Enhancement of COVID-19 Detection by Unravelling its Structure and Selecting the Optimal Attributes

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Abstract*—According to the current unprecedented pandemic, we realise that we cannot respond to every contagion novel virus as fast as possible, either by vaccination or medication. Therefore, it is paramount for the sustainable development of antiviral urban ecosystems to promote early detection, control, and prevention of an outbreak. The structure of an antivirus-based multi-generational smart-city framework could be crucial to a post-COVID-19 urban environment. Humanitarian efforts in the pandemic's framework deployed novel technological solutions based on the Internet of Things (IoT), Machine Learning, Cloud Computing and Artificial Intelligence (AI). We aim to contribute by improving real-time detection using data mining in collaboration with machine learning techniques through our research work. Initially, for detection, we propose an innovative system that could detect in real-time virus propagation based on the density of the airborne COVID-19 molecules—the proposal based on the detection through the isothermal amplification RT-Lamp [1]. We also propose real-time detection by spark-induced plasma spectroscopy during the internal airborne transmission process [17]. The novelty of this research work, called characteristic subset selection, is based on identifying irrelevant data. By deducting the unrelated information dimension, machine learning algorithms would operate more efficiently. Therefore, it optimises data mining and classification in high-dimensional medical data analysis, particularly in effectively detecting COVID-19. It can play an essential role in providing timely detection with critical attributes and high accuracy. We elaborate the teaching-learning method optimisation to achieve the optimal set of features for the detection.

***Keywords*—covid-19, coronavirus, data mining, machine learning, teaching-learning, pandemic**

I. INTRODUCTION

Before 2019 exhalate, humanity faced an unprecedented pandemic until roughly 70% of the population worldwide has been vaccinated. The eternal vicious circle of the COVID-19 epidemic reveals that we need to find ways to escape the new normal of isolation. We should not focus on social distancing according to the definition that is commonly disseminated in social media. Instead, we should elaborate on ways for spatial distancing by disrupting the proper nodes from the chain of COVID-19 transmission. The main objective is to elaborate on the aspects that could construct a sustainable and effective against disease outbreaks and an intelligent urban ecosystem based on technological initiatives. Our proposal is an indispensable weapon against humanity's invisible foe as it can enhance real-time detection. It is out of paramount importance to reliably visualise the density of virus strains in real-time to control its spread, especially in crowded indoor environments, e.g., trains, aeroplanes, school classes etc. Therefore, we elaborate the case of intelligently integrating with intelligent environments a framework that could detect COVID-19. The goal is to unobtrusively control the spread from human synchronicity by measuring coronavirus concentration.

Detection based on RT-Lamp isothermal amplification that could be applied without thermal circulators is an alternative to current PCR and Rapid-test tests. It also enables the detection process without viral extraction due to its structure based on disposable cartridges. Also, it can target the sequence due to its resistance to inhibitors as well as its high specificity, using four to six primers that identify six to eight regions in the standard for amplification.

Visualising the air transmission and propagation of coronavirus virtually can also be conducted by spark-induced plasma spectroscopy, according to Jung et al. and Yang et al. [2], [3]. Their experimental procedures proved that the method is efficient to analyse elements in the atmospheric air. Also, processing transitions to atomic signals with distance and propagation time in a chamber system concludes that the leading cause of air diffusion and concentration of airborne elements has been recognised as related to measurement time and spray distance. Subsequently, Yang et al. introduced a framework based on real-time spark-induced plasma spectroscopy analysis to measure a virus's density floating in ambient air at different spray distances. The method used to detect coronavirus and other viruses where the risk of infection from droplets adsorbed on surfaces or floors is higher [22].

Our motivation arises from the absence of a method that could instantaneously detect the virus's concentration within an indoor space. Therefore, contributing to the development of that initiative could be crucial to prevent the spread and enable the continuation of humanity's daily tasks in a natural environment. The virtual has become the new normal. We present the modified binary teaching-learning machine learning technique through our research work, aiming to generate optimal data attributes and apply the classification of this data. The objective is to improve virus strain identification by eliminating the irrelevant data grounded by the unrelated characteristics [4]. Thus, we can detect the virus accurately, understand its biology and unravel its structure based on that approach. Initially, we review the literature focusing on current technological initiatives and new research works that could help eradicate the pandemic and real-time detection. Thereafter, we investigate coronavirus attributes, specifically the spike protein molecule in which its complex spatial structure is emphasised. Finally, we present our proposal based on a supervised machine learning method to enable data clustering through a data mining technique based on the virus molecule's appropriate characteristics.

II. RELATED WORKS

Datasets gathered worldwide since January 2020 regarding COVID-19, and the information is accumulating at a fascinating pace. A modern trend of mathematical methods and knowledge is out of paramount importance to help users retrieve pertinent data to derive beneficial information from rapidly growing quantities of coronavirus data [5]. The application of specific data mining techniques for forecasting models and smart-excavation is fundamental for the procedure. Deriving the valid data for validation and interpretation from datasets requires strategic planning implementation [6]. The process of discovering knowledge in a database based on data mining through machine learning techniques will be essential. Subsequently, it demands complex procedures to identify and derive the predominantly patterns from the datasets [7]. State of the art data mining techniques comprises the following methods: generalisation, classification, clustering analysis, correlation, tracking patterns, etc. Also, it can be classified into three categories: Learning optimisation, Supervised and unsupervised data analysis through machine learning, where the process includes predictable and unidentified data sets, respectively [8], [9].

Recently A. Andreou and C. X. Mavromoustakis et al. present the idea of an IoT cloud-based framework aiming to inhibit the rampant spread of the virus [10]. A. Andreou, C. X. Mavromoustakis and G. Mastorakis et al. developed an innovative system for confidential healthcare data exchange, including fundamental cryptographic techniques for sharing medical images [11]. Based on the same motivation, Lalos A.S. et al. thoroughly analyse IoT networks' confidentiality problems by surveying ML and Dee Learning techniques [12]. C. X. Mavromoustakis and G. Mastorakis et al. proposed a novel offloading methodology that hosts a "resource-aware" recommendation scheme, which allows the efficient monitoring of energy-draining applications that run in an IoT ecosystem [13]. In addition, C. X. Mavromoustakis and G. Mastorakis et al. presented and identified the different ways to implement the edge computing paradigm by using M2M communications in dense networked systems via social connectivity from two different perspectives: the offered reliability for delay-tolerant (delay-sensitive) services and the energy conservation over reliability provision [14].

Naglaa and Ehab et al. state that "Architecture and urbanism after the Covid-19 epidemic will never be the same," and they are correct [15]. Their scope was to research the current pandemic situation to enhance the response to future similar outbreaks. Chanjuan and Zhiqiang et al., aiming to prevent coronavirus spread, elaborated the research fields where the effectiveness of spatial distance and indoor ventilation efficiency [16]. Based on the same research area Antony, Velraj, and Fariborz et al. studied the spread of COVID-19 under several different climates and environmental conditions, indoor and outdoor [17]. To overcome the several lockdown policies' adverse economic impact due to continually pandemic waves, this paper [18] proposed a real-time data-driven dynamic clustering framework. Xing-Yi et al. examined the coronavirus's risk of spreading to health and care ecosystems to enhance sustainable work in the hospital environment [19]. Andreou, C. X. Mavromoustakis and G. Mastorakis et al. implemented a novel machine learning technique to forecast the pandemic's progress accurately. Their study proved to be correct as the cumulative infectivity curve's progression followed the progression that had been predicted [20].

Anurup et al. conducted experiments on coronavirus detection through a portable device based on RT-Lamp isothermal amplification [21]. Yang et al. introduced a novel idea for real-time coronavirus detection using spark-induced plasma spectroscopy [22]. Zhou et al. developed BioAider, for quick sequence annotation and mutation analysis on large-scale genome-sequencing data. Based on BioAider, they detected 14 substitution hotspots within 3,240 COVID-19 genome sequences, with three groups of theoretically associated substitution [23]. Yong and Hua et al. developed a framework aiming to obtain the spatial distribution to forecast infection. They combine the method of spatial flow impact factor with the Wells-Riley model. Their model can identify people's optimised arrangement and air purifiers in an indoor environment [24].

III. UNRAVELLING THE STRUCTURE OF COVID-19

The sluggishness of immunisations in some countries may allow the proper time interval for the virus to mutate, and immune evasion may occur. Therefore, we should be equipped with alternative solutions based on edge computing to enhance virus detection in atmospheric indoor environments if immunodeficiency emerges. The goal is to enable efficient and sufficient solutions to escape the new normal of isolation that has been established in our lives since early 2020. The innovative technological improvement will have the opportunity through machine learning to detect

COVID-19 mutations and novel viruses that could cause an outbreak. We are motivated by the fact that the scientific community focused on, then out of paramount importance, vaccination development to optimise individual diagnostic testing. Herein, the consideration to study the detection of the virus in the environment was limited. However, it will be beneficial as it will enable finite testing in indoor environments unobtrusively.

A. Morphology and genomic structure

COVID-19 belong in the positive-strand RNA viruses, which means that the positive-sense genome can act as a messenger for the viral proteins by the host cell's ribosomes. The structure of coronavirus, as presented in Fig.1, comprises of the following proteins:

- Spike protein, which is vital for host cell receptor bindings to allow the entry of the host cell;
- Membrane protein which is the dominant manager for the concentration of the virus;
- Envelope protein which shape determined by membrane protein and forms viral envelope;
- Nucleocapsid protein binds to the RNA genome for nucleocapsid production. Also, it constitutes an essential attribute for drug production and vaccine progression.

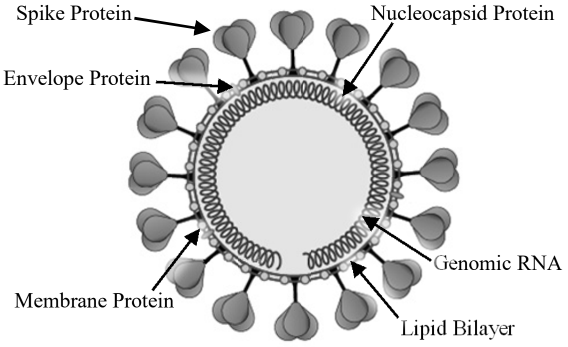

Fig. 1. Illustration of the Schematic Structure of COVID-19

B. Focusing on the structure of the Spike protein

The fundamental characteristic of coronavirus structure that could be identified is the spike protein due to the spike that enables airborne transmission and adhesion. The spike protein's size is approximately 190 kDa, where 1-Dalton is equivalent to $1.66053906660 \times 10^{-27}$ kg. According to the visual representation of Figure 2, spike protein is a trimer that schematically forms a bulb, a halo around the viral particle. As shown, the S1 and S2 subunits entail the bulbous head and stem region [26]. In addition, the receptor bindings are coated with polysaccharide molecules to cover them, avoiding monitoring the host's immune system upon entry [27]. The length of the spike is 1273 amino acids and comprises the S1 subunit and the S2 subunit. In the S1 subunit, there is an N-terminal domain and a receptor-binding domain. The S2 subunit consists of the transmembrane domain and cytoplasm domain.

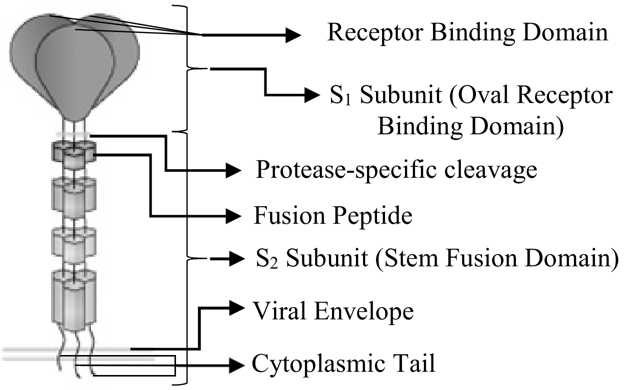

Fig. 2. Visual Illustration of Spike Protein

1) S_1 - Oval Receptor Binding Domain

Initially, the infection from COVID-19 occurs due to the indissoluble bond among the virus particles and the cell receptors on the host cell's surface. The receptor-binding domain is an essential target for identification due to the initial contact with the hosts and the distinguishing characteristics. The S1 subunit comprises the N region at one end of the protein and the C-terminal domain. The individual details at the binding boundary form basic residue substitutions in the COVID-19 strain. The mutations of crucial residues play an imperative role in enhancing the interaction with the angiotensin-converting enzyme.

2) S_2 - Stem Fusion Domain

The S_2 subunit, responsible for viral fusion and penetration, consists of a sequential fusion peptide, repeat sequence heptapeptide 1 and 2, and a transmembrane cross-section. The fusion peptide is a segment of approximately 17.5 amino acids that comprise hydrophobic residues. It hooks with a membrane when the spike protein adopts the pre-hairpin modulation. Heptapeptide sequences 1 and 2, positioned at the C-terminus and the N-terminus of the transmembrane domain, respectively, consists of a repetitive heptapeptide. Also, shape the six-helical beam, which is vital for the viral fusion and ingress process of the S_2 subunit.

IV. PROPOSED ORIENTATION FRAMEWORK

Through our research work, we enable a novel modification of binary teaching–learning-based optimisation. This technique aims at selecting subset characteristics and demonstrating the precision of the support vector machine for binary recognition as a function of suitability for implementing the characteristic subset selection process. Furthermore, our objective is to implement the proposed technique to classify COVID-19 datasets.

A. Motivation

Akhlaghi, Emami, and Nozhat et al. proposed the binary teaching–learning-based optimisation algorithm [25]. The displacement of the velocity vector V_i^n which determines the probability of change from 1 to 0 and vice versa according to (1) and (2); Occurs along with generations *n* during the teaching process. Binary values are included within the set Y^n with all learners, $i.j$ denotes the learner and $j \neq i$. Tutor and learning knowledge mean in the ith iteration presented from Y_t and Y_m respectively, and F represents teaching. R is determined as 0 or 1, selected randomly, and the teaching factor is computed by (3).

$$V_i^n = R_i Y_t^n - F Y_m^n \tag{1}$$

$$V_i^n = R_i\left(Y_i - Y_j\right) \tag{2}$$

$$F = round(random + 1) \tag{3}$$

Through the hyperbolic tangent function (4), we normalise velocity to be within the interval [0,1], and the new function of j in each iteration n with the *i-learner* presented in (5).

$$tanh\left(\left|V_{i,j}^n\right|\right) = \frac{e^{\left|2V_{i,j}^n\right|} - 1}{e^{\left|2V_{i,j}^n\right|} + 1} \tag{4}$$

$$Y_{i,j}^n = \begin{cases} 1, if\ tanh\left(\left|V_{i,j}^n\right|\right) > range(0,1) \\ 0, \qquad alternatively \end{cases} \tag{5}$$

B. Tutor selection process

Initially, we identify the adjacent points A among each end of the population individually (6). Let O be centred among the population and consider as m the quantity of the adjacent points. Euclidean distance between O_i and O_j is presented in (7) for d dimensions. We arrange them in ascending order based on the spaces among the points from each centred point Oi. Density computes at (8) the magnitude-per-unit area from point topographies belonging to a neighbourhood around each centred point. Figure 1 illustrates a paradigm of density calculation among data points.

$$A(O_i) = \left\{O_J/R \le \left(O_i, O_J\right) \le \left(O_i, O_m\right)\right\} \tag{6}$$

$$\left(O_i, O_J\right) = \left\|O_i - O_J\right\| = \sqrt{\sum_{l=1}^{d}\left(O_{i,l} - O_{J,l}\right)^2} \tag{7}$$

$$den_{O_i \in O}(O_i) = \text{den}(O_i, A) = \sum_{j=1}^{A}\left(O_i, O_J\right) \tag{8}$$

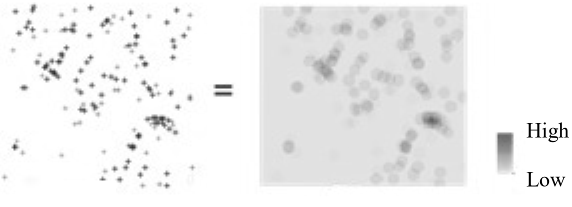

Fig. 3. Density Illustration

Finally, we select the point with the maximum density as a tutor, which means that the specific point must have the minimum cumulative distances among data points.

C. Data Update Mechanism

By conducting a modification on the proposed algorithm by Akhlaghi, Emami, and Nozhat et al. [24], intending to discreet the suitable subset of characteristics from the dataset. We manage to achieve an optimised execution of a feature selection process for COVID-19 diagnosis. The proposed framework is based on the fact that the update function does not depend on the current position in a binary search space. Thus, the current status does not select the next part, and the velocity is the subject (9). The exponential function $\frac{1}{1+e^{-\left(Y_{i,j}^{n+1}-Y_{i,j}^{n}\right)}}$ at (10) determined by the position of each term for two consecutive steps. Furthermore, j=1, 2,…,d is denoted as 1, indicating that the attributes have been chosen as necessary for the next iteration. The position and velocity of the term are updated when the stop criterion is accomplished.

$$Y_{i,j}^{n+1} = Y_{i,j}^n + V_{i,j}^{n+1} \tag{9}$$

$$Y_{i,j}^n = \begin{cases} 1, if\ random < \dfrac{1}{1 + e^{-\left(Y_{i,j}^{n+1} - Y_{i,j}^n\right)}} \\ 0, \qquad alternatively \end{cases} \tag{10}$$

D. Characteristic Selection Technique

The algorithm is a simulation of a lesson in a classroom. The tutor aims to modify the learning process by developing learners to be taught by communicating with other classroom learners. We applied the support vector machine method to select the fitness function, a specific type of objective function of the population.

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Algorithm
  Requirements:
$P$: Input the size of the population
$g$: Input the number of generations
d: Input the number of characteristics
t: Threshold parameter (termination criterion)
  Process:
  for $n \in [1, g]$
  for $i \in [1, P-1]$
  for $j \in [1, d]$
     $Y_{i,j}^{n} \leftarrow \mathrm{rand}\{0|1\}$
     fitness $\left(Y_{i,j}^{n}\right) \leftarrow$ classification through support-vector machine method
        end for $i$
        end for $j$
     Similar neighbourhood $(P, R) \leftarrow (6)$
     Similarity density $\left(Y_{i,j}^{n}\right) \leftarrow (8)$
     Tutor $\leftarrow$ max $\left[E\left(max\left(density\left(Y_{i,j}^{n}\right)\right)\right)\right]$
     $V_{i}^{n} \leftarrow R_{i}Y_{t}^{n} - FY_{m}^{n}$
  for $i \in [1, P]$ do
     learners $\leftarrow V_{mean}^{n}$
Tutor stage
     $V_{new}^{(n)}(i) \leftarrow (1)$
     $Y_{new}^{(n)}(i) \leftarrow (9), (10)$
        if $fitness\ Y_{old}^{(n)}(i) < fitness\ Y_{new}^{(n)}(i)$ then
     $Y_{new}^{(n)}(i) \leftarrow Y_{old}^{(n)}(i)$
     $V_{new}^{(n)}(i) \leftarrow V_{old}^{(n)}(i)$
Learner stage
     $learners \leftarrow \mathrm{rand}\{j|m\}$
     $V_{new}^{(n)}(i) \leftarrow (3)$
     $Y_{new}^{(n)}(i) \leftarrow (9), (10)$
        if $fitness\ Y_{old}^{(n)}(i) < fitness\ Y_{new}^{(n)}(i)$ then
     $Y_{new}^{(n)}(i) \leftarrow Y_{old}^{(n)}(i)$
     $V_{new}^{(n)}(i) \leftarrow V_{old}^{(n)}(i)$
        end if
        end for i
        end for j
        end for g
     $Y_{optimum} \leftarrow$ max $\left(\mathrm{fitness}\left(Y_{i,j}^{n}\right)\right)$
  end procedure
```

V. CONCLUSION & FUTURE ORIENTATION

Based on the paramount importance to establish an anti-pandemic intelligent framework to contribute to smart-cities ecosystems. This framework will be a significant step in improving digitalisation and responding in a post-COVID 19 multi-generational society. We proposed integrating the isothermal Reverse-Transcription lamp (RT-lamp) or implementing spark-induced plasma spectroscopy analysis through our research work. Our contribution is based on the data mining procedure of the attributes aiming to enhance the system that could enable the unobtrusive nucleic acid-based detection of COVID-19 instantaneously. Furthermore, we have proposed optimising the COVID-19 characteristic set of options to allow efficient detection to benefit detection processes. The proposed method's innovation is based on the leading trainer's choice through the binary teaching-learning algorithm with the support-vector way that calculates the optimisation's suitability function. Consequently, the new modification of the binary teaching-learning based optimisation algorithm can define the optimum subset of characteristics of the COVID-19 strain.

The eternal vicious circle of the COVID-19 epidemic reveals that we need to find ways to escape the new normal of isolation. But, unfortunately, recovered coronavirus patients are not immune to reinfection. Therefore our research orientation in the future is developing a Radio-Frequency IDentification (RFID), aiming to capture the interactions between infected and uninfected users through the network and collect this information. By thoroughly elaborating on this data, we will trigger an alert message to susceptible users. Also, the system will detect the proximity interaction between them [28].

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