IJRTSM

INTERNATIONAL JOURNAL OF RECENT TECHNOLOGY SCIENCE & MANAGEMENT

"CORONAVIRUS DISEASE 2019 (COVID-19) IMPACT AND DETECTION AND PREVENTION IN USING ML/DL TECHNIQUES: A LITERATURE REVIEW"

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ABSTRACT

In December 2019, a new disease with pneumonia-like symptoms was spreading throughout Wuhan in China which was entitled as novel coronavirus disease or COVID -19 caused by the virus SARS CoV-2. Within a span of a few days, this disease became a global threat and was termed as a pandemic by the World Health Organization (WHO) on March 11, 2020, since then the disease has affected more than 1.5 crore people worldwide and around 6.9 lakh people in India as of July 5, 2020. The origin of the COVID-19 disease has been traced back to the bats, but the intermediary contact is unknown. The disease spreads by respiratory droplets and contaminated surfaces. In most cases, the virus shows mild symptoms like fever, fatigue, dyspnea, cough, etc. which may become severe if appropriate precautions are not adhered to. For people with co morbidities (usually elderly) the disease may turn deadly and cause pneumonia, Acute Respiratory Disease Syndrome (ARDS), and multi-organ failure, thereby affecting a person's ability to breathe leading to being put on the ventilator support. The reproduction number (R𝜎) of COVID-19 is much higher than its predecessors and genetically similar diseases like SARS-CoV and MERS-CoV. This paper discusses the epidemiological characteristics of the SARS-CoV-2 virus, its phylogenetic relationship with the previous pandemic causing viruses such as SARS-CoV-1 and MERS-CoV and analyzes the various responses to this global pandemic worldwide, focusing on the actions taken by India and their outcomes.

Key Words: Machine Learning ,Deep learning, COVID, SARS-CoV-1.

I. INTRODUCTION

The current global pandemic is caused by the "novel corona virus disease (2019-nCoV) or severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) popularly known as COVID-19 disease" originated in the city of Wuhan in Hubei Province, China, during December in 2019. The virus quickly spread throughout the world. Many countries reacted too late to implement preventive measures leading to a sudden upsurge in the number of cases worldwide. Genomic analysis of the virus SARS-CoV-2 was found to be phylogenetically similar to other bat originated corona viruses like SARS-Cov-1 and MERS-CoV, thereby confirming that bats are the primary reservoir of the virus, however, the intermediate source of origin and its transfer to humans is not yet known [1]. As of July 5, 2020, there is no clinically approved antiviral drug treatment or vaccine available to be used against COVID-19, however, in the month of July 2020 certain organizations worldwide are claiming to be working on a vaccine to treat the novel coronavirus. Drugs like Remdesivir (GS-5734) and Dexamethasone are being evaluated in late-stage clinical trials but have not been approved anywhere. The transmission of COVID-19 is confirmed to be through human to human interactions [2], the maximum amount of viral load shedding is done by symptomatic carriers, however, there are confirmed cases of asymptomatic carriers also transmitting the disease [3].
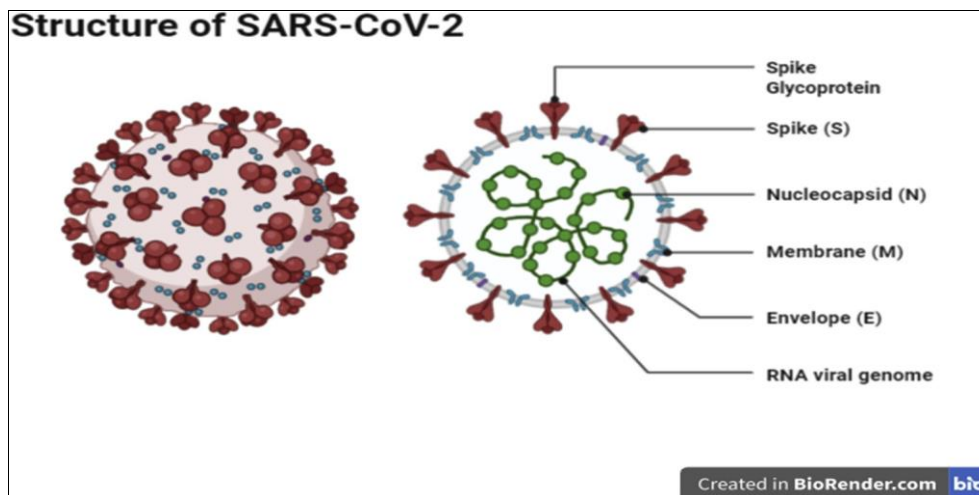
Fig.1. : Structure of the corona virus

The human body is exposed to a variety of infectious microorganisms, such as viruses, bacteria, fungi, protozoa, and helminths, which cause tissue damage through different mechanisms. Viruses are unique among these types of infectious organisms in that they can manipulate the host-cell machinery in a unique way and continuously evolve to survive and prosper in all species [4]. COVID-19 is the disease caused by a new corona virus called SARS-CoV-2. learned of this new virus on 31 December 2019, following a report of a cluster of cases of 'viral pneumonia' in Wuhan, People's Republic of China.Since December 2019, a novel coronavirus disease had rapidly spread throughout China, leading to a global outbreak, and causing considerable public health concern. World Health Organisation (WHO) announced the outbreak of COVID-19 as a global public health emergency on 30 January 2020. In India, the First case of COVID-19 was reported on January 27, 2020, in Kerala district. Since then, there is a wide variation in the reporting of cases across the country. The case reporting is based on the SARS-CoV-2 antigen testing by Real-Time Reverse Transcription Polymerase Chain Reaction (RT-qPCR) or by Rapid Antigen Test (RAT) [5]. Coronavirus (CoV) is clustered under the viral family group that causes disease in mammals and birds. A pandemic novel corona virus was named as ''Corona Virus Disease 2019'' (2019-nCoV) by World Health Organization (WHO) in Geneva, Switzerland. As its RNA pattern is closer to SARS, the 2019 Coronavirus is renamed as SARSCoV- 2 pandemic. It belongs to the subfamily Orthocoronavirinae inside the family Coronaviridae, order Nidovirales, and the realm Riboviria [6]. A two-dimensional view of Corona beneath a transmission electron microscopy reveals a characteristic look of ''paying homage to a crown'' around the virions. This lead to naming the virus ''Corona'', meaning ''crown'' or ''halo'' in Latin This is the deadly third-generation virus in Corona family preceded by severe acute respiratory syndrome (SARS) in 2003, killed almost 10% of total affected patients (8429) across 29 international locations and Middle East Respiratory Syndrome (MERS) in 2012, even more lethal with a mortality rate of 30% of the infected patients.

Structure of SARS -CoV- 2

The size of corona viruses ranges from 60 to 140 nm in diameter, its linearly stranded and positive-sense RNA genome is quite large, ranging from 26 to 32 Kb in size [7]. These spherical or pleomorphic viruses have envelopes that contain helical nucleocapsid of nucleoproteins(N) which is associated with the RNA genome. Embedded in the envelope is a 2 nm trimer of spike glycoprotein (S) that facilitates the virus's attach- ment to the receptor of host cells. Its envelopes also consist of integral membrane (M) and envelope (E) proteins. Coronaviruses that belong to the genus Beta-coronavirus have additional membrane glycoprotein hemagglutinin esterase which forms 5–7 nm long spikes (N.J., et al., 2019) these spike-like projections on its surface give it a crown-like appearance under the electron microscope, hence the name coronavirus [8]. The common cold which has a mild effect on our respiratory system is also a form of corona virus.

II. RELATED WORK

Convolutional Neural Networks

Convolutional neural networks, specifically artificial neural networks, are a branch of deep learning methods that are inspired by the natural visual perception mechanism of living organisms [9]. CNNs are nothing but stacked multilayered neural networks. There are three major categories of layers, namely, convolutional layers, pooling layers and fully connected layers. The first layer of any CNN model is an input layer, where the width, height and depth of the input image are specified as the input parameters. Immediately after the input layer, convolutional layers are defined with the number of filters, filter window size, stride, padding and activation as the parameters. Convolutional layers are used to extract meaningful feature maps for the input location by calculating the weighted sum [10].

Then, each feature map is passed through an activation function, and bias is added to form the output. Usually, rectilinear unit (ReLU) activation is used as the activation function [11]. Pooling layers are used to reduce the size of the output from the convolutional layers. As the model increases in size with an increasing number of filters in the convolutional layer, the output dimensionality also increases exponentially, this makes it hard for computers to handle. Pooling layers are added to reduce the dimensions for easy computation and sometimes to suppress noise. The pooling layer can be a max pooling, average pooling, global average pooling, or spatial pooling layer. The most commonly used pooling layer is a max pooling layer. The output is flattened to form a single-array feature vector, which is fed to a fully connected layer. Finally, a classification layer is defined with activation functions such as sigmoid, softmax and tanh functions [12]. The number of classes is specified in this layer, and the extracted features are aggregated into class scores. Batch normalization layers are applied after the input layer or after the activation layers to standardize the learning process and reduce the training time [22]. Another important parameter is the loss function, which summarizes the error in the predictions during training and validation. The loss is back propagated to the CNN model after each epoch to enhance the learning process.

Several Available Architectures

Generalize well irrespective of the dataset or application. Various popular architectures, such as AlexNet, VGG, Inception, ResNet, DenseNet, MobileNet, and Xception, are summarized in this section. AlexNet is a simple five-layer convolutional neural network. There are two variants of the VGG network – VGG16 and VGG19 [26]. The VGG architecture was originally proposed for image recognition applications. In VGG16 and VGG19, 16 and 19 wt layers are used with a smaller convolutional filter size of 3×3. The network won first and second places in the ILSVR (ImageNet) competition [13] in 2014. The size of the input image is fixed to 224×224. The model is trained on the ImageNet dataset, which contains millions of images [28]. In contrast to CNN architectures, in which the layers are stacked, a new architecture with an inception block is introduced in InceptionNet.Several variants are available in the inception family. The inception network is also used for image classification and localization and participated in the ILSVR (ImageNet) competition [4] in 2014. Instead of increasing the depth of the model by adding additional layers, the authors apply various filter sizes to the input image simultaneously in the inception block. This leads to the growth of the model width. All the outputs of the inception block are concatenated and fed to the next inception block. Available versions include InceptionV1 (GoogLeNet) [16], InceptionV2 and InceptionV3 [15], InceptionV4 and InceptionResNet [17]. The input image size that is accepted by the model is 224×224.

DL applications in COVID-19 and DL Methods In General

AI-based methods are frequently employed to identify, classify, and diagnose medical images. Recent AI innovation has significantly enhanced COVID-19 screening, diagnoses, and prediction, resulting in superior scale-up, timely response, most reliable and efficient outcomes, and occasionally outperforming humans in certain healthcare activities. Out of the various fields of AI, ML and DL are the two most well-known. In the following sections, we will look at how both ML and DL can be used to battle and mitigate the COVID-19 epidemic. DL-based techniques, such as CNN, RNN, and LSTM for COVID-19 detection, diagnosis, and classification, have recently been applied by several researchers to tackle the COVID-19 pandemic. Screening, drug repurposing, prediction, and forecasting are all things that can be done. Furthermore, ML techniques have been routinely employed to discover epidemic trends. Various

studies have attempted such strategies to screen, classify, diagnose, repurpose drugs, and anticipate COVID-19 in the context of the COVID-19 pandemic. Concerning the COVID-19 outbreak, several of the most effective ML techniques, including SVM, logistic regression, random forest, and decision tree, are applied [18].[Also, one of the major accomplishments for contemporary AI is DL which is recognized as hierarchical learning .DL approaches are now being successfully extended to various AI-based medical applications, including the study of Magnetic Resonance Imaging (MRI) images for cancer diagnoses. Because of their capacity to learn from context, Neural Networks (NN) and DL have exploded in popularity in modern scientific research. These two approaches have been widely utilized in various applications, including classification and forecast issues, smart homes, image recognition, self-driving vehicles, etc. Due to their ability to adjust to numerous data types in many areas .DL mirrors the human brain's filtering of information for correct decision-making. However, DL trains a device to process inputs utilizing various layers, similar to the human brain, to support data prediction and classification. These layers serve as input to the next layer, similar to the layered filters used by NNs in the brain. The feedback loop is continued until the output is the same as before. Weights are assigned to each layer to create the precise output, and they are adjusted throughout training to get the accurate output. There are three types of DL techniques: supervised, semi-supervised, and unsupervised. Each known value serves as an input vector for the supervisory signal, which is the desired value.

The method predicts the desired output labels by using existing labels. Classifications methods employ supervised learning and can traffic signals, detect spam in a file, convert speech to text, recognize faces, and other scenarios Semi-supervised learning is a procedure that bridges the gap between supervised and unsupervised ML techniques. Semi-supervised learning uses both labeled and unlabeled values as training data. Semi-supervised learning is the middle ground between unsupervised and supervised learning. When combined with a small amount of labeled data, the unlabeled data will significantly increase learning accuracy

Certain theoretical theories arise about DL techniques. The first is that data nearby share the same name. The second possibility is the cluster assumption, which states that all data in a cluster have the same name. The third point is that rather than using the entire input space, the data is restricted to a single dimension.Unsupervised learning determines the interrelationships between the elements and then classifies them. Clustering, anomaly detection, and NN use these techniques. Unsupervised learning is commonly used in security domains to detect anomalies .Most DL techniques utilize Artificial Neural Networks (ANN) for feature processing and extraction. A feedback mechanism is used in the learning process, in which each level changes its input data to produce a summary representation. The term "deep" in the DL technique refers to the number of layers needed to transform the data .Throughout that transformation, a Credit Assignment Path (CAP) was being used. The depth of CAP in a feed-forward NN is determined by multiplying the number of hidden layers by the number of output layers. The CAP depth cannot be calculated since an RNN's layer may have numerous signals that travel many times.Also, CNN is the most extensively utilized NN technique for image processing. Besides, since the feature extraction approach is automated and conducted throughout the CNN training on pictures, DL is the most precise image processing field.

DL is recognized as a brilliant technique for offering innovative ideas in the COVID-19 pandemic.

[20] described recent attempts about the COVID-19 outbreak for smart and safe cities, inspired by DL applications for medical image processing. COVID-19 disruption was accomplished using DL in several ways, including disease prediction, virus spread monitoring, diagnosis and treatment, vaccine development, and drug testing. Data protection, the variability of outbreak patterns, control and reliability, and the difference between COVID-19 and non-COVID-19 symptoms were among the problems and issues they found in previous studies. Eventually, they addressed a variety of potential directions for DL applications in medical image processing using COVID-19. Also, as another work,

[21] indicated the impressive area of study on DL for the COVID-19 treatment plan. Their research illuminated the literature regarding DL technology and the numerous approaches established to prevent COVID-19 disease. They looked at a data-efficient CNN that could detect COVID 19 on CT scans. Their survey identified the areas of research on DL for COVID-19 diagnosis. They classified the papers based on DL and ML approaches and quickly compared ML and DL mechanisms. Their survey did not include a large number of works. Furthermore, it did not compare techniques. Plus,

[22] looked into AI-based ML and DL methods to diagnose and treat COVID-19 diseases. They also summarized AI-based ML and DL approaches and the available datasets, tools, and performance. The paper provided a concise overview of current state-of-the-art methods and implementations for ML and DL investigators and the broader health community and examples of how ML, DL, and data could prevent COVID-19 outbreaks. They classified the ML approaches to diagnosis and treatment, assessed these works, and then proposed future research on these topics. They also investigated the prediction performance of AI-based ML, and DL approaches for diagnosing COVID-19 using chest X-ray and CT images, COVID-19 speech and audio analysis, and COVID-19-based medication development.

In addition, [23] investigated how DL dealt with the pandemic and offered suggestions for potential COVID-19 studies. They studied Natural Language Processing (NLP), life sciences, computer vision, and epidemiology DL applications. They explained how the availability of big data affects both of these applications and how learning tasks are built. They assessed the current state of DL and DL's main limitations for COVID-19 applications. Their study focused on how DL might be applied to protein structure prediction, precision diagnostics, and medication repurposing in the life sciences. In epidemiology, DL was also used in spreading forecasting. DL systems to combat COVID-19 were found in abundance in their literature review. They hoped that by conducting this survey, they would be able to speed up the usage of DL in the COVID-19 study. Finally, [24] 2020 discussed the benefits and drawbacks of deep TL approaches, edge computing, and related problems in A. Heidari et al. Computers in Biology and Medicine 141 (2022) 105141 5 combating the COVID-19 epidemic. Also, they introduced a hypothetical combined model, outlining the context and potential implications of working at sensitive sites with real data.

[25] Proposed a method to classify large-scale screening of people infected with COVID-19 differently; this work can be used to identify various breathing patterns and we can bring this tool for practical use in the real world. In this paper, first, a new and strong RS (Respiratory Simulation) Model is introduced to fill the gap between a huge amount of training data and inadequate actual data from the real-world to considering the characteristics of real respiratory signals. To identify six clinically important respiratory patterns, they first applied bidirectional neural networks like the GRU network attentional tool (BI_at_GRU) Eupnea, Biots, Cheyne-Stokes, Bradypnea, and Central-Apnea). The research results show that six distinct respiratory trends with 94.5%, 94.4%, 95.1%, and 94.8% respectively, precision, accuracy, recall, and F_1 can be identified by the proposed model. In comparative studies, the acquired BI_at_GRU specific to the classification of respiratory patterns outperforms the existing state-of-the-art models. The proposed deep model and design concepts have enormous potential to be applied to large-scale applications such as sleeping situations, public environments, and the working environment.

III. Conclusion

COVID-19 is a serious and dangerous infectious disease with symptoms similar to SARS in the form of fever, cough and fatigue. The disease is mostly transmitted through respiratory droplets and close contact. This disease is a major threat to world health and safety. Bioanalytical methods designed to diagnose COVID-19 disease are superior to other diagnostic methods due to their lower cost, higher accuracy, better detection limit and lower error. The advantages and disadvantages of various biosensing methods used to detect the SARS-CoV-2 virus are given in Table S2. Electrochemical methods can be used in further studies of this disease and similar diseases, and even by simulating the disease using relevant biosensors due to their high response speed, which in addition to helping the advancement of science, also offers the possibility of rapid diagnosis and achievement. It provides the appropriate treatment method, so it is recommended to use the simulation and design of appropriate biosensors to make the necessary predictions to prevent or even diagnose and treat similar emerging diseases that may occur. Nanotechnology has the potential to accelerate the development of unique diagnostic sensors, the integration of novel devices, improved optimization/validation and improvements in sensing performance at the point of care. Future research should focus on developing novel and next-generation non-invasive, specific, inexpensive and quick biosensing techniques and technologies for diagnostic applications, particularly in the management of pandemics and life-threatening infectious illnesses. However, certain difficulties require further investigation and attention. For starters, the majority of these technologies and materials have been studied on a laboratory scale, implying that employing them in real-world circumstances may not be as precise as in the lab .Furthermore, none of these biosensors has yet been developed for detecting the SARS-CoV-2 virus. As a result, the commercialization of numerous efficient biosensors should be

hastened. Aside from the approaches and biosensors given, innovative methods such as AI-based technologies, wearable biosensors for continuous public monitoring and single-use disposable sensors for individual testing should be researched for SARS-CoV-2 mass screening

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