



# COVID-19 IMAGE CLASSIFICATION USING DEEP LEARNING: A SYSTEMATIC LITERATURE REVIEW AND FUTURE DIRECTIONS

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**Abstract:** Corona Virus Disease-2019 (COVID-19), which was caused by the severe acute respiratory syndrome-Corona Virus-2 (SARSCoV-2), is a very contagious illness that has killed millions of people all over the world. Imaging methods like computed tomography (CT) and chest x-rays (CXR) are often used to make a quick and accurate COVID-19 diagnosis. Because COVID-19 is a pandemic that is spreading quickly, it must be found quickly in order to stop the virus from spreading. Pictures of the lungs can be used to tell if someone has a corona virus infection. COVID-19 can be found with the help of images from computed tomography (CT) and chest x-rays (CXR). Deep Learning (DL) techniques, and more specifically Convolutional Neural Networks (CNN), have become one of the most popular ways for artificial intelligence (AI) to classify COVID-19. In this work, some of the most important research papers on DL-based categorization of COVID19 using CXR and CT images are looked at, and a summary of those studies is given here. We also give an overview of the latest developments in the field and a critical analysis of the problems that still need to be solved. So that we can come to a conclusion about this work, we will list some possible directions for future research in the COVID-19 imaging classification. The COVID-19 pandemic has quickly spread to all parts of the world. The virus is spreading quickly, which is a danger that makes it harder to stop the disease from spreading. Because of the pandemic, a lot of medical facilities had to switch from giving care in person to doing it over the phone or computer. This is called telemedicine. In order to prevent COVID-19, the goal of this study is to do a literature review on telemedicine applications that use machine learning. Between 2015 and 2022, all of the research that was published in six different electronic databases was looked at in depth. The data that was found during this quick evaluation suggests that machine learning and telemedicine might be able to help stop epidemics by allowing for smart triage of patients and monitoring of their conditions from a distance. There could also be more research and development done on how telemedicine could be used in case of future epidemics.

## I. Introduction

The rapid spread of the corona virus infection was called a pandemic by the World Health Organization (WHO) in March 2020. The COVID-19 pandemic is another name for this one. The current corona virus epidemic is caused by the severe acute respiratory syndrome corona virus 2. (SARS CoV 2). The first known case of the disease was found in Wuhan, China, and from there it quickly spread to the rest of the world [1]. The corona virus can spread from one person to another through the droplets that come out of their nose and mouth when they cough or sneeze. These droplets could make the surfaces even more contaminated, which would make it easier for the disease to spread. When a person is infected with the corona virus, they may have mild to severe respiratory disease that may require them to use a breathing machine [2]. Corona virus infections are common in older people and people with diseases that make them age faster than normal. As a result, many governments have limited their citizens' freedom of movement and closed their borders in an effort to break the pandemic's cycle and stop it from spreading further [3]. Due to the sequencing of the ribonucleic acid (RNA) that the corona virus makes, many vaccines are being made all over the world right now. Conventional and next-generation technologies are used to make the vaccines, and each one is based on one of six vaccination platforms: live attenuated virus, inactivated virus, viral vector-based, messenger RNA (mRNA), or deoxyribonucleic acid (DNA). Even though vaccines can slow the rate at which a disease spreads and help people become immune by causing the body to make antibodies that fight the disease, they only work 95% of the time. When it comes to giving the vaccine, there are a lot of problems, such as problems with the supply chain, hesitation about the vaccine, and a lack of concern about the vaccine. A vaccine's main goal is to stop disease from happening, not to treat it [4]. Even though there is a vaccine for the corona virus, it is still very important to find it early. This is because it can help find people who have come into contact with the disease either directly or indirectly. To stop the pandemic from spreading further, it is important to find these people. If you have COVID-19, you will get a lung infection. Images from computed tomography (CT) and chest X-rays (CXR) are the main diagnostic tools used to figure out what kind of lung infection a

person has [5]. Clinicians and other clinical staff are working with researchers and technicians to find ways to spot corona virus infections early. According to PubMed [6,] there were 755 scholarly articles written about "corona virus" in 2019, and that number rose to 1245 in the first 80 days of 2020.

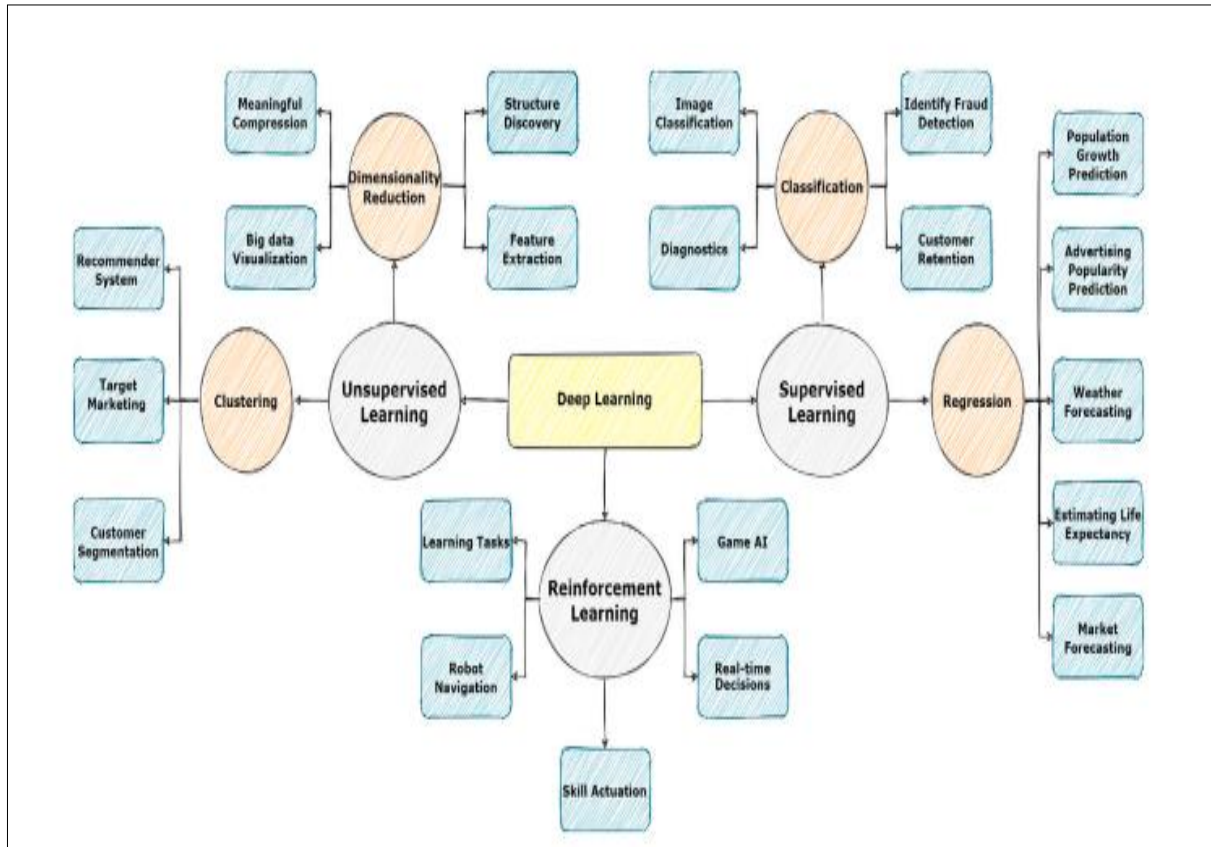


Fig.1 Deep Learning Application

Artificial intelligence and deep learning methods are the most commonly used methods by researchers for the detection of coronavirus infection from CT and CXR images. Deep learning methods have shown significant performance in many research applications, such as computer vision [7], object tracking [8], gesture recognition [9], face recognition [10], and steganography [11–13]. Deep learning methods are widely used because of their improved performance compared to traditional methods. In contrast to traditional methods and machine learning methods, the features need not be hand-picked. By changing the parameters and configurations of the deep learning convolutional neural network (CNN) architecture, a model can be trained to learn the best possible features for the dataset in use. Researchers have used deep learning methods to explore the field of medical imaging even before the coronavirus pandemic. With the recent pandemic, the use of deep learning methods for the detection of coronavirus infection from images has increased tremendously. A detailed survey of the available deep learning approaches for the detection of coronavirus infection from images such as CT scans or CXR images is conducted in this paper. Although other surveys are available in the literature, most of them cover a wider scope. For example,

Ulhaq et al. there was a thorough look at all of the ways that corona viruses can be stopped. These methods include medical image processing, data science methods for modelling pandemics, artificial intelligence (AI) and the Internet of things (IoT), AI for text mining and natural language processing (NLP), and AI in computational biology and medicine. This gives a big picture view of what's happening in the world of research right now. In a survey [15] that looked at the use of computer vision technologies to COVID-19, the segmentation of lung images was looked at and written down. The only goal of this study is to explain how deep learning techniques can be used to find corona viruses. In order to help researchers come up with better ways to find corona viruses, this study gives a summary of all the methods that have been written about in the scientific literature. Along with the method, this paper talks about the datasets that were used, the common metrics that were used for evaluation and comparison, and the future of the field.

### Convolutional Neural Networks

Convolutional neural networks, which are also called "artificial neural networks," are a type of deep learning method that is based on how living things naturally understand what they see [16]. CNNs are nothing more than neural networks that have been layered and stacked. There are three main types of layers, which are called convolutional layers, pooling layers, and fully connected layers, in that order. For the CNN model's first layer, called the "input layer," the width, height, and depth of the image must be given as input parameters. This is a layer that must be in any CNN model. The phase where the convolutional layers are set up comes right after the input layer. The number of filters, the size of the filter window, the stride, the padding, and the activation are some of the parameters for these layers. In the process of figuring out the weighted sum [17,18], convolutional layers are used to get meaningful feature maps for the place where the input was given. After that, each feature map is fed into an activation function, and bias is added to the final product before it is sent out. Rectilinear unit activation, also called ReLU activation, is the most common type of activation function [19]. By adding pooling layers to the process, the output from the convolutional layers can be made easier to handle. When the size of the model and the number of filters in the convolutional layer both grow, the output dimensionality grows exponentially. This makes it hard for computers to process. Pooling layers are used to reduce the number of dimensions in a model in order to make computations easier and sometimes to get rid of noise. Pooling layers can be max pooling, average pooling, global

average pooling, or spatial pooling. The max pooling layer is the most commonly used type of pooling layer [20]. After the output has been flattened, a single-array feature vector is made and sent to a fully linked layer. As the last step, [21] activation functions like sigmoid, softmax, and tanh are used to define a classification layer. In this layer, the number of classes that will be used is set, and the aggregated class scores are calculated from the retrieved features. Batch normalisation layers are used either after the input layer or after the activation layers to standardize the learning process and shorten the amount of time spent training [22]. Another important part is the loss function, which adds up all of the wrong predictions made during the training and validation processes. After each epoch, the loss is recalculated and sent back to the CNN model to improve the learning process [23].

#### Transfer Learning and Fine-Tuning

After designing, making, and building a deep learning model, the number of epochs needed to start training is figured out. During training, initial weights are chosen at random, and at the end of each epoch, these weights will be changed again so that the final result is closer to the classification score. With transfer learning, on the other hand, the model can be set up with the weight values of already-trained models instead of using random weight values, which is the more common way to do things. Transfer learning works best when there isn't enough training data to go around. When transfer learning is done, the last layer of the architecture of the model that has already been trained is changed to a fully connected layer that has the same number of classes as the new dataset. The architecture of the DenseNet model, on the other hand, is made up of  $L(L+1)$  2 direct connections. A feed-forward structure is made when every layer is linked to every other layer. All of the feature maps from the layers that came before the one that is currently active are used by the layer that is currently active, and the feature map from the layer that is currently active is sent to all of the other layers.

The maximum size of an image that can be sent in is 224 pixels on each side. MobileNets are small designs that can be used in cell phones and other devices with embedded software [33]. These architectures have convolutional layers that are separated by depth. In depthwise separable convnets, on the other hand, only two 1D convolutional layers are used instead of the two 2D convolutional layers that are usually used. By doing this, the number of parameters could be cut down, which helped reduce the time needed for computation and training as well as the amount of memory that was used. There are 54 layers in the input image, which is 224 pixels by 224 pixels. The designs of Xception [34] are like those of the Inception family. In both cases, the architectures are made up of inception blocks and convolutional layers that can be separated by depth. The input image is 229 pixels wide and 229 pixels tall, and it has a total of 71 layers. Retrained so that the model could be used with the new data [24]. Another method, called "fine-tuning," is also used when the dataset is small. Specifically, the very top layer of the architecture is changed by a process that is very similar to transfer learning. The only difference between the two is that fine-tuning lets only certain layers be redefined and retrained based on the application, while transfer learning retrains all of the layers. [25] One of the biggest problems with these methods is that the size of the image that is sent in cannot be changed. So, if the pretrained model uses a smaller image dimension than the dataset being used for transfer learning, the picture must be enlarged in order to use transfer learning on a dataset with a bigger image dimension. If a large image is shrunk down to a smaller size, it may hurt the performance of the model in some situations. Careful thought needs to go into putting transfer learning and fine-tuning into action.

## II. Methodology Of Research

The SLR approach is used in this section to help you understand the DLCOVID-19 applications better. The systematic literature review is an analysis that looks at all of the research that has been done on a certain topic in the past. With the help of this section, a full investigation into how DL approaches were used in COVID-19 is done. Then, we look into how reliable the ways were that the studies were chosen. The search process, research topics, and selection criteria are all explained in more detail in the sections that follow.

The goal of this paper is to give an overview of the different machine learning and deep neural network techniques that have been used to find COVID-19 infections by looking at pictures of infected rice plants. In the review method, the following steps are included:

- 1.Data Collection
- 2.Searched databases

Science Direct, Scopus, Springer, the Association for Computing Machinery, and the Institute of Electrical and Electronic Engineers (IEEE) were among the five databases consulted in this study (IEEE Explore Digital Library). This poll was conducted between the years of 2015 and 2020.

#### Searched Terms:

For the survey of papers, the following search expression was defined: ("Convolutional Neural Network" OR "Machine Learning" OR "Artificial Neural Network" OR "DeepLearning") AND ("COVID-19 Diseases" OR "Crop Diseases Detection & Classification" OR "Crop Pest Classification"" COVID-19 diseases")

#### Inclusion criteria:

in order to find the paper that meets the criteria given, The first part of the selection process was to look at the titles and abstracts of the papers. The second part was to get rid of any papers that were already there.

#### Exclusion criteria

Papers that are not specifically dealing with Rice or other plant diseases detection and classification using deep learning/CNN were excluded from the study.

#### Data Analysis

After more than 100 publications that seemed right for the evaluation were chosen, the data was analyzed with the following in mind:

#### Year of Publication

Over the past few decades, researchers have paid more and more attention to a field of study called CNN/deep learning for identifying diseases. Because of this, it's important to know when it was published if you want to find out what caused this interest to grow.

**Purpose of the study**

In this study, different rice diseases were looked at. Different tasks were done, such as identifying discolorations and lesions, classifying the diseases, and separating them into groups. All of these jobs were done for different reasons.

**Deep Learning Architecture**

Deep learning architectures like Deep Neural Networks, Convolution Neural Networks, and Recurrent Neural Networks have been used to find illnesses in COVID-19.

**The process of article selection**

The search for and selection of relevant articles for this study can be broken down into four steps. this step-by-step process. the search terms and keywords that you should use when looking through the publications for the first time. The papers in this collection were found by running a query against several different electronic databases. Scopus, IEEE Explore, Springer Link, Google Scholar, ACM, Elsevier, Emerald Insight, MDPI, Taylor and Francis, Wiley, Peerj, JSTOR, Dblp, DOAJ, and ProQuest are some of the electronic databases that can be used for applied research. Scopus, IEEE Explore, Springer Link, DOAJ, and ProQuest are some of the other databases. Also found are books, chapters, notes, technical studies, special journal issues, and conference papers and journal articles. The total number of papers from Stage 1 was 100 Figure 3, which was given by the publisher,

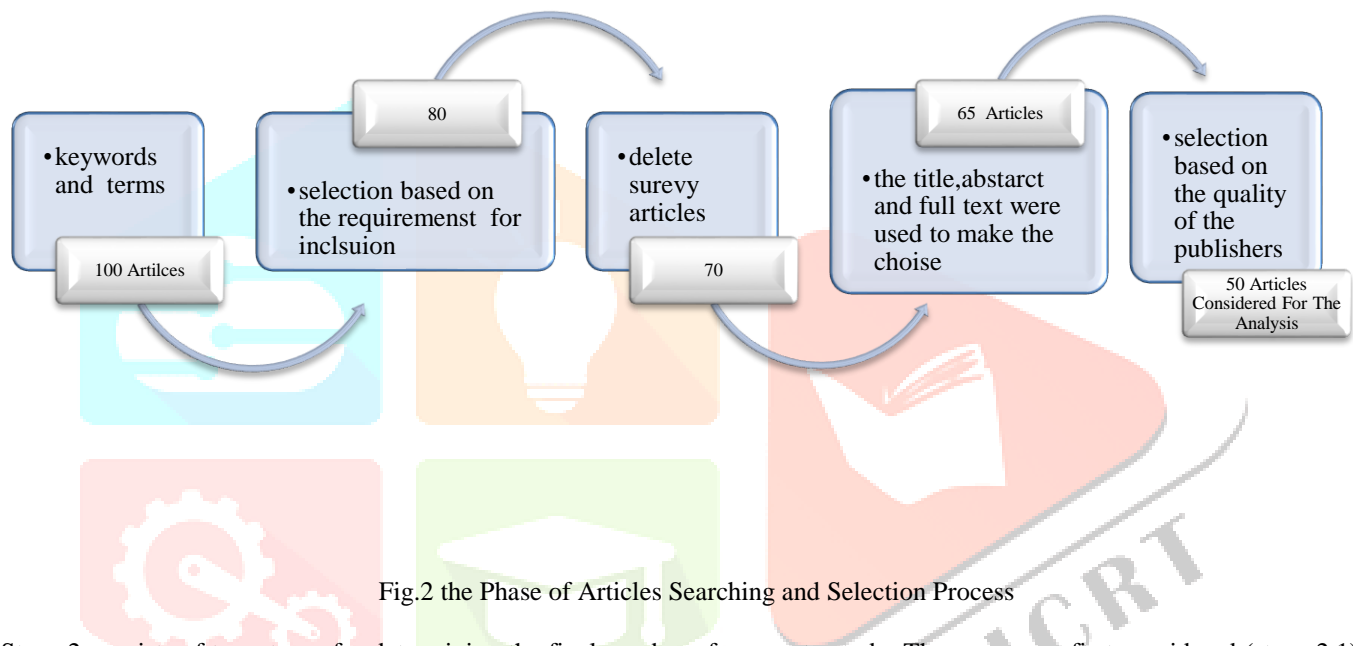


Fig.2 the Phase of Articles Searching and Selection Process

Stage 2 consists of two stages for determining the final number of papers to study. The papers are first considered (stage 2.1) At this time, 80 papers are remaining. Most research papers are published by Elsevier and Springer and Elsevier .At this point, there are 230 articles left. The title and abstract of the papers were reviewed in Stage 3. The papers' methodology, assessment, discussion, and conclusion have also been checked to ensure they apply to the research. At this point, 70 papers have been chosen for further consideration and then 65 papers. Finally, 50 papers that met the strict standards were chosen to review and examine the remaining articles

Table 1 the publisher's distribution of the papers.

Journals	Number Of Papers
Other Journals	24
MDPI	15
Elsevier	16
Springer	20
ACM	15
Hindawi	10
IEEE	23

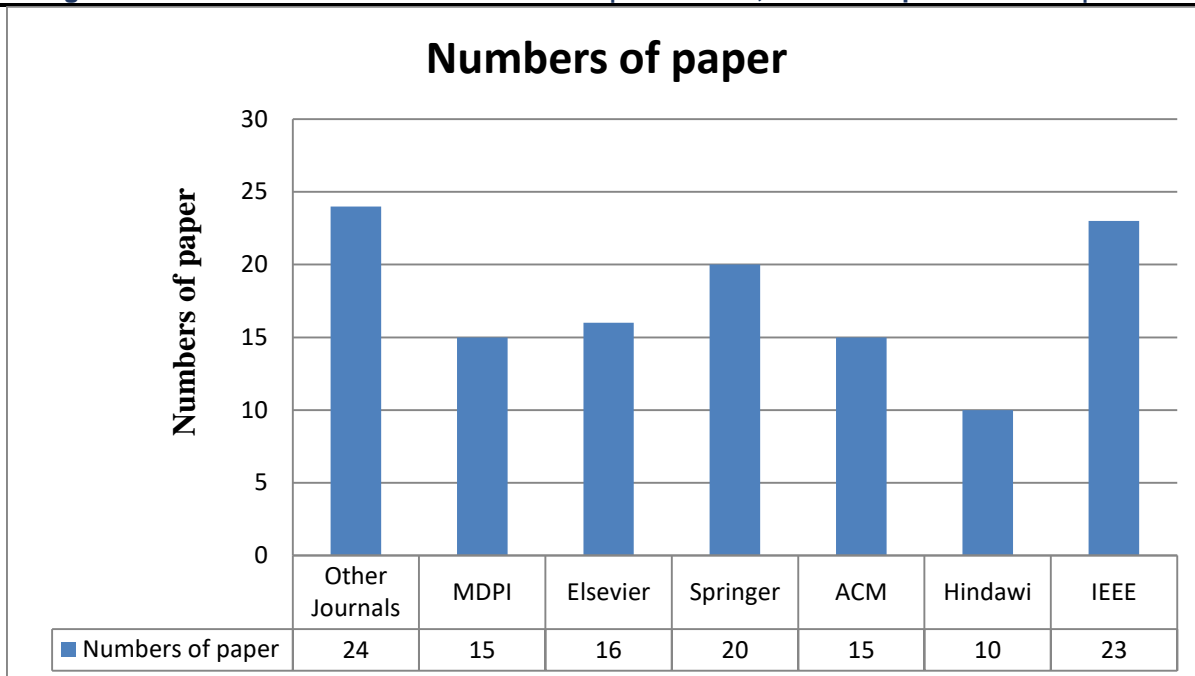


Fig. 3. Stage 1 is the publisher’s distribution of the papers.

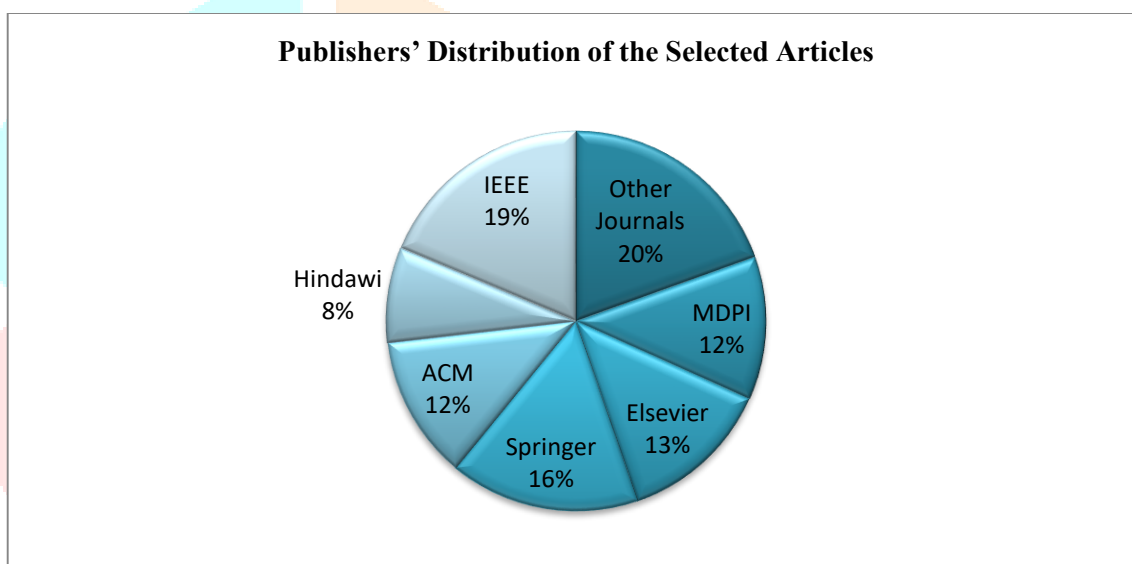


Fig. 4 the publishers’ distribution of the selected articles.

Fig 6 shows the distribution of the chosen articles by their publishers. Other journal publishes most selected articles (20%,24 articles). The lowest number is related to hindawi 8%, 10 articles, springer (16 % 20 article), ,ACM (12%,15 journals), MDPI (12% 15 journals),IEEE (19%,23 journals) selected for the review

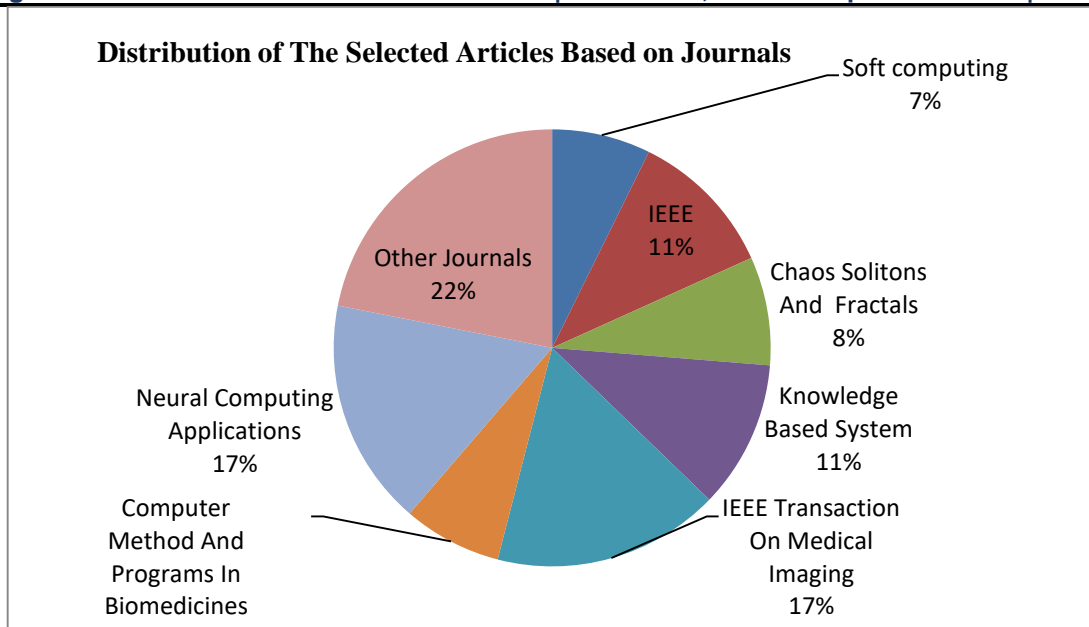


Fig.5 the papers are distributed by the publishers.

Fig 6 shows the distribution of the chosen articles by journals. Other journal publishes most selected articles (22%, 30 articles). The lowest number is related to Computer Method and Programs (7%, 10 articles). And Soft computing (7%, 10 articles). In Neural Computing Applications (17%, 23 articles), in IEEE (17%, 15 articles), Chaos Solitons And Fractals (8%, 11 articles), Knowledge Based System (11%, 15 articles), IEEE Transaction On Medical Imaging (17%, 23 articles), selected for the review.

Table 2 Distribution of the Selected Articles Based on Journals

Selected Articles	Number of Articles.
Computer Method And Programs In Biomedicines	10
Neural Computing Applications	23
Other Journals	30
Soft computing	10
IEEE	15
Chaos Solitons And Fractals	11
Knowledge Based System	15
IEEE Transaction On Medical Imaging	23

### III. Literature Survey

This article gives a short analysis of how AI can be used in covid-19. This article looks at the ways in which AI could be used in countries that aren't as well off. In [1], an in-depth analysis of how DNN algorithms can be used to find and predict covid-19 on their own is given. In the article [2], a new survey of algorithms based on AI is done to help fight the epidemic. In [3], some of the machine learning techniques that are used to process medical pictures related to the condition are reviewed. [4] gives an overview of the different AI methods that can be used to run covid-19. A review of data-driven approaches to tracking, modelling, and predicting the pandemic is given as a presentation. [5] Talks about the different models for how the disease might spread that have been suggested. In [3], a conversation about how big data can help with better management of the epidemic is shown. The article [1] gives an overview of the data science techniques that can be used to fight the disease. [8] gives a summary of recent research that looked at how machine learning could be used to fight the disease. [4] gives an in-depth look at the research done on how machine learning algorithms can be used to make predictions about the total number of cases. In [7], there is a review of how AI is being used to find new drugs. In [6], a review of the studies on how AI can be used to treat critical covid-19 patients is given. This review is now finished.

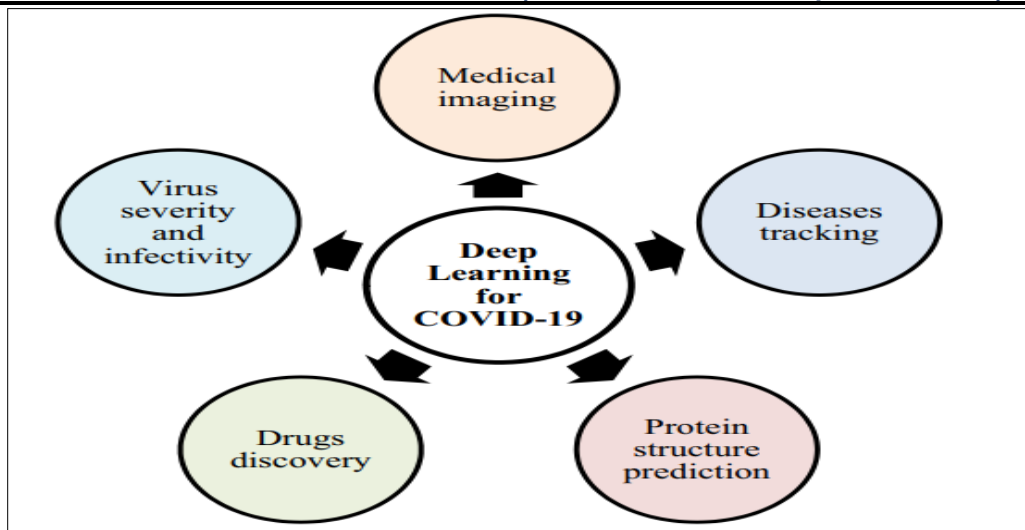


Fig.6 deep learning techniques to control COVID

**L. J. Muhammad et.al.** Even though no vaccine or treatment has been shown to work against the novel coronavirus (COVID-19 or 2019-nCoV) that is causing the 2019-nCoV pandemic, patients are making a full recovery with the help of antibiotics, antivirals, chloroquine, and vitamin C supplements. The spread of COVID-19 around the world needs to be stopped and fought with the help of non-clinical methods like data mining and augmented intelligence. This will help lower healthcare costs and give patients the best tools they can get to diagnose the 2019-nCoV pandemic. Using a South Korean epidemiological dataset of COVID-19 patients, data mining models were made to predict how well COVID-19 patients who were infected would get better. Using the programming language Python, the dataset was used to create the decision tree, support vector machine, naive Bayes, logistic regression, random forest, and K-nearest neighbour algorithms. The model predicts that people who get the COVID-19 pandemic should feel better in a few days to a few weeks. The decision tree data mining algorithm did a better job than the support vector machine, naive Bayes, logistic regression, random forest, and K-nearest neighbour algorithms at predicting whether or not COVID-19 patients will get better. Overall, they were 99.85 percent right. [1]

**Xinggong Wang et.al** (2020) So that patients can be quarantined and treated quickly, it is important to make a correct diagnosis of suspected COVID-19 cases as soon as possible. To stop the spread of SARS-CoV-2, it would be helpful to make a model that uses deep learning and can automatically identify COVID-19 using chest CT. 3D CT volumes were used to build a framework for deep learning that is only partially supervised. This was done so that COVID-19 could be used to classify and locate lesions. First, a pre-trained UNet was used to separate the lung area of each patient. Next, the 3D segmented lung area was put into a 3D deep neural network to figure out how likely it was that COVID-19 would be infectious. Lastly, the COVID-19 lesions were found by combining the classification network's activation regions with the unsupervised connected components. During the training phase, you had to finish 499 CT volumes. During the assessment phase, you had to finish 131 CT volumes. The ROC AUC for our method was 0.959, and the PR AUC was 0.976. With a probability threshold of 0.5, the algorithm was able to tell the difference between COVID-positive and COVID-negative cases with an accuracy of 0.901%. The method also had a very high negative predictive value of 0.982 and a positive predictive value of 0.840. The algorithm only needed 1.93 seconds to process the CT volume of a single patient when it was running on a dedicated GPU. Our deep learning model, which is only partially supervised, can accurately predict the chance of a COVID-19 infection and find the location of lesions in a chest CT scan without having to label the lesions in order to learn. An algorithm for deep learning that is easy to train and very effective makes it possible to find COVID-19 patients quickly. This is very helpful in the fight against the spread of SARS-CoV-2. [2]

**Mohamed Almansoor et.al** (2020) The COVID-19 pandemic is a worldwide event that happened between 2019 and 2020 and caused a lot of money to be lost. Every day, hundreds of thousands of people who might have an infection are tested, and the results are added up and looked at. In more developed countries, it usually only takes a few hours to get the results of a virus test. In less developed countries, however, it can take several days. The goal of this study is to answer the question of whether or not normal blood tests can help find covid-19 by using a number of different machine learning algorithms. If this is the case, it would show which people should take the virus test. In this research, we use a number of different machine learning algorithms, such as support vector machines, adaptive boosting, random forest, and k-nearest neighbours. After that, a number of algorithms are used to create ensemble learning, which leads to classification in the end. The research shows that the ensemble learning method has the highest true positive rate, at 30%. The results show that standard blood tests aren't very good at giving accurate information about the presence of COVID-19.[3]

**Furqan Rustam et.al** (2020) Forecasting methods based on machine learning (ML) have shown how important they are by being able to predict outcomes in advance, which helps make better decisions about what to do in the future. ML models have been used for a long time in a wide range of situations where it was important to find and rank the most dangerous parts of a threat. Several different ways of making predictions are used widely today to deal with problems related to predicting. This work shows that machine learning algorithms can accurately predict how many patients will get COVID-19 in the near future. People now think that this virus could be dangerous for all of humanity. In this study, four standard forecasting models were used to make a prediction about the potentially dangerous factors related to COVID-19. These models were linear regression (LR), least absolute shrinkage and selection operator (LASSO), support vector machine (SVM), and exponential smoothing (ES). Each model makes three different kinds of predictions: how many people will get sick, how many will die, and how many will get better in the next ten days. The results of the study show that it would be a good idea to use these methods to deal with the COVID-19 pandemic right now. The results show that out of all the models used, ES works the best, followed by LR and LASSO, which do a good job of predicting new confirmed cases, death rate, and recovery rate. SVM, on the other hand, doesn't do well in any of the prediction scenarios given the data they were given. [5]

**Richard F. Sear et.al (2020)** A lot of false information that could be dangerous is being spread about COVID-19 on the internet. Here, we show how machine learning can be used to measure COVID-19 content among online opponents of well-known health guidelines, especially vaccinations ("anti-vax"). We've found that the group of people who don't like vaccinations (called the "antivax" community) is building a COVID-19 debate that is less focused than the group of people who do like vaccinations (known as the "provac" community). But the anti-vaccine community offers a wider range of "flavours" of COVID-19 topics. As a result, it can reach a wider range of people who are looking for COVID-19 advice online. Some of these people may be afraid of a fast-tracked, mandatory COVID-19 vaccine or looking for other ways to treat the disease. So, it looks like the people who are against vaccines are in a better position than those who are for them to bring in new support in the future. This is a cause for concern because, if a COVID-19 vaccine doesn't get widely used, the world won't be able to provide herd immunity, leaving countries vulnerable to future COVID-19 outbreaks. We give a mechanical model that helps explain these results and may help figure out how likely it is that different kinds of intervention will work. Our method is flexible, and as a result, it solves the urgent problem that social media platforms are facing right now, which is that they need to evaluate a lot of online health information that is wrong or misleading. [6]

**Ekta Gambhir et.al (2020)** The Novel Corona virus, which is also called COVID-19, has spread to different parts of the world. This has affected the whole planet and caused the deaths of millions of people. This should be a strong warning to the people in charge of the public's health, and it will be remembered as one of the worst pandemics ever. The goal of this article is to help you learn more about how different Machine Learning models can be used in the real world. In particular, the paper will be about: In this research, the statistics for the whole world were looked at, and the current pattern or trend of Covid-19 transmission in India was also looked at. This study, which was done with data from India's Ministry of Health and Family Welfare, shows different trends and patterns that have been seen in different parts of the world. The data that will be looked at was collected over 154 days, from January 22, 2020, to June 24, 2020. More analysis can be done on the data so that it can be used in future research, and more results can be found. [7]

**Zhao Wang et.al (2020)** The pandemic of corona virus disease 2019 (COVID-19), which has spread to hundreds of countries, has caused a global public health emergency. It would be great if CT imaging could be used to automatically find COVID-19. This would help doctors make better diagnoses and make it easier to understand images. This is because the number of new infections is always on the rise. It is important to combine examples from different medical systems to make models that are both stable and generalizable. This is done to increase the datasets that are used to develop machine learning methods. In this paper, we propose a new joint learning framework for accurate COVID-19 identification by making good use of heterogeneous datasets with different distributions during the learning process. We make a strong backbone by reworking the recently proposed COVID-Net in terms of network architecture and learning strategy in order to improve the accuracy of predictions and the speed with which they are learned. This helps us learn new things faster and better. In addition to our improved backbone, we do independent feature normalisation in latent space to deal with the cross-site domain shift. This is done with the help of our stronger backbone. We also suggest using a contrastive training target as a way to improve the domain invariance of semantic embeddings in order to improve the performance of classification across all datasets. Our method is built and tested using two large COVID-19 diagnosis datasets made up of CT images that are available to the public. Extensive tests show that our method improves the performance of both datasets in a consistent way. It does better than the original COVID-Net trained on each dataset by 12.16 and 14.23 percent in AUC, and it also does better than the best multi-site learning methods that are already available. [8]

**Rachna Sethi et.al (2020)** As a pandemic, a new corona virus spillover event is hurting people's health all over the world. To stop the spread of disease, a lot of people need to be checked out at once. In pathology, real-time polymerase chain reaction is one of the most common ways to find out what's wrong (PCR). Because the number of false positives is going up, people are now looking into other ways to test. Screening for COVID-19 has shown that chest X-rays of COVID-19 patients are a useful alternative indicator. To be sure of accuracy, though, you need to know a lot about radiology. If a diagnosis recommender system can help the doctor look at a patient's lung images, it will make it easier for the doctor to make a diagnosis. Using deep learning techniques, especially Convolutional Neural Networks (CNN), to sort medical images has been a huge success. For the diagnosis of COVID-19, four different deep CNN architectures were used to look at pictures of chest X-rays. Using the ImageNet database, these models have already been trained, so huge training sets aren't needed. Using CNN-based architectures, it has been found that COVID-19 disease can be found. [9]

**Yuxiang Li et.al (2020)** Since the 2019 Corona virus Disease (COVID-19) was first reported, it has quickly spread to every part of the world. For both controlling the disease and taking care of patients, it is important to find COVID-19 as soon as possible. Even though non-contrast thoracic computed tomography (CT) has been found to be a useful diagnostic tool, the disease outbreak has put a lot of stress on radiologists who have to read the tests, which could lead to wrong diagnoses because of fatigue. Automatic classification algorithms that work well can be very helpful, but they often need a large number of COVID-19 examples to be properly trained, which can be hard to get in a timely manner. In the meantime, one of the challenges is figuring out how to make the most of the existing archive of non-COVID-19 data, which is often called the negative samples, when there is a big difference between the classes. The disease is also spreading quickly, which means that algorithms must be made quickly. In this work, we propose a new way to train COVID-19 classification networks to work well and quickly by using a small number of COVID-19 CT exams and an archive of data from negative samples. This method uses a small number of samples that are not positive and a small number of COVID-19 CT test results that are positive. To explain this in more detail, we show a brand new method of self-supervised learning for extracting features from the COVID-19 and negative samples. Then, two kinds of soft-labels ('difficulty' and 'diversity') are generated for the negative samples by computing the earth mover's distances between the features of the negative and COVID-19 samples, from which data 'values' of the negative samples can be assessed. So, a certain number of negative samples are chosen ahead of time and then put into the neural network to train it. The results of our experiments show that our method can get better results with about half as many negative samples, which greatly cuts down the amount of time needed to train a model. [10]

**T. Padma et.al (2020)** Since it started in China in December 2019, the COVID-19 pandemic has quickly spread around the world, causing life-threatening problems. So that the Corona virus doesn't spread through the population, it is important to find positive cases quickly. Recent studies have used CT and X-ray images of the chest to show how bad the corona virus is in the lungs. These images show that the corona virus affects the lungs in a clear way. As AI gets better at medical imaging, it will be able to handle huge amounts of data quickly and accurately, making it easier and more accurate to find diseases even in remote places. Convolution 2D techniques are used on open source datasets of COVID-19 from GitHub and Kaggle to create a proposed method for analyzing



chest X-ray images to detect COVID-19 for binary classes with a 98 percent accuracy and a 98 percent validation accuracy, with a loss of about 0.15 percent. [11]

**Mohammad Jamshidi et.al (2020)** COVID-19 has put the whole world in a tough situation that has never happened before. It has put a scary stop to life everywhere in the world and killed thousands of people in the process. Even though COVID-19 has spread to 212 different countries and territories and the number of infections and deaths has gone up to 5,212,172 and 334,915, respectively, it is still a major threat to public health (as of May 22nd, 2020). In this study, an AI-based way of dealing with the problem of fighting viruses is shown (AI). Several Deep Learning (DL) strategies, like Generative Adversarial Networks (GANs), Extreme Learning Machines (ELMs), and Long/Short Term Memories, have been described and shown to help reach this goal (LSTM). It describes an integrated bioinformatics approach, which is one in which different pieces of information from a continuum of structured and unstructured data sources are put together to make platforms that are easy for academics and medical professionals to use. The main benefit of these AI-based platforms is that they can speed up the time it takes to diagnose and treat COVID-19 disease. Researchers looked at the most recent articles and medical reports that were relevant in order to choose inputs and targets for the network. This could make it easier to find a reliable Artificial Neural Network-based solution to COVID-19's problems. There are also some inputs that are unique to each platform, such as the different types of data, such as clinical data and medical imaging, which can help the introduced approaches work better and give the best answers in real-world applications. These inputs can help improve how well the new ways of doing things work to get the best results. [12]

Gciniwe S. Dlamini et.al (2020) the 2019 new SARS-CoV-2 virus caused the COVID-19 pandemic, which is making a lot of trouble all over the world. To learn more about this newly discovered virus and how it is related to other infectious agents, scientists need to find new ways to look at the genome. In this study, whole genome sequence data were used to look at the intrinsic dinucleotide genomic signatures of SARS-CoV-2 and seven other pathogenic species. Before they were put through the classification process with the help of the extreme gradient boosting (XGBoost) model, the genome sequences were changed into the relative frequencies of dinucleotides. The classification models were trained to do two things: a) tell the difference between the sequences of all eight species, and b) tell the difference between the sequences of SARS-CoV-2 that come from different places. In the eight-species classification challenge, our method got a perfect score of 100% for all tasks and all measures of performance. Also, the models were able to classify SARS-CoV-2 sequences into the six continental regions with a balanced accuracy of 67 percent. Also, the models were able to classify SARS-CoV-2 samples as either coming from Asia or not coming from Asia with a balanced accuracy of 86 percent. All eight species' dinucleotide genomic profiles were looked at, and the results showed that the viral sequences of SARS-CoV-2 and MERS-CoV are very similar. More research on the SARS-CoV-2 viral genomes from all six continents showed that samples from Oceania had the most TT dinucleotides and the fewest CG dinucleotides compared to the other continents. Other dinucleotide signatures had very different frequencies, but the dinucleotide signatures of AC, AG, CA, CT, GA, GT, TC, and TG were very similar in most genomes. Taken as a whole, the results of this study show that the relative frequencies of dinucleotides can be used to tell different species apart that are genetically similar.[13]

**Elena Casiraghi et.al (2020)** More than 34 million people were infected with the SARS-CoV-2 virus between January and October of 2020, resulting in more than one million deaths globally (data from the Johns Hopkins University). Because of the outbreak of COVID-19, emergency departments were overrun with patients who needed to be admitted or discharged quickly. Due to the low sensitivity of chest radiographs (CXR), additional variables and criteria are needed to effectively estimate the probability of infection. To better anticipate patient risk, we propose an automated computer system that uses radiological, clinical, and laboratory information, as well as an explainable machine learning approach that may give doctors with easy choice criteria for assessing patient risk. Random Forest (RF) and Boruta are combined in a 10-fold cross-validation technique to provide a variable importance estimate that is not influenced by the existence of surrogates. Training an RF classifier with these most significant variables results in an associative tree that is particularly appealing because of its simplicity. The results reveal that the radiological score automatically computed by a neural network is strongly correlated with the score computed by radiologists, and that laboratory variable, coupled with the number of co-morbidities, aids risk prediction. ' Our method outperformed generalised linear models in terms of prediction accuracy and robustness. For speedy and accurate risk prediction in COVID-19 patients, the suggested machine learning-based computational method can be simply installed and used in emergency rooms. [14]

Nugroho Setio Wibowo et.al (2020) The Covid-19 epidemic, which has spread all over the world, including to Indonesia, has forced the government to take steps to stop the spread of the virus. People are getting together to talk about how they should keep their distance and stay inside. Twitter is one of the media platforms that can be used for this purpose. Even though people have tried to be more social, the number of people who have caught Covid-19 has not gone down yet. A lot of analysis is needed to figure out how to make things better. One thing that needs to be looked at is how well the community follows the rules about how Covid-19 is given out. The goal of this study is to find out how well people in Indonesia follow the rule to stay at home and how that relates to the number of people who test positive for Covid-19. The information for this study comes from the tweets that people in Indonesia sent out. The two individual algorithms that are used are logistic regression and random forest. These two algorithms are combined with bagging, which is the ensemble algorithm. The Twitter posts that were looked at were those that were made in Indonesia between March 3, 2020 and July 7, 2020 and had the words "covid19," "tetapdirumah," "stayathome," "mudik," and "psbb" in them. Based on the data from 705 tweets, the non-compliance community has grown since the middle of June 2020. This is in line with the trend of more Covid-19 cases in Indonesia, which has also been rising. [15]

**Zhongyi Han et.al (2020)** During the SARS-CoV-2 pandemic that will hit the whole world in 2020, automated COVID-19 screening based on chest CT will be very important and necessary. The spatial complexity of 3D volumes, the difficulty of identifying infection sites, and the small difference between COVID-19 and other viral pneumonias on chest CT all make screening for COVID-19 very hard. Even though there have been a few pioneering works that have made a lot of progress, most of these works are either hard to understand or require that infection locations be marked by hand. In this study, we talk about what we did to make COVID-19 screening from chest CT very accurate and easy to understand by using weak labels. In this paper, we talk about these efforts. In the attention-based deep 3D multiple instance learning (AD3D-MIL) method we propose, a 3D chest CT, which is treated as a bag of instances, is given a label at the patient level. AD3D-MIL is able to build semantically correct deep 3D instances by following the likely infection area. AD3D-MIL also uses an attention-based pooling method on 3D instances to show how each instance affects the bag label. AD3D-MIL has finally learned the Bernoulli distributions of the bag-level labels. This will make them much easier to learn. We looked at 460 chest CTs, including 230 CTs from 79 people who were diagnosed with COVID-19, 100 CTs from 100 people who were diagnosed with common pneumonia, and 130 CTs from 130 people who did not have

pneumonia. Several real-world experiments have shown that our algorithm has an overall accuracy of 97.9%, an area under the curve (AUC) of 99.0%, and a Cohen kappa score of 95.70%. Because of these benefits, our algorithm is a good tool that can be used to help screen COVID-19 and get good results. [16]

**Ulhaq et al.** There was a thorough look at all of the ways that corona viruses can be stopped. These methods include medical image processing, data science methods for modelling pandemics, artificial intelligence (AI) and the Internet of things (IoT), AI for text mining and natural language processing (NLP), and AI in computational biology and medicine. This gives a big picture view of what's happening in the world of research right now. In a survey [15] that looked at the use of computer vision technologies to COVID-19, the segmentation of lung images was looked at and written down. The only goal of this study is to explain how deep learning techniques can be used to find corona viruses. In order to help researchers come up with better ways to find corona viruses, this study gives a summary of all the methods that have been written about in the scientific literature. Along with the method, this paper talks about the datasets that were used, the common metrics that were used for evaluation and comparison, and the future of the field.

### 2.1 Convolutional Neural Networks

Convolutional neural networks, which are also called "artificial neural networks," are a type of deep learning method that is based on how living things naturally understand what they see [16]. CNNs are nothing more than neural networks that have been layered and stacked. There are three main types of layers, which are called convolutional layers, pooling layers, and fully connected layers, in that order. For the CNN model's first layer, called the "input layer," the width, height, and depth of the image must be given as input parameters. This is a layer that must be in any CNN model. The phase where the convolutional layers are set up comes right after the input layer. The number of filters, the size of the filter window, the stride, the padding, and the activation are some of the parameters for these layers. In the process of figuring out the weighted sum [17,18], convolutional layers are used to get meaningful feature maps for the place where the input was given.

After that, each feature map is fed into an activation function, and bias is added to the final product before it is sent out. Rectilinear unit activation, also called ReLU activation, is the most common type of activation function [19]. By adding pooling layers to the process, the output from the convolutional layers can be made easier to handle. As the size of the model and the number of filters in the convolutional layer continue to grow, the output dimensionality will continue to grow at an exponential rate. This will make it hard for computers to figure out what to do with the data. Pooling layers are used to reduce the number of dimensions in a model in order to make computations easier and sometimes to get rid of noise. Pooling layers can be max pooling, average pooling, global average pooling, or spatial pooling. The max pooling layer is the most commonly used type of pooling layer [20].

After the output has been flattened, a single-array feature vector is made and sent to a fully linked layer. As the last step, [21] activation functions like sigmoid, softmax, and tanh are used to define a classification layer. In this layer, the number of classes that will be used is set, and the aggregated class scores are calculated from the retrieved features. Batch normalisation layers are used either after the input layer or after the activation layers to standardise the learning process and shorten the amount of time spent training [22]. Another important part is the loss function, which adds up all of the wrong predictions made during the training and validation processes. After each epoch, the loss is "back propagated" to the CNN model to make the learning process more effective. [23].

### 2.3 Several Available Architectures

No matter the dataset or the application, keep a high level of generaliz ability. This section gives a brief overview of some well-known architectural styles, such as AlexNet, VGG, Inception, ResNet, DenseNet, MobileNet, and Xception. AlexNet is a five-layer convolutional neural network that is easy to understand. The two different versions of the VGG network are called VGG16 and VGG19 [26]. The VGG architecture was first thought of as a way to help programmes that recognize images. In VGG16 and VGG19, 16 and 19 wt layers are used with a three-by-three convolutional filter size. In 2014, the network took first and second place, respectively, in the ILSVR (ImageNet) competition. The size of the image you send in is always 224 pixels by 224 pixels. The ImageNet dataset, which has millions of different pictures, was used to train the model [28]. In contrast to CNN designs, which stack the layers, InceptionNet's [29] new architecture includes a "inception block" as part of the structure.

There are many different kinds of the inception family to choose from. In 2014, the inception network took part in the ILSVR (ImageNet) competition [27], in addition to being used for image classification and localization. In the inception block, instead of adding more layers to the model to make it deeper, the authors apply multiple filter sizes to the input image at the same time. This makes it look like the model is more detailed than it really is. As a result, the width of the model gets bigger. After each inception block, all of the block's outputs are added together and sent to the next inception block. Inception is currently available in the following versions: InceptionV1 (GoogleNet) [29], InceptionV2 and InceptionV3 [18], InceptionV4 and InceptionResNet [30]. The model can handle images that are no bigger than 224 pixels by 224 pixels.

ResNet [31] was the winner of the ILSVRC 2015 [27] competition and it is also used in algorithms for classifying images. The ResNet family uses the residual block, which can be thought of as a network inside a network, in their design. The network is made up of five phases, some of which are convolutional blocks and others are identity blocks. The size of the input image is 224 by 224 pixels, which is the same size as the VGG family. Many versions are available. The inception block and the residual block have been combined into a single part of the hybrid architecture called Inception-ResNet [30]. Images with a size of 229 by 229 pixels can be sent to InceptionResNet. The ResNet design has been changed to the DenseNet architecture [32] because it has been made bigger and better. The architecture is built using a residual identity block, just like the ResNet family. However, instead of summation, concatenation is used during the building process. In traditional CNN model hierarchies, L links stand for L levels.

DL applications in COVID-19 and DL Methods In General

AI-based approaches are often used to identify, classify, and diagnose medical images. Recent improvements in artificial intelligence have made it much easier to screen for, diagnose, and predict COVID-19. These improvements have led to better scaling up, faster responses, more reliable and efficient results, and in some cases, machines that are better at some healthcare tasks than people. Machine learning (ML) and deep learning (DL) are the two parts of AI that have been getting the most attention lately (DL). In the sections that follow, we'll look at how both machine learning and deep learning can be used to fight the COVID-19 outbreak and lessen its effects. In order to stop the COVID-19 pandemic, researchers have recently started to use DL-based methods like CNN, RNN, and LSTM for COVID-19 detection, diagnosis, and classification. These methods are meant to find the virus, figure out what it is, and put it into a group. There are a lot of things that can be done, such as screening, repurposing medications, making predictions, and making forecasts. Machine learning techniques have also been used a lot to find patterns that are linked to

epidemics. In the context of the COVID-19 pandemic, many studies have tried to screen, classify, diagnose, repurpose medications, and predict COVID-19 using these methods. Several of the best machine learning strategies, like support vector machine, logistic regression, random forest, and decision tree, have been used to fight the COVID-19 epidemic [20]. [ Also, deep learning (DL), which is also called hierarchical learning [21], is one of the most important new developments in AI. At the moment, DL methods are being used successfully in a wide range of AI-based medical applications, such as analyzing MRI (magnetic resonance imaging) pictures to find out if someone has cancer. Neural Networks (NN) and Deep Learning (DL) have become very popular in modern science because they can learn from their surroundings. These two methods are used a lot in many different areas of research, such as categorization and forecasting problems, smart homes, image recognition, self-driving cars, and other similar fields. Because they can work with many different data formats in many different areas [22].

DL is a model of how the human brain sorts through information to make the best decisions possible [23]. On the other hand, DL teaches a machine to understand inputs in a way similar to how the human brain does. It does this by using a number of layers to predict and classify data. These layers are used as input for the next layer, just like how neural networks (NNs) in the brain use stacked filters [24]. Keep moving around in the feedback loop until the output is the same as it was before. Each layer is given a weight so that the right output can be made, and these weights are changed as the training goes on so that the right output can be made [25]. There are three types of DL approaches that can be found in [26]. They are supervised, semi-supervised, and unsupervised. Each known value is used as an input vector for the supervisory signal, which stands for the desired value [27].

Based on the labels that are already there, the method makes guesses about the labels that will be put on the output [28]. Classification approaches use supervised learning and can recognise faces, traffic signals, spam in a file, convert speech to text, and do many other things [29]. The goal of the process called "semi-supervised learning" is to bridge the gap between "supervised learning" and "unsupervised learning." For training data, semi-supervised learning uses both values that have been labelled and values that have not been labelled. Semi-supervised learning is a type of learning that falls between unsupervised learning and supervised learning [30]. If the unlabeled data are combined with a small amount of labelled data, the accuracy of learning will improve by a lot [11].

DL approaches give rise to a number of theoretical hypotheses. The first problem is that the same name is given to data that is close together. The second idea is the cluster assumption. This idea says that all the data in a cluster should have the same name. The third and last thing to think about is that the data are limited to one dimension [31] instead of using the whole input space. Learning without supervision starts by figuring out how the parts fit together, and then it sorts the parts based on how they fit together. Clustering, Anomaly Detection, and NN all use these methods. Unsupervised learning is a method that is often used in the security industry to find things that aren't normal [31].

Artificial Neural Networks (ANN) is used by the vast majority of DL methods to process and extract features. During the learning process, there is a feedback mechanism where each level changes its own input data to make a summary representation. In the DL approach, the number of layers needed to successfully convert the data is called the "depth" [32]. CAP, which stands for Credit Assignment Path, was used for the whole process of that change. In a feed-forward NN, the number of hidden layers is multiplied by the number of output layers to get the depth of CAP. This shows how many layers are in the network as a whole. Because an RNN's layer could have a lot of signals that go through the network more than once [13], the CAP depth cannot be calculated. Also, the technique for processing images that is used most often is called CNN and is based on neural networks. Deep learning is also the most accurate way to process images because the technique for extracting features is automated and done all the way through the CNN training on photos. [33].

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

Bhattacharya, Maddikunta et. al. 2020 It was talked about how the COVID-19 outbreak led to the development of medical image processing DL apps for smart and safe cities. DL was used to stop COVID-19 from spreading by making and testing a vaccine and other drugs. It was also used to predict illness and keep track of how the virus spread. In past investigations, they found problems with data protection, the different ways that outbreaks happen, control, and reliability, and the difference between COVID-19 symptoms and those of other diseases. Researchers eventually looked at a number of DL applications in medical image processing that used COVID-19. As a separate project,

**Alsharif et. al. 2021** shown that the COVID-19 treatment plan does a lot of research on DL. There are a few ways to avoid getting COVID-19 disease, and their research made the literature on DL technology clearer. A data-efficient CNN was used to find COVID 19 on CT scans. The results of their poll showed that more DL research is needed to figure out how to diagnose COVID-19. They put the studies into two groups: those that used DL techniques and those that used ML techniques. They then compared the ML and DL mechanisms right away. In their survey, they didn't look at very many works. This study also didn't compare how things were done.

**Alafif, Tehame et. al. 2021** AI-based ML and DL methods for diagnosing and treating COVID-19 illness have been looked into. They talked about AI-based machine learning (ML) and deep learning as part of their presentation (DL). The study gives an overview of the most up-to-date methods and applications for ML/DL researchers and the health community as a whole. It also gives examples of how ML/DL and information could be used to stop the spread of COVID-19 outbreaks. As part of this effort, they put the ML ways of diagnosing and treating into groups and gave these works ratings. For the COVID-19 diagnosis, they also tested AI-based ML and DL techniques using chest X-ray and CT images, COVID-19 speech/audio analysis, and COVID-19-based drug formulation, among other things.

In addition, Shorten, **Khoshgoftaar et. al. 2020** The response of DL to the pandemic was looked at, and ideas were made for future COVID-19 investigations. They looked into how DL could be used in NLP, biosciences, computer vision, epidemiology, and other related fields. Researchers say that big data changes both of these applications and the way learning tasks are set up. For COVID-19, they looked at where DL is now and what its main problems are. Their research focused on how DL could be used in the life sciences to predict the structure of proteins, do precise diagnostics, and find new uses for old medicines. In the field of epidemiology, DL was also used to spread predictions. In their review of the literature, they found a lot of DL strategies to fight COVID-19. They planned to do this poll to speed up the use of DL in the COVID-19 study.

Sufian, Ghosh et. al. Computers in Biology and Medicine 141 (2022) 105141-5 by A. Heidari et al. looked at the pros and cons of deep TL methods, edge computing, and other problems related to them in the context of controlling the COVID-19 outbreak. Using real data, they also showed a hypothetical integrated model that described the background and the possible effects of working in sensitive areas.

**Wang Yunlu et al. 2021** This work can be used to figure out how different people breathe, and we can put this technology to use in the real world. We came up with a way to put people infected with COVID-19 into different groups for large-scale screening. In the beginning of this paper, a new and powerful RS (Respiratory Simulation) Model is shown. The goal of this model is to bridge the gap between a lot of training data and not enough real-world data, so that it can take into account how real-world respiratory signals look. They started by using two-way neural networks like the GRU network attentional tool (BI at GRU) to find the six clinically important breathing patterns (Eupnea, Biots, Cheyne-Stokes, Bradypnea, and Central-Apnea). The study's results show that the suggested model can correctly identify six different respiratory trends with a precision of 94.5 percent, an accuracy of 94.4 percent, a recall of 95.1 percent, and an F1 of 94.8 percent. Comparison tests show that the new BI at GRU, which is designed to classify breathing patterns, is better than the most advanced models that were already available. The deep model and design principles that have been suggested have a lot of potential to be used in big ways, like at work, in public places, and in sleeping situations.

In their study [3], **Jiang Zheng et al.** showed a portable, non-contact way to track the health of people wearing masks by looking at parts of their respiratory systems. This was done by paying attention to how the person breathed. The most important parts of this device are an Android phone and a FLIR-equipped thermal imaging camera (forward-looking infrared). This can help tell the difference between COVID-19 patients and other patients in more realistic situations, like pre-screening in institutions and clinical centres. In this study, health screening was done by using cameras based on the DL architecture to record thermal and RGB footage. In the first step, they used techniques for analyzing lung data to find out who was wearing a mask. In the second step, they took the results for pulmonary disease and used a BI at GRU function on them to get the health screening result. In the third and final step, they were able to classify the respiratory health of a sick person with an accuracy rate of 83.7%.

**Imran Ali et al. 2020** A screening solution based on artificial intelligence (AI) that could find COVID was thought up, built, and then tested after it was put into use. This solution could be sent to someone else using an app on a smart phone. AI4COVID-19 is the name of the mobile app that records and sends triple 3-second cough sounds and a response back to AI-based clouds running in the cloud within two minutes. Coughing is a common sign of about 30 different illnesses that are caused by non-COVID-19. Because of this, COVID disease is hard to diagnose based on coughing alone because it is a multidisciplinary issue. The accuracy of the respiratory system can be raised to 88.76% by studying morphological direction changes that are different from cough.

**Brown Chloe et. al.** proposes an Android/iOS app to collect COVID-19 sounds data from crowd-sourced sounds respiratory data of more than 200 positives for COVID-19 from more than 7,000 unique users; Brown Chloe et al. have taken a lot of general parameters and three major sets of COVID-19 tasks based on the sounds of a person's breath and cough. Here, the parameters are i) COVID-positive/non-COVID, ii) COVID-positive with cough/non-COVID with cough, and iii) COVID positive with cough/non-COVID asthma cough. In task one, we got 80% accuracy for 220 users whose modality was cough + breath, 82.5% accuracy for 29 users whose modality was cough only, and 80% accuracy for 18 users whose modality Because the net isn't designed to catch every COVID-19 cough, the recall function is a little lower (72%).

**Hassan Abdelfatah et al.** Recurrent Neural Networks (RNNs) were used to make a system for finding COVID-positive patients by analysing the sounds of coughing, breathing, and speaking. Long-Short-Term Memory (LSTM) was used to analyse the sounds of coughing, breathing, and speaking in order to find the COVID-19 virus. When the results of the speech test are compared to recordings of coughing and breathing, they show that the test wasn't accurate enough.

**Orlandic Lara et al.** COUGHVID, a crowdsourced data set that can be used to analyse coughs, has been added to the COVID-19 symptom; There are more than 20,000 cough recordings from the general public in the COUGHVID collection. These recordings show a lot of different things, like gender, age, location, and COVID-19 status. For training the classifier, they have directly collected a set of 121 cough sounds and 94 sounds that don't sound like a cough. There are voices, laughter, silence, and many other sounds in the background. They decided how to label the recordings based on the following self-reported status variables: 25% of the sound recordings had healthy values, 25% had COVID values, 35% of the sound recordings had symptomatic values, and 25% had healthy values. Also, 15 percent of the cough sounds had to be labelled by all three reviewers. The numbers of people who tested positive for COVID, who showed symptoms of COVID, and who were healthy were 7.5%, 15.5%, and 77.5%, respectively. 65.5 percent of the people in the study were men, and 34.5 percent were women. In 632 COVID-19 cough data, it showed up as dyspnea that could be heard (93% of the time), wheezing (90% of the time), stridor (98.7% of the time), choking (99.1% of the time), or nasal congestion (99.2% of the time).

#### **A-CNN Methods**

CNN is one of the most important and most important ways to DL. It has been used in almost every area of medicine, and researchers find it to be one of the most interesting methods. As we talked about in the second section, the technique is most often used to identify CT scans, MRI pictures, and the backgrounds of these scans. In this section, we'll talk about five different ways to do things.

**Kedia and Katarya [57]** Deep CNNs were used to automatically predict COVID-19. These scientists wanted to make an ensemble model that could use Chest X-ray scans to tell the difference between healthy, uninfected people and sick people. Also, they used binary classification to compare chest X-rays of COVID-19 and non-COVID-19 patients. The dataset was put together with information from a number of free and open-source online sources. There was no cost to use these resources for academic purposes. With the help of these public datasets, we were able to train a complicated DNN and get great results. Also,

**Wang, Nayak** COVID-19 detection in CCTs is supposed to be based on CSHNet. CSHNet. The four groups they looked at in their research were CAP, Second Pulmonary Tuberculosis, and Community-Acquired Pneumonia (COVID-19) (SPT). The method they use in their research is called Deep CCT Fusion Discriminant Correlation Analysis (DCFDA). They made a pre-trained network selection algorithm for fusion so they could choose the best models that had already been trained. With the help of the proposed TL algorithm, the learning of model features was finished. Results showed that when CCTs are used, the CSHNet gives the best results, making it easier for radiologists to diagnose COVID-19. The results show that using CCTs to find lung diseases can help people make decisions. Using cloud computing, their algorithm can be easily moved to the server of a new hospital. Also, to tell the difference between COVID-19 and normal X-ray images,

**Ismael and S, engür** The DL approach used deep feature extraction, fine-tuning of a CNN that had already been trained, and full-scale training of a CNN model that had already been trained. Deep CNN models that had already been trained on the data were used to pull out deep features from the data. The deep features were put into groups using kernel functions that ranged from Linear and Quadratic to Quadratic and Gaussian (SVM). Deep CNN models that had already been trained were used to fine-tune the algorithm. The success of the study was measured by how well it classified things, and the results showed a high level of accuracy.

## B-Hybrid Method

In COVID-19 domains, hybrid approaches are one of the more advanced ways to do things. These plans use two or more methods to help people deal with problems. In these evaluations, we made a list of the mechanisms that were built with the methods being evaluated. It is a common way to deal with this disease in a wide range of fields. This section looks at ten different ways of doing things.

AbdelBasset, Chang By using a new semi-supervised two-path architecture-based segmentation model, COVID-19 segmentation from axial CT images can be made better. To make training easier, the encoder was made based on a version of ResNet34 that had already been trained. In addition to recombination and recalibration, it was suggested that the information learned from the support set be moved to the question slice segmentation. The model was better at generalisation when unlabeled CT slices were added and one slice was labelled during semi-supervised training. On COVID-19 CT images that were available to the public, the suggested FSS-2019-nCov and a number of baselines were studied. They also sent in detailed architectural selection studies with RRblocks, Skip connections, and the suggested building blocks. Due to the limited monitoring, the suggested FSS-2019-nCov segmentation output could not get very accurate segmentation. This can be fixed with a generative learning schema. Another problem was that they couldn't show volumetric data. This could be fixed by adding 3D CT images of COVID-19 to their model. Also,

Pereira, Guerin LSTM is the name of the network model that Data Training-SAE uses (LSTM-SAE). They put together all of the places in the world where the epidemic is at an advanced stage so that they could find countries that could be used to train ANN models. Using the different groups, the right countries for training models are chosen. The features that go into making them by hand show how a country dealt with the early spread of the pandemic. The final models were changed auto encoder models that were trained on these clusters and learned to predict possible data for Brazilian states. These predictions are used to estimate important facts about the condition, like when the number of cases will peak and how many people have been diagnosed with it so far. It will be used in the end to see if the distribution better reflects the results of MAE and to improve estimates of the peak of the pandemic. The pandemics are expected to end between June and August 2020, when 97 percent of the cases will be over.

Chaves-Maza and Martel to give some background, after the COVID-19 was made, an investigation was done into the policies on entrepreneurship in 20 countries. AI was used to look at factors that have a big impact on how long businesses last. In this study, researchers wanted to find out if it is necessary to help entrepreneurs by making predictions about how likely it is that a business project will be successful based on other factors that affect both the entrepreneur and the community in which they work. By putting SOM and MLP together, a technique based on artificial intelligence (AI) could be made. There are two different kinds of artificial networks used: SOM and MLP. From 2008 to 2012, when the economy was getting back on its feet after the financial crisis, data on 2221 Andalusian entrepreneurs and 769 other factors were used to make NNs. It was found that over 98 percent of those who were evaluated had good ideas about how likely it was that their business would survive and how well it would do. Besides, Leichtweis, de Faria Silva The Global Health Security Index (GHSI) and the SARS-basic CoV-2 reproduction number (R0) were looked at to see if they had anything in common (GHS). The climates of 52 countries and the COVID-19 cases and their GHS notes were looked at. The GAN was used to find out how temperature, sun radiation index, relative humidity, and GHS score affect the rate of COVID-19 spreading. By putting countries close to each other in the same group, SOM was used to figure out how each variable affected the spread of a disease. The relationship between relative humidity and R0 was not linear ( $p = 0.001$ ), but the relationship between temperature and R0 was linear (with a 36.2 percent explained difference). The sun radiation response curve showed a difference of 32.3% that could be explained ( $p 0.001$ ). COVID-19's control variables included the GHS index, which accounted for 38.4% of the difference, and climate variables, which had a significant nonlinear effect on countries with higher GHS index scores ( $p 0.001$ ).

Al-Waisy, Mohammed The COVID-DeepNet system was made as a hybrid multimodal DL system to help professional radiologists look at CX-R pictures quickly and accurately to find viruses. With contrast-limited adaptive histogram equalisation (CLAHE), the images from the CX-R were clearer and brighter. Then, a DBN and a DBN with loops were looked at using two different DL methods. Radiologists were told to use the parallel design because it gives them a lot of confidence that COVID-19 can tell the difference between healthy and sick people. In large datasets, the accuracy of detection is 99.93%, the sensitivity is 99.90%, the specificity is 100%, the precision is 100%, the F1-score is 99.93%, the mean square error (MSE) is 0.02%, and the root mean square error (RMSE) is 0.01%. In other words, this method has been tested and shown to work. It can be used in a real clinical setting in less than 3 seconds per picture to find the COVID-19 virus early and keep track of treatment. Furthermore,

Rosa, De Silva proposed a method for predicting events based on early changes in user activity in Online Social Networks (OSNs). This method can be used for many different things because it can figure out the specific case of any problem. The framework for event detection that is being proposed is made up of five main parts. These are: 1) figuring out where the user is; 2) getting messages out of an OSN; 3) recognising subjects using NLP and DBN; 4) figuring out how user behaviour changes in an OSN; and 5) using a tree-CNN to make an effective and useful evaluation for figuring out how people feel. Community and public health officials can only take steps to fix problems if they know about them early enough. Because of this, the COVID-19 is used as a case study. In the performance evaluation, the event detection system had a precision of more than 0.90, while other similar systems had a precision of less than 0.74. They also have a technology that could find a problem about three days earlier than the other choices. Case data can also be used to figure out what are the most important parts of a situation, such as keywords and emotional messages. Hooshmand, Ghobadipublished their work on the MMRBM (Multimodal Restricted Boltzmann Machine Method), which connects information from different modes to solve the problem of repurposing medications. In their method, they used MM-RBM, which brings together both small molecule perturbations and the chemical structures of small molecules. Two RBMs were used to figure out each datum's characteristics and specific probability distributions. RBM was used to find out how the found features were likely to be distributed so that the data could be analysed further. The clusters in the model were shown to be important by the results. Because of these groups, researchers found medicines that were very similar to the COVID-19 treatments that had been planned. The chemical structures of small molecules that had genes that were out of sync with each other suggested that they could be used to treat COVID-19. The results of the study suggest that this method could also be used to find very effective COVID-19 therapies with few side effects. Also, researchers will look into what caused COVID-19 to grow and die in order to find out what caused it to spread.

Another study about DL has been finished. During this outbreak, COVID-19 researchers found that 14 articles (37.83%) used applications to classify CT/X-ray pictures of patients' chests that were used to diagnose them. These benefits include helping

radiologists diagnose diseases with the least amount of error, figuring out different kinds of pneumonia and COVID-19, and quickly figuring out what's wrong with a patient. The second-place prediction is that COVID 19 will cause more new cases and deaths, which is what nine publications (24.32 percent) said would happen. As the third most interesting topic, with four articles (11 percent), predicting the future needs for COVID-19, estimating the number of hospital beds, or figuring out how many medical ventilators are needed in the hospital is one of the most important uses of DLs in this sector. There has also not been much work done to find drugs and drug combinations that can be used to fight COVID19.

#### **C-RNN Methods**

One of the most interesting methods for researchers to think about is the RNN method, which has been shown to be very useful in the fields of health care and medicine. As was said in the second section, this is the method that is most often used to make predictions and forecasts. In this section, we look at five different ways to solve the problem.

Alakus and Turkoglu A method based on protein mapping could be used to guess how COVID-19 nonstructural proteins will work together. To find the links, a bidirectional RNN model was used. In the first part of the study, which used NCBI proteins, protein sequences were mapped with the help of the AVL model and three separate mapping algorithms. After the protein sequences were mapped, the Deep BiRNN model was used to normalise them and put them into groups. The proposed method worked about 85.33 percent of the time in interactions.

#### **D-GAN Method**

As we talked about in the second section, the GAN method is the one that is used most often when it comes to detecting and classifying images. It's one of the most appealing methods for researchers to use, and it's only recently become common in the medical and healthcare fields. In this part, we'll look at four different approaches that have been used in this area.

Goel, Murugan COVID-19 could be kept an eye on with the help of CT images and software that recognises pictures automatically. They use a GAN to make more CT images because it's hard to train DL networks on small datasets. We use the Whale Optimization Algorithm to get the most out of GAN's generator (WOA). Using the SARS-CoV-2 CT-Scan dataset, which has both COVID-19 and non-COVID-19 pictures, the proposed system is tested and proven to work. Specificity, sensitivity, accuracy, and the F1-score of 98.79%, as well as the positive predictive value of 97.82% and the negative predictive value of 99.77%, all show that the generative model is better than the competition. Their method could be used to help automate the screening of COVID-19 patients. This would lower the cost of health care. X-ray pictures can also be helpful.

Rasheed, Hameed Using machine learning techniques, they found people who had COVID-19. Using this method, patients can be quickly identified, so they can get the right medical care as soon as possible. This method is a cheap alternative for poor countries where standard testing kits are either not available or too expensive to buy. In order to avoid overfitting, a GAN-based data augmentation strategy was used to improve classification accuracy. The method had a maximum accuracy of 100% and a standard deviation of 0.99%. Because of this, when PCA was used, training time was cut down by a lot, but testing data was still accurate to the letter.

Elzeki, Shams The CXRVN was put forward as a way to classify the X-ray COVID-19 images. GAN networks were used to fill in gaps in a small number of datasets from different sources that were not balanced and to manage them well. When it came to managing the features extracted from each convolutional layer, the suggested framework was more stable and better than other benchmark approaches. In the first experiment, GAN method images were used, and the testing accuracy was 92.85%. In the second experiment, 455 GAN method images were used. The GAN method is the most common way to classify and find things in images. In the last few years, it has become more popular in the healthcare and medical fields, and researchers find it to be one of the most useful tools. Here, we will look at four possible ways to solve this problem.

Goel, Murugan COVID-19 could be kept an eye on with the help of CT images and software that recognises pictures automatically. They use a GAN to make more CT images because it's hard to train DL networks on small datasets. We use the Whale Optimization Algorithm to get the most out of GAN's generator (WOA). Using the SARS-CoV-2 CT-Scan dataset, which has both COVID-19 and non-COVID-19 pictures, the proposed system is tested and proven to work. Specificity, sensitivity, accuracy, and the F1-score of 98.79%, as well as the positive predictive value of 97.82% and the negative predictive value of 99.77%, all show that the generative model is better than the competition. Their method could be used to help automate the screening of COVID-19 patients. This would lower the cost of health care. X-ray pictures can also be helpful.

#### **E-SOM Methods**

As was mentioned in the second part of this article, the SOM method is the one that is used most often to figure out where and when something is found. It has become one of the most interesting approaches in the COVID-19 domains, and it is one of the most interesting approaches for scholars right now. In this part, we'll look at four different ways to get things done.

Melin, Monica a certain kind of unsupervised NN was used to look into how the COVID-19 disease epidemic changed over time and space around the world. Using the clustering feature of SOMs, they were able to figure out which countries were doing similar things and could therefore benefit from using different methods to stop the spread of the virus. The researchers got their information from databases of COVID-19 cases from all over the world that were free to use. There have been some interesting discoveries that could help find the best ways to fight the infection. Another thing that was thought about was how their strategy affected the way people with diabetes and high blood pressure was spread out in Mexico. Even though time is an important part of the problem, most of the earlier work on Corona virus data focused on forecasting based on numbers.

Galvan, Effting Using a SOM-like algorithm, unsupervised NNs were used to figure out where and when COVID-19 was found in Brazil based on the number of cases and deaths. The SOM doesn't decide how to stop the virus from spreading, but the datasets show what the government has done. Because of this plan, it has been shown that the spread of the disease in Brazil is not the same in all of the country's cities and states. Researchers found that the disease affected cities and states in the north the most, with the most cases and deaths per 100,000 people. The SOM clustering could be used to sort cities, states, and regions by how many corona virus outbreaks are happening there. Similar strategies could be used to stop the spread of viruses in these cities, states, and regions. There are a number of other choices. Using a model that has already been trained, the deep features of a custom dataset can be pulled out [77]. The extracted deep characteristics are put into groups using a linear support vector machine (SVM) and a one-versus-all support vector machine (SVM) classifier. AlexNet, DenseNet201, GoogleNet, InceptionV3, ResNet18, ResNet50, ResNet101, VGG16, VGG19, XceptionNet, and InceptionResNetV2 are used to pull deep features from the ImageNet dataset. The authors take a different approach to putting X-ray pictures into groups [77]. in a similar way to Ref [77]. CT images are put into groups based on features from VGG-16, GoogleNet, and Resnet-50 [78].

It is used to rank features based on how often they are used, so that fewer features are used more than once. The final feature vector is put into one of two groups using a binary SVM classifier. A depth-separable convolution neural network (DWS-CNN) takes the X-ray pictures of the patient and pulls out the features. The collected features are sent to a deep support vector machine for classification (DSVM). Devices that can connect to the IoT are used to gather data. The raw data are run through a Gaussian filter [79] before the features are extracted and the data are put into groups. For COVID-19 identification, a pre-trained VGG16 network is used, and the output is upsampled to a depthwise separable convolutional network. This is followed by a shallow 3D CNN block and spatial pyramid pooling. A hierarchical classification system could be used instead of a flat classification system[81]. In a hierarchical structure, the relationships between classes are taken into account when classifying, local classification is done, and classification models are trained. Even after being changed, the dataset is still small, so data augmentation techniques are used to add to what's already there to keep the model from being underfit or Overfit

Table 1 Summary of Related Works

Bhattacharya, Maddikunta [53]	Reviewing the papers associated with DL usage for COVID-19 medical image processing	Reviewing the challenges of DL image processing. •Taking into account critical variables.	•The article selection process is not clear. •There was no talk about future projects. •The methods are not compared.
Alsharif, Alsharif [54]	Discussing studies on the various applications of DL in the detection and diagnosis of COVID19.	There is a complete introductory guide to the research relating to DLCOVID-19.	•The article selection process is not clear. •There is no comparison between the articles.
Alafif, Tehame [55]	Investigating ML and DL methods for COVID-19 treatment and diagnosis.	Challenges and potential guidance are discussed.	•The article selection process is not clear
Shorten, Khoshgoftaar [56]	Covering DL applications in NLP, computer vision, life sciences, and epidemiology.	•Cover a significant portion of the papers Limitation on the amount of literature provided responsibly	•The article selection process is not clear. •There is no comparison between the articles. •There has not been any indepth review of the papers.
Sufian, Ghosh [52]	Examining Covid19's deep TL methods	•In the context of COVID-19, brief evaluations and challenges have been given. •The article selection process is not clear. •A precedent pipeline model of DTL over edge computing has been drawn up for a future scope to mitigate any outbreaks.	The article selection process is not clear. •There is no comparison between the articles.

#### IV. Public Imaging Datasets For Covid-19

detection Researchers looked at and used about 35 public datasets (CXR and CT scans) to verify the methods discussed in the articles that were reviewed for this work. You can find these sets of data online. Table 2 gives a full list of all the information. Some of these datasets have CXR images and CT-scan images of COVID-19, while others have images of both healthy participants and patients with a wide range of pulmonary diseases. Using the second type of datasets makes it possible to make algorithms that can find COVID-19 in a larger number of different types of radiography images. This is why these sets of information are being used. For the readers' sake and to get them interested in doing more research, we give a brief overview of some of these datasets and put download links for each dataset in Table 2. CXR dataset We have included a total of 20 datasets for CXR images. The most popular is the one published by Kermany et al. (2018) [48], which focuses on normal and pneumonia CXR images. There are a total of 5856 photos in this dataset [48], 2780 of which show bacterial pneumonia, 1493 showing viral pneumonia, and 1583 showing normal patients. The place where people were asked to take part was the Guangzhou Women and Children's Medical Center. The Mooney dataset from 2017 [49] is a CXR dataset for classifying viral and bacterial pneumonia. With the help of this dataset, it was made. The dataset is now available as a competition on Kaggle. This study is made up of 5247 CXR images of normal, viral, and bacterial pneumonia, each with a different level of resolution. Out of the 5247 CXR images, 3906 were of people with pneumonia. Of these, 2561 were of people with bacterial pneumonia and 1345 were of people with viral pneumonia. The other 1341 photos were taken from people who were healthy. Wang et al(2017) .'s dataset [125] has also been used in a number of different research projects. The National Institutes of Health (NIH) made this dataset public. It has 108,948 CXR pictures of healthy lungs that don't have lung infections or pneumonia that isn't caused by COVID. Ali [50] made a Kaggle dataset with only pictures of pneumonia. It has CXR images from 53 patients with both viral and bacterial pneumonia. The only pictures in the set are of pneumonia. The Radiology Society of North America (RSNA), the Society of Thoracic Radiology, and MD.ai worked together to make a database for the Pneumonia-Detection-Challenge on Kaggle [111]. This collection has CXR pictures of 6002 normal people and 20599 people with pneumonia.

**Open Issues** - This section talks about a wide range of important problems and roadblocks that will need more research in the future. Most people who study machine learning and deep learning that are based on AI have a background in computer science. Still, adding more medical data to the use of ML and DL in the COVID19 war will require a lot of expertise in medical imaging, bioinformatics, virology, and other related fields. To deal with COVID-19, experts from many different fields will need to work together and include the results of many different lines of research. Also, it might be hard to work with written descriptions that aren't clear or have wrong information. Large amounts of information from many different sources could have mistakes. Also, when there's too much data, it's impossible to pick out the useful bits. Trying to deal with COVID-19 data that isn't balanced because of a lack of good medical imaging and a long training period, and not being able to explain the results. By making social networks and knowledge graphs, an AI-based machine learning and deep learning system can keep an eye on and track the characteristics of the people who live near COVID-19 patients. This lets the system predict and keep track of how the disease is likely to spread. Also, AI-based ML and DL algorithms can find possible drugs and vaccines and simulate drug-protein and vaccine-receptor interactions. This lets the systems predict how people with different COVID-19 illnesses will react to drugs and vaccines in the future. In biological research, AI-based ML and DL systems can be used to accurately analyse biomedical knowledge, such as important protein structures, genetic sequences, and viral trajectories, in order to figure out protein composition and viral factors. This can be done with the help of techniques like deep learning and machine learning. Here are some ideas that could be looked into by researchers in the future.

## V. Limitations

It's important to admit that the research we already have has some limits. The research can only use certain search terms, databases, and selection criteria. This study was done over the course of a certain amount of time. On the other hand, COVID-19 is used so often and is so important that every day, more and more studies are done on it. Because this research included a thorough review of the literature, it is important to limit the scope of the investigation. So that this wouldn't ruin the study too much, questions about what papers should be included and what papers should be left out were made. In order to do the review, seven web databases were looked through. Queries can also be run on other databases, though. If the investigation is made bigger, there is room for the number of databases to grow. There are a lot of other studies besides the ones that were chosen for this research. It's important not to forget that some rules were set up to limit the research. For example, studies that didn't say what algorithm was used or didn't say much about how the implementation was done were thrown out. Most of the time, Applied AI/ML studies are used to reach different goals without taking COVID-19 issues into account. Because of this, the papers don't say directly what the problems are with COVID-19. By looking at each study on its own and analysing the results, it was decided which issue would be looked at. It's possible that there have been books that haven't been read up until now.

## VI. CONCLUSION

This study looks at how techniques like machine learning (ML) and deep learning (DL) can be used to fight COVID-19. The systematic review is being done. The review found that the number of confirmed cases can be accurately predicted by ARIMA models with different orders, PR, RIDGE, and SVR models, logistic models, and the hybrid wavelet ARIMA model. Also, it has been found that many machine learning techniques, like the multilayer perceptron, SVM, random forest, and XGBoost, can help tell the difference between people with COVID-19 and normal people. In one specific case, the random forest method is able to classify things with 95.95 percent accuracy. For DL-based COVID-19 diagnosis, there are several steps, such as image preprocessing, segmentation, feature extraction, and classification. All of these steps happen separately. This research also shows that deep learning methods like CNN, ResNet, COVIDNet, VGG-16, VGG-19, and hybrid neural networks can accurately diagnose COVID-19 when used on X-ray and CT scan images. In the future, there are a number of problems that will need to be solved before AI can be used in real life. Some of the biggest problems are regulations, a lack of trustworthy large datasets, inaccurate or noisy data, a big gap where AI and medicine meet, and not enough protection for personal data. Also, in the not-too-distant future, it will be very important to have high-quality medical datasets with large sample sizes. Also, the datasets should include COVID-19 individuals at different stages of development. In particular, the number of cases that are on the edge will be a key factor in figuring out how well a classifier works. Each person who might have COVID-19 should have more than one imaging test, such as an ultrasound, X-ray, computed tomography (CT), and magnetic resonance imaging (MRI), to make the diagnosis more accurate and improve patient care. This is because a multi-modal system uses the best parts of each imaging method. Because there are a lot of COVID-19 medical photos without the needed labels, it can be helpful to use unsupervised learning methods. In conclusion, it is thought that if new machine learning and deep learning algorithms are made, the COVID-19 epidemic will be able to be dealt with successfully around the world.

Most of the time, the CNN approach was used to either put things into groups or make a diagnosis. Before using CNN for the COVID-19 experiments, the authors should keep in mind the limitations we've already talked about.

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