than 5,000 viral genomes within minutes from scratch. This shows that, for new viral and pathogen genome sequences, unmatched genome-wide machine learning methods can provide reliable real-time courses of action for taxonomic classification.

Mei *et al.* [48] developed an ensemble model to identify COVID-19 infections, which can allow early identification of COVID-19 patients at an early stage based on the initial chest CT scans and related clinical information. This model combines a deep convolutional neural network with three classifiers: random forest, support vector machine, and multilayer perceptron. The deep convolutional neural network is utilized for imaging the characteristics of COVID-19 patients, and the three classifiers form an ensemble model to classify COVID-19 patients based on extracted characteristics of COVID-19 and other clinical information. This ensemble model showed significant performance in terms of sensitivity (84.3%), specificity (82.8%), and AUC (0.92).

Apostolopoulos *et al.* [49] extended their previous work [19] by using transfer learning to train deep CNNs since there are many pre-trained models that can be retrieved from open sources, such as VGG-19 [52], MobileNets V2 [30], Inception V4 [53], and Xception [54]. Unlike their previous work [19], which straightforwardly utilized MobileNets V2 to build an image recognition model for classifying COVID-19 patients, Apostolopoulos *et al.* [49] applied transfer learning on the pre-trained models and used a dataset that consists of 224 chest CT images of patients with COVID-19, 700 chest CT images of confirmed common bacterial pneumonia, and 504 chest CT images of no diseases to fine-tune the pre-trained models.

Based on the papers surveyed in this section, some insightful findings can be made:

1) Although deep learning has become the most popular notion recently, some classical computational learning theory approaches, such as support vector machine, random forest, and decision tree, could still be useful while the amount of data is limited. The studies [46]–[48] reveal that the shallow learning method can be utilized as an initial model for building a classification model to distinguish COVID-19 patients.

2) With a bigger dataset, the concept of model ensembles can be used to combine initial models with some deep learning methods. The work in [45] and [47] provides possible solutions for model ensembles. Besides model ensemble, the concept of domain adaptation is a possible solution to combine two models. The transfer learning techniques utilized in Apostolopoulos *et al.*'s study [48] are also a possible solution.

VII. Probabilistic Methods for Combating COVID-19
In computational intelligence, a probabilistic method is applied by calculating the expected value of a random variable. The probabilistic method is typically used for analysis of the risk factors correlated with COVID-19 and explains why they are crucial. Table VI shows the issues that have been addressed by probabilistic methods.

Cássaro and Pires [55] assume that the number of infected patients grows exponentially over the time. As a result, the probabilistic model can be formulated as

$$I(t) = I(t_0)e^{rt}, \tag{3}$$

TABLE V Issues addressed by existing computational learning theory methods.

	TPVP	CSVI	TRD	PD	PHPM
DUFFEY AND ZIO'S STUDY [44]	✓				
WANG *ET AL*.'S STUDY [45]		✓			
BARSTUGAN *ET AL*.'S STUDY [46]		✓		✓	
RANDHAWA *ET AL*.'S STUDY [47]		✓			
MEI *ET AL*.'S STUDY [48]		✓			
APOSTOLOPOULOS *ET AL*.'S STUDY [49]		✓			

TABLE VI Issues addressed by existing probabilistic methods.

	TPVP	CSVI	TRD	PD	PHPM
CÁSSARO AND PIRES'S STUDY [55]	✓				
ZHANG *ET AL*.'S STUDY [57]	✓				
KUCHARSKI *ET AL*.'S STUDY [56]	✓				

where $I(t)$ is the number of diagnosed infections over time, t_0 is initial time, and r is the growth rate, which can be determined through learning from the time-series data of diagnosed infections by minimizing the mean absolute error. Cássaro and Pires [55] utilized the time-series data of diagnosed infections collected from eight countries (Greece, Italy, Spain, Germany, France, Netherlands, the UK, and the USA) to learn the growth rate, r. The prediction results show that the exponential model can accurately predict the number of confirmed cases within 14 days when the first infection is observed; however, it is unable to make long-term predictions.

Zhang et al. [57] proposed a logistic growth probabilistic model that considers both the power law and the exponential law to estimate the number of infected patients. Unlike the exponential model that can only deal with the estimation of uncontrolled prevalence, the logistic growth probabilistic model is initially approximated to the exponential law, but the upper bound of the model is set and used to reduce the growth rate. Accordingly, the logistic growth probabilistic model is formulated as

$$I(t) = \frac{N}{1 + e^{b - c(t - t_0)}},\qquad(4)$$

where $I(t)$ is the number of diagnosed infections over time, N is the predicted upper bound, b and c are the fitting coefficients that can be learned from the dataset, and t_0 is the time when the first infection is observed. The prediction results show that the logistic growth probabilistic model can make long-term predictions that have a low prediction error within 3 months.

Kucharski et al. [56] designed a stochastic transmission dynamic model to estimate the variation in transmission over time during January and February of 2020. A dataset that consists of the COVID-19 population in or from Wuhan was collected. The transmission was modelled as a geometric random walk. Based on the proposed stochastic transmission dynamic

model, the probability of outbreak in other areas was estimated. To train the proposed stochastic transmission dynamic model, the model was fitted into four publicly available datasets: 1) daily numbers of new global confirmed cases beginning January 26, 2020; 2) daily numbers of new confirmed cases in Wuhan between December 1, 2019 and January 1, 2020; 3) daily numbers of new confirmed cases in China between December 29, 2019, and January 23, 2020; and 4) proportions of confirmed cases on evacuation flights between January 29, 2020 and February 4, 2020.

VIII. Real-World Systems and Tools Using Computational Intelligence for Combating COVID-19

Many industries and nonprofit organizations have been utilizing computational intelligence to develop systems or tools for combating COVID-19. According to the report published by the Organization for Economic Co-operation and Development (OECD) [58], these real-world systems and tools for combating COVID-19 can be utilized to support decision makers, the medical community, and society to manage every stage of the COVID-19 crisis; these stages consist of detection, prevention, response, and recovery. Based on the OECD's report, several AI-powered tools, including BlueDot [59], EpiRisk [60], CRUZR robot [61], Canada's COVID-19 chatbot [62] and Satellites Monitor [63], can be used for combating COVID-19. However, the details of these systems and tools were not stated in the report or other relevant literature. In fact, their results are still worth introducing and promoting to the community of computational intelligence. Instead of introducing how they work, in this section, we focus on what they have done.

BlueDot [59] is a software that evaluates the outbreak risk of infectious diseases caused by over 150 different pathogens, toxins, and syndromes. In fact, COVID-19 is the most crucial disease whose outbreak risk is detected by BlueDot. The main technique behind BlueDot is a crawler that can scan over 100,000 official and mass media sources in 65 languages per day. Based on the data crawled, natural language processing and text mining are applied to extract important information for the evaluation of outbreak risk of infectious diseases. Although BlueDot is recognized by the OECD's report to support decision makers at the detection stage, it provides a user-centric view that can also be utilized to calculate an individual's probability of infection (i.e., issues at the prevention stage). Unlike BlueDot, EpiRisk [60] is a web-based application that calculates an individual's probability of infection based on a topology structure of airline transportation networks. Since the data source of EpiRisk is quite narrow and might miss some crucial data, the evaluation results are doubtful, even if it is very convenient to use. For example, as shown in Fig. 2, EpiRisk shows that the probability of infection in Taipei is higher than 45%, which is completely untrue, with zero new confirmed domestic cases over the past 80 days in Taiwan.

When the outbreak began, how to effectively isolate infection was a key issue. The operating site might be divided into
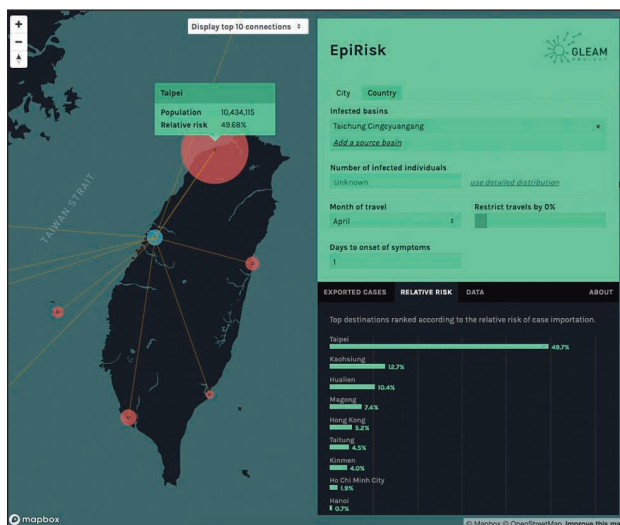

FIGURE 2 A snapshot of EpiRisk.

two parts: hospital and home. To isolate suspected infections in hospitals, many hospitals have been utilizing robots to serve patients that arrive. For example, at Antwerp University Hospital, Cruzr Health [61] takes patients' body temperatures and checks whether they are wearing masks when patients arrive. If the patients are wearing masks and their body temperatures are within the normal range, Cruzr Health leads them to their appointment. To take care of home isolation, Canada developed a chatbot [62] that provides information for home isolation and reminders for those who are suspected to be infected. As shown in Fig. 3, we can see that the chatbot provides information on COVID-19 symptoms at users' requests.

At the end of the pandemic, the most important task for every country would be economic recovery. However, the timing of enforcing policies for economic recovery is a difficult problem. Researchers at WeBank [64], a private Chinese neobank, collected data from satellites, GPS, and social media to detect the hot spots of actual steel manufacturing inside the factories in China [63]. They believe that the detection results may reflect economic recovery in China. Although this system was built for internal use, the data from satellites, GPS, and social media can be crawled easily, implying that computational intelligence researchers can build a model according to this concept.

IX. Conclusions

In this survey, we reviewed several critical issues on combating COVID-19 that have been or can be resolved using computational intelligence techniques. Computational intelligence is classified into five different principles: neural networks, fuzzy logic, evolutionary computation, computational learning theory, and probabilistic methods. Our survey found that most research studies have been designed based on neural networks for addressing the issues on characterization of the symptoms of viral infections. Meanwhile, Panwar *et al.* [16]'s method achieved the highest performance (97.62% true–positive rate), which means that using deep neural networks to detect symp-

toms from CT images is well-developed, and we may devote our efforts to other issues.

Theoretically, all issues we listed in Section II can be solved by at least one of the principles of computational intelligence. Unfortunately, based on our survey, many COVID-19 pandemic issues have not yet been addressed in computational intelligence studies. On the contrary, most reported studies have focused only on specific issues, such as the characterization of the symptoms of viral infection. This may be because computational intelligence is a data-driven technique that can work well mostly when the amount of data is sufficient. Currently, the data that we can most easily crawl is chest CT images. Therefore, existing works have focused on discovering the characteristics of COVID-19 patients based on their chest CT images to build classification models. As more and more patients are cured, many treatment records will be produced. Such treatment records could be viewed as a set of time series data. Many computational intelligence techniques could be then applied to analyze treatment records. To address the issues on TrD and PD, future works can combine time-series analysis mechanisms with previous works. For example, if we obtain COVID-19 patients' CT images for each stage, the characteristics at each stage can be modeled and utilized for treatment design.

Finally, we observe that some existing works, such as [42], [46]–[48], utilized more than two principles to design hybrid models that can balance the strengths and weaknesses of two principles so that the applicability of these works could be improved. For example, evolutionary computation could be used to optimize the hyperparameters of deep learning models so that some deep learning models might be built from limited data. We believe, in the near future, the computational intelligence community will invent new algorithms by combining multiple principles to address the critical issues described in this survey using limited data or under strict conditions, such as visual analytics techniques and applications for propagation modeling and monitoring, vaccine design or drug repositioning, as well as IoT for smart care in COVID-19.

Acknowledgment

FIGURE 3 A snapshot of Canada's COVID-19 chatbot.

References
[1] F.S. Lu et al., "Accurate influenza monitoring and forecasting using novel internet data streams: A case study in the Boston metropolis," *JMIR Public Health Surveill.*, vol. 4, no. 1, p. e4, 2018. doi: 10.2196/publichealth.8950.
[2] S. Jang, S. Lee, S.M. Choi, J. Seo, H. Choi, and T. Yoon, "Comparison between SARS CoV and MERS CoV using Apriori algorithm, decision tree, SVM," in *Proc. MATEC Web Conf.*, 2016, vol. 49, p. 08001. doi: 10.1051/matecconf/20164908001.
[3] D. Kim, S. Hong, S. Choi and T. Yoon, "Analysis of transmission route of MERS coronavirus using decision tree and Apriori algorithm," in *Proc. 18th Int. Conf. Advanced Communication Technology (ICACT)*, Pyeongchang, 2016, pp. 559–565.
[4] "COVID-19 Open Research Dataset Challenge (CORD-19)." Accessed: Aug. 3, 2020. [Online]. Available: https://www.kaggle.com/allen-institute-for-ai/CORD-19-research-challenge
[5] J. C. Bezdek, "What is computational intelligence?" in *Computational Intelligence: Imitating Life*, J. Zurada, R. Marks, and C. Robinson, Eds. Piscataway, NJ: IEEE Press, 1994, pp. 1–12.
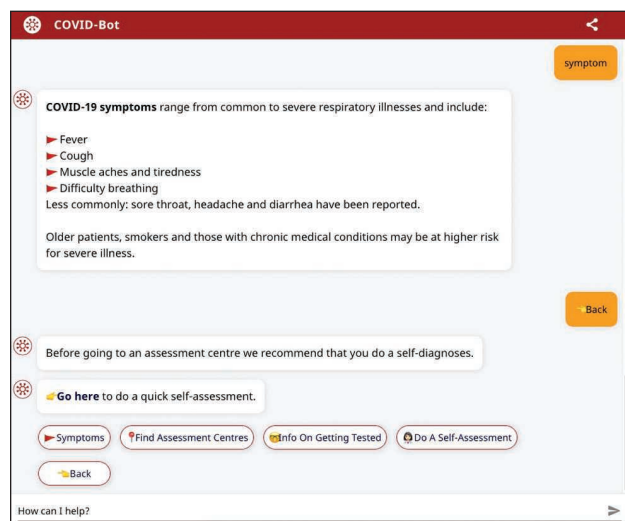
[6] N. Siddique, H. Adeli, *Computational Intelligence: Synergies of Fuzzy Logic, Neural Networks and Evolutionary Computing*. Hoboken, NJ: Wiley, 2013.

[7] R. Marks, "Intelligence: Computational versus Artificial," *IEEE Trans. Neural Netw.*, vol. 4, no. 5, pp. 737–739, 1993.

[8] C. Stergiou and D. Siganos, "Neural networks," *Imperial Coll. London Surprise J.*, vol 4, p. 1.

[9] M. J. Somers, J. C. Casal, "Using artificial neural networks to model nonlinearity," *Organ. Res. Methods*, vol. 12, no. 3, pp. 403–417, 2009. doi: 10.1177/1094428107309326.

[10] V. Novák, I. Perfilieva, J. Močkoř, *Mathematical Principles of Fuzzy Logic*. Dordrecht: Kluwer, 1999.

[11] K. De Jong, *Evolutionary Computation: A Unified Approach*. Cambridge, MA: MIT Press, 2006.

[12] A. K. Palit and D. Popovic, *Computational Intelligence in Time Series Forecasting: Theory and Engineering Applications*. New York: Springer-Verlag, 2006, p. 4.

[13] F. Gaillard, "Normal chest CT - Lung window." Accessed: June 28, 2020. [Online]. Available: https://radiopaedia.org/cases/normal-chest-ct-lung-window-1?lang=us

[14] S. Roy et al., "Deep learning for classification and localization of COVID-19 markers in point-of-care lung ultrasound," *IEEE Trans. Med. Imag.*, vol. 39, no. 8, pp. 2676–2687, Aug. 2020. doi: 10.1109/TMI.2020.2994459.

[15] L. Wang and A. Wong, "COVID-Net: A tailored deep convolutional neural network design for detection of COVID-19 cases from chest radiography images," 2020, arXiv:2003.09871.

[16] Z. Han et al., "Accurate screening of COVID-19 using attention based deep 3D multiple instance learning," *IEEE Trans. Med. Imag.*, vol. 39, no. 8, pp. 2584–2594, Aug. 2020, doi: 10.1109/TMI.2020.2996256.

[17] H. Panwar, P.K. Gupta, M. K. Siddiqui, R. Morales-Menendez, and V. Singh, "Application of deep learning for fast detection of COVID-19 in X-rays using nCOVnet," *Chaos, Solitons, Fractals*, vol. 138, p. 109,944, 2020. doi: 10.1016/j.chaos.2020.109944.

[18] Y. J. Oh, S. J. Park, and J. C. Ye, "Deep learning COVID-19 features on CXR using limited training data sets," *IEEE Trans. Med. Imag.*, vol. 39, no. 8, pp. 2688–2700, Aug. 2020. doi: 10.1109/TMI.2020.2993291.

[19] I. Apostolopoulos, S. Aznaouridis, and M. Tzani, "Extracting possibly representative COVID-19 biomarkers from X-ray images with deep learning approach and image data related to pulmonary diseases," *J Med. Biol. Eng.*, 2020. doi: 10.1007/s40846-020-00529-4.

[20] S. Wang et al., "A fully automatic deep learning system for COVID-19 diagnostic and prognostic analysis," *Eur. Respir. J.*, vol. 56, no. 1, p. 2,000,775, 2020. doi: 10.1183/13993003.00775-2020.

[21] S. Ayyoubzadeh, S. M. Ayyoubzadeh, H. Zahedi, M. Ahmadi, and S. R. N. Kalhori, "Predicting COVID-19 incidence through analysis of google trends data in Iran: Data mining and deep learning pilot study," *JMIR Public Health Surveill.*, vol. 6, no. 2, p. e18828, 2020. doi: 10.2196/18828.

[22] S. Vaid, R. Kalantar, and M. Bhandari, "Deep learning COVID-19 detection bias: Accuracy through artificial intelligence," *Int. Orthop.*, vol. 44, pp. 1539–1542, 2020. doi: 10.1007/s00264-020-04609-7.

[23] L. Huang, R. Han, T. Ai, P. Yu, H. Kang, Q. Tao, and L. Xia, "Serial quantitative chest CT assessment of COVID-19: Deep-learning approach," *Radiol., Cardiothorac. Imag.*, vol. 2, no. 2, p. e200075, 2020. doi: 10.1148/ryct.2020200075.

[24] B. Hurt, S. Kligerman, and A. Hsiao, "Deep learning localization of pneumonia: 2019 coronavirus (COVID-19) outbreak," *J. Thoracic Imag.*, vol. 35, no. 3, pp. 87–89, May 2020. doi: 10.1097/RTI.0000000000000512.

[25] O. Ronneberger, P. Fischer, and T. Brox, "U-net: Convolutional networks or biomedical image segmentation," in *Proc. 2015 Int. Conf. Medical Image Computing and Computer-Assisted Intervention*, Munich, Oct. 5, pp. 234–241.

[26] Z. Zhou, M. M. R. Siddiquee, N. Tajbakhsh, and J. Liang, "Unet++: A nested u-net architecture for medical image segmentation," in *Proc. Workshop Deep Learning Medical Image Analysis and Multimodal Learning Clinical Decision Support*, Granada, Spain, Sept. 20, 2018, pp. 3–11.

[27] L.-C. Chen, Y. Zhu, G. Papandreou, F. Schroff, and H. Adam, "Encoder-decoder with atrous separable convolution for semantic image segmentation," in *Proc. 2018 European Conf. Computer Vision (ECCV)*, Munich, Sept. 8–14, 2018, pp. 801–818.

[28] S. Jégou, M. Drozdzal, D. Vazquez, A. Romero, and Y. Bengio, "The one hundred layers tiramisu: Fully convolutional densenets for semantic segmentation," in *Proc. 2017 IEEE Conf. Computer Vision and Pattern Recognition Workshops*, Honolulu, HI, pp. 11–19.

[29] K. He, X. Zhang, S. Ren, and J. Sun, "Deep residual learning for image recognition," in *Proc. 2016 IEEE Conf. Computer Vision and Pattern Recognition (CVPR)*, Las Vegas, NV, pp. 770–778. doi: 10.1109/CVPR.2016.90.

[30] M. Sandler, A. Howard, M. Zhu, A. Zhmoginov, and L.-C. Chen, "MobileNet V2: Inverted residuals and linear bottlenecks," in *Proc. 2018 IEEE Conf. Computer Vision and Pattern Recognition*, Salt Lake City, UT, pp. 4510–4520.

[31] G. Huang, Z. Liu, and K. Q. Weinberger, "Densely connected convolutional networks," in *Proc. 2016 IEEE Conf. Computer Vision and Pattern Recognition (CVPR)*, Las Vegas, NV, pp. 4700–4708

[32] T.-Y. Lin, P. Doll´ar, R. Girshick, K. He, B. Hariharan, and S. Belongie, "Feature pyramid networks for object detection," in *Proc. 2017 IEEE Conf. Computer Vision and Pattern Recognition (CVPR)*, Honolulu, HI, pp. 936–944. doi: 10.1109/CVPR.2017.106.

[33] N. Dhiman, and M. Sharma, "Fuzzy logic inference system for identification and prevention of coronavirus (COVID-19)," *Int. J. Innov. Technol. Exploring Eng.*, vol. 9, pp. 2278–3075, 2020. doi: 10.35940/ijitee.F4642.049620.

[34] D. M. Nazarov, "Fuzzy model of digital assessment of donation systems' level in COVID-19," in *Proc. 2nd Int. Scientific and Practical Conf. "Modern Management Trends and Digital Economy: From Regional Development Global Economic Growth" (MTDE 2020)*, Yekaterinburg, Russia, 2020. doi: 10.2991/aebmr.k.200502.199.

[35] N. Van Tinh, "Forecasting of COVID-19 Confirmed cases in Vietnam using fuzzy time series model combined with particle swarm optimization," *Comput. Res. Progr. Appl. Sci. Eng.*, vol. 6, no. 2, pp. 114–120, 2020.

[36] Z. Yang, X. Li, H. Garg, and M. Qi, "Decision support algorithm for selecting an antivirus mask over COVID-19 pandemic under spherical normal fuzzy environment," *Int. J. Environ. Res. Public Health*, vol. 17, p. 3407, 2020. doi: 10.3390/ijerph17103407.

[37] Z. Ren, H. Liao, and Y. Liu, "Generalized Z-numbers with hesitant fuzzy linguistic information and its application to medicine selection for the patients with mild symptoms of the COVID-19," *Comput. Ind. Eng.*, vol. 145, p. 106,517, July 2020, doi: 10.1016/j.cie.2020.106517.

[38] A. Yousefpour, H. Jahanshahi, and S. Bekiros, "Optimal policies for control of the novel coronavirus COVID-19 outbreak," *Chaos, Solitons Fractals*, p. 109,883, 2020. doi: 10.1016/j.chaos.2020.109883.

[39] M. Niazkar, and H. R. Niazkar, "COVID-19 outbreak: Application of multi-gene genetic programming to country-based prediction models," *Electron. J. General Med.*, vol. 17, no. 5, p. em247, 2020.

[40] R. Salgotra, M. Gandomi, and A. Gandomi, "Time series analysis and forecast of the COVID-19 pandemic in India using genetic programming," *Chaos, Solitons, Fractals*, vol. 138, p. 109,945, 2020. doi: 10.1016/j.chaos.2020.109945.

[41] R. Salgotra, M. Gandomi, and A. Gandomi, "Evolutionary modelling of the COVID-19 pandemic in fifteen most affected countries," *Chaos, Solitons Fractals*, vol. 140, p. 110,118, Nov. 2020. doi: 10.1016/j.chaos.2020.110118.

[42] S. Dilbag, Singh, V. Chahar, Vaishali, and M. Kaur, "Classification of COVID-19 patients from chest CT images using multi-objective differential evolution–based convolutional neural networks," *Eur. J. Clin. Microbiol. Infect. Dis., Official Publ. Eur. Soc. Clin. Microbiol.*, vol. 39, no. 7, pp. 1379–1389, 2020. doi: 10.1007/s10096-020-03901-z.

[43] K. Price, R. M. Storn, and J. A. Lampinen, *Differential Evolution: A Practical Approach to Global Optimization*. New York: Springer-Verlag, 2006.

[44] R. Duffey, and E. Zio, "Analysing recovery from pandemics by learning theory: The case of COVID-19," *IEEE Access*, vol. 8, pp. 110,789–110,795, 2020. doi: 10.1109/ACCESS.2020.3001344.

[45] G. Wang et al., "A noise-robust framework for automatic segmentation of COVID-19 pneumonia lesions from CT images," *IEEE Trans. Med. Imag.*, vol. 39, no. 8, Aug. 2020. doi: 10.1109/TMI.2020.300014.

[46] M. Barstugan, U. Ozkaya, and S. Ozturk, "Coronavirus (COVID-19) classification using CT images by machine learning methods," 2020, arXiv:2003.094.

[47] G. S. Randhawa, M. P. M. Soltysiak, H. El Roz, C. P. E. de Souza, K. A. Hill, and L. Kari, "Machine learning using intrinsic genomic signatures for rapid classification of novel pathogens: COVID-19 case study," *PLoS ONE*, vol 15, no. 4, pp. 2653–2663, 2020. doi: 10.1371/journal.pone.0232391.

[48] X. Mei et al., "Artificial intelligence–enabled rapid diagnosis of patients with COVID-19," *Nature Med.*, pp. 1–5, 2020.

[49] I. D. Apostolopoulos and T. A. Mpesiana, "COVID-19: Automatic detection from x-ray images utilizing transfer learning with convolutional neural networks," *Phys. Eng. Sci. Med.*, vol. 43, pp. 635–640, 2020. doi: 10.1007/s13246-020-00865-4.

[50] A. Tarvainen and H. Valpola, "Mean teachers are better role models: Weight-averaged consistency targets improve semi-supervised deep learning results," in *Proc. 31st Conf. Neural Information Processing Systems (NIPS 2017)*, Long Beach, CA, pp. 1195–1204.

[51] L. Yu, S. Wang, X. Li, C. W. Fu, and P. A. Heng, "Uncertainty-aware self-ensembling model for semi-supervised 3D left atrium segmentation," in *Proc. 22nd Int. Conf. Medical Image Computing and Computer Assisted Intervention*, Shenzhen, China, 2019, pp. 605–613.

[52] K. Simonyan and A. Zisserman, "Very deep convolutional networks for large-scale image recognition," 2014, arXiv:1409.1556.

[53] C. Szegedy, S. Ioffe, V. Vanhoucke, and A. A. Alemi, "Inception-V4, inception-resnet and the impact of residual connections on learning," in *Proc. 31st AAAI Conf. Artificial Intelligence*, San Francisco, 2017, pp. 4278–4284.

[54] F. Chollet, "Xception: Deep learning with depth-wise separable convolutions," in *Proc. 2017 IEEE Conf. Computer Vision and Pattern Recognition (CVPR)*, Honolulu, HI, pp. 1251–1258. doi: 10.1109/CVPR.2017.195.

[55] F. A. Cássaro and L. F. Pires, "Can we predict the occurrence of COVID-19 cases? Considerations using a simple model of growth," *Sci. Total Environ.*, vol. 728, p. 138,834, 2020. doi: 10.1016/j.scitotenv.2020.138834.

[56] A. J. Kucharski et al., "Early dynamics of transmission and control of COVID-19: A mathematical modelling study," *Lancet Infect. Dis.*, vol. 20, no. 5, pp. 553–558, 2020. doi: 10.1016/S1473-3099(20)30144-4.

[57] X. Zhang, R. Ma, and L. Wang, "Predicting turning point, duration and attack rate of covid-19 outbreaks in major western countries," *Chaos, Solitons, Fractals*, vol. 135, p. 109,829, 2020.

[58] "Using artificial intelligence to help combat COVID-19." Accessed: June 28, 2020. [Online]. Available: https://www.oecd.org/coronavirus/policy-responses/using-artificial-intelligence-to-help-combat-covid-19-ae4c5c21/

[59] BlueDot. Accessed: June 28, 2020. [Online]. Available: https://bluedot.global/

[60] EpiRisk. Accessed: June 28, 2020. [Online]. Available: https://epirisk.net/

[61] J. Parrock, "Coronavirus: Belgium hospital employs robot to protect against COVID-19," *Euronews*, Accessed: June 28, 2020. [Online]. Available: https://www.euronews.com/2020/06/02/coronavirus-belgium-hospital-employs-robot-to-protect-against-covid-19

[62] "Canada's COVID-19 Chatbot." Accessed: June 28, 2020. [Online]. Available: https://covidchatbot.com/

[63] T. S. Perry, "Satellites and AI monitor Chinese economy's reaction to coronavirus." Accessed: June 28, 2020. [Online]. Available: https://spectrum.ieee.org/view-from-the-valley/artificial-intelligence/machine-learning/satellites-and-ai-monitor-chinese-economys-reaction-to-coronavirus/

[64] WeBank. Accessed: June 28, 2020. [Online]. Available: https://www.webank.com/#/home