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NEXT-GENERATION AI AND MACHINE LEARNING MODELS FOR ENHANCING HEALTHCARE RESILIENCE: A REVIEW OF PANDEMIC PREPAREDNESS STRATEGIES

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ABSTRACT

The COVID-19 pandemic posed unprecedented challenges to global healthcare systems, particularly in resourceconstrained environments like India. This study explores the role of data mining and artificial intelligence (AI) in addressing these challenges through predictive modeling, diagnosis, and genomic analysis. AI techniques such as machine learning algorithms were applied to analyze large datasets, optimize resource allocation, and improve patient screening and triage. The paper discusses methods including supervised, unsupervised, and transfer learning, as well as evaluation metrics like accuracy and F1 scores to validate AI models. Findings highlight AI's transformative role in diagnostics, epidemiological predictions, and genomic research, demonstrating its potential to strengthen preparedness for future health crises. Recommendations focus on integrating AI with healthcare systems to address disparities and enhance decision-making. This review underscores the critical role of AI-driven data mining in improving public health responses, offering insights into future applications.

KEYWORDS: Artificial Intelligence, COVID-19, Data Mining, Epidemiology, Machine Learning, Supervised Learning, Transfer Learning, Unsupervised Learning.

1. INTRODUCTION

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The COVID-19 pandemic, which began in December 2019 in Wuhan, China, quickly turned into a global health crisis, affecting millions of lives and challenging health systems worldwide. The emergence of the SARS-CoV-2 virus and its rapid spread forced the World Health Organization (WHO) to officially declare a pandemic in March 2020 [1]. In India, the impact was especially severe, with over 44 million confirmed cases and more than 530,000 deaths recorded by May 2024 [2]. The country's health system faced significant challenges, exacerbated by the dense population, varying access to healthcare, and regional disparities in medical infrastructure.

Throughout the pandemic, science and technology played crucial roles in responding to the crisis. The accelerated development of vaccines, such as Covaxin and Covishield, and the implementation of new therapeutic approaches brought significant advances in the fight against COVID-19. However, the rapid evolution of the virus, with the emergence of variants like Delta and Omicron, presented ongoing challenges, requiring continuous adaptations in control and treatment strategies [3]. In this context, artificial intelligence (AI) technologies and data mining became essential tools for analyzing and predicting epidemiological patterns, managing healthcare resources, and supporting the discovery of new therapeutic solutions.

In India, AI's application during the pandemic was diverse. AI-driven platforms, such as Aarogya Setu, helped track COVID-19 exposure and monitor the spread of the virus [4]. In addition, AI was leveraged for hospital triage, patient diagnosis, and optimizing the allocation of medical resources, improving efficiency and accuracy in the healthcare system [5]. AI also played a pivotal role in genomic analysis, supporting the development of vaccines and therapies in record time. These technological advancements highlighted the immediate benefits of AI during the pandemic and demonstrated its vast potential to address future health emergencies.

Given this context, this article seeks to answer the following question: How can data mining be applied to the COVID-19 pandemic in India to identify patterns and provide insights that can help in addressing future public

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health crises? This study aims to explore how data mining was utilized in India during the COVID-19 pandemic, focusing on advanced applications like hospital triage, imaging diagnosis, and genomic analysis. Through a comprehensive literature review, we seek to understand the state of the art in these technologies, offering valuable insights for improving responses to current health crises and better preparing for future global emergencies.

2. LITERATURE REVIEW

This section addresses aspects of the emergence and classification of this new etiological agent, as well as genetic information about SARS-CoV-2 and viral epidemiology, and especially about the basis and applicability of data mining methods in COVID-19.

2.1 COVID-19

The most recent CoV epidemic began in December 2019 in Wuhan, China, in a food market that sold live animals, where bats were identified as hosts and the causative agent was classified as SARS-CoV-2 [6]. In early 2020, the Chinese Center for Disease Control and Prevention detected the new CoV in hospitalized people, which led to the naming of the virus as CoV-19. In addition to China, Thailand announced in January 2020 the laboratory confirmation of the first case that was imported from Wuhan [7]. Gradually, cases were reported in Macau, the United States, Hong Kong, and cases of spread by people who had traveled to Wuhan. The rapid spread and contagion of the virus led the WHO (World Health Organization) to declare the COVID-19 pandemic on March 11, 2020 [7].

The first case of COVID-19 in India was reported on January 30, 2020, in the state of Kerala, and by September 2020, the country had already recorded approximately 100,000 deaths [8]. By August 2021, India had the secondhighest number of cumulative cases of COVID-19 in the world, following the United States [9]. The state of Maharashtra was the most affected by the pandemic until mid-2021, with over 120,000 deaths recorded by July 2021 [10]. In March 2020, the first peak began, reaching its maximum in September 2020, which was associated with the spread of the B.1.617.2 (Delta) variant. Subsequently, the second peak began in April 2021, with a maximum in May 2021, when the Delta variant surged across the country, overwhelming hospitals and healthcare resources.

As of May 2024, India has reported over 44 million confirmed cases and more than 530,000 deaths [9], while worldwide the numbers exceed 704 million cases, with over 7 million deaths. On May 31, 2021, the WHO announced the new variants of COVID-19, using Greek letters to classify them (Alpha, Beta, Gamma, Delta). Many of these strains had mutations linked to the virus's spike protein, which affected their behavior, pathogenesis, and ability to partially evade immunity [11]. According to the Our World in Data Dashboard (https://ourworldindata.org), as of June 18, 2024, more than 13.58 billion doses of the COVID-19 vaccine had been administered globally. In India, the vaccination drive began in January 2021, with Covaxin and Covishield being the primary vaccines used. Despite the rapid vaccine production, the new variants of COVID-19, especially Delta and Omicron, exhibited genetic modifications that reduced the effectiveness of conventional vaccines [11].

2.2 Coronavirus Taxonomy

Coronaviridae is a monophyletic group within the order Nidovirales, family Coronaviridae, subfamily Orthocoronavirinae, and genus Betacoronavirus. Members of this family are divided into four genera: Alphacoronavirus, Betacoronavirus, Gammacoronavirus, and Deltacoronavirus (Coronaviridae Study Group of the International Committee on Taxonomy of Viruses). The taxonomic classification of Coronaviridae, according to the International Committee on Taxonomy of Viruses (ICTV), is presented in Figure 1.

Coronaviruses have been identified in several reservoir species, such as bats, mice, rats, chickens, dogs, cats, horses, and camels [12], [13]. Some species cause pandemic diseases in domestic and wild mammals and birds, leading to livestock mortality and economic losses. These viruses include chicken coronavirus (Infectious bronchitis virus, IBV), Beluga whale coronavirus (BWCoV-SW1), bat coronaviruses (CDPHE15 and HKU10), Porcine epidemic diarrhea virus (PEDV), and Swine acute diarrhea syndrome coronavirus (SADS-CoV), as compiled by [12] and reproduced in Figure 1.

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Figure 1: Taxonomy of human coronavirus according to ICTV source: European centre for disease prevention and control (ECDC) [12]

The genera Alphacoronavirus and Betacoronavirus are known to infect humans. Within these genera, six species of coronaviruses can cause disease in humans. Coronaviruses 229E, OC43, NL63, and HKU1 are prevalent and typically cause symptoms of the common cold. The severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome coronavirus (MERS-CoV) strains are of zoonotic origin and have been associated with more severe and sometimes fatal diseases. Regarding SARS-CoV-2 (Severe Acute Respiratory Syndrome Coronavirus), phylogenetic studies [14], [15] point to similarities with bat coronaviruses, SARS-CoV, and MERS-CoV [16], [13].

2.3 Pathogenesis

SARS-CoV-2 infection begins in nasal and bronchial epithelial cells. As viral replication progresses to later stages, the virus directly infects endothelial cells in various organs, potentially causing disruption of the endothelial barrier and diffuse endothelial cell damage [17], [18].

Infection is initiated by binding of the viral particle on the external surface to the host surface receptor via the spike glycoprotein [19], [20]. Studies on the mechanism of entry of the SARS-CoV-2 virus into the host cell indicate that the cellular receptor ACE2 is used, similar to the mechanism described for the SARS-CoV virus [19], [21]. The ACE2 receptor is present in the cell membranes of several organs, including the lungs, arteries, kidneys, heart, and intestines [20], [17].

The virus enters the cell through pH- and host receptor-mediated endocytosis, a process in which the viral nucleocapsid is delivered into the cytoplasm. Upon infecting the host cell, host factors interact with the viral RNA at these sites and participate in viral RNA synthesis. In this way, the genome acts as an mRNA for translation of the replicase polyproteins required for viral replication [19], [21], [17]. The schematic representation of the pathogenesis is shown in Figure 2.

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Figure 2: Human Coronavirus Pathogenesis [19]

2.4 Symptomatology and Epidemiology of the Virus

At the beginning of the pandemic, as it was an emerging disease, the forms of transmission were still being studied. It was believed that the disease was transmitted only from animals to humans, and then only between symptomatic people [22], until the first case of human-to-human transmission from an asymptomatic carrier was documented in Germany [23]. It is understood that SARS-CoV-2 is transmitted between humans by direct contact, aerosol droplets, fecal-oral route, and intermediate fomites from symptomatic and/or asymptomatic patients during the incubation period [22]. The estimated incubation period ranges from 2 to 14 days, with a median time of 6 days. However, some cases have presented different incubation periods, comprising 21, 24, or even 27 days [22], [23]. The pathophysiology and severity of COVID-19 disease vary among patients and depend in part on underlying risk factors and chronic diseases. Usually, COVID-19 presents with symptoms such as fever, dry cough, dyspnea, sneezing or sore throat, and diarrhea [22]. In severe cases, the disease progresses to the development of pneumonia, metabolic acidosis, septic shock, and bleeding associated with low leukocyte and lymphocyte counts; marked inflammatory response and abnormal coagulation parameters [24], [23], [25]. Regarding preventive measures and precautions related to limiting exposure to the virus and reducing its spread, the following stand out: (1) washing hands frequently with soap and water or alcohol-based hand sanitizer, (2) coughing or sneezing etiquette, recommending covering the mouth, (3) avoiding touching the eyes, nose, and mouth if hands are not clean, (4) avoiding close contact with sick people, (5) avoiding sharing dishes, cups, bedding, and other household items with sick people, (6) cleaning and disinfecting surfaces that are frequently touched, and (7) staying home from work, school, and public areas when feeling sick [22].

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2.5 Artificial Intelligence in Healthcare

The recent pandemic caused by COVID-19 highlights the importance of conducting research related to emerging and highly infectious viruses in a globalized scenario. Both science and technology are in continuous evolution processes, and the large number of studies on SARS-CoV-2 demonstrate the agility and capacity of the global scientific community. The pandemic contributed to stimulating this development, as well as better preparing the globalized society for the next pandemics that may arise. To assist in this aspect, data analysis projects with data mining approaches have applicability.

2.5.1 Data Mining: Process and Applications

Analytical data mining projects involve five phases, namely: data selection, pre-processing, application of Artificial Intelligence (AI) algorithms, validation of results, and finally the knowledge generated [26], [27]. Thus, through algorithms that return patterns and trends in the analyzed data, it is possible to make inferences that are analyzed and validated by domain experts [28], [29]. Figure 3 illustrates the flow of activities related to an artificial intelligence project.



Figure 3: KDD (Knowledge Discovery in Databases) processes [33]

Specifically, when dealing with data of biological origin, there is an additional difficulty in artificial intelligence applications, mainly due to the natural heterogeneity of biological systems. Biological data range from single chemical or molecular structures to complex systems on a genome-wide scale or even complete metabolic networks. Thus, they vary in complexity, format and scale, including: (i) sequences (DNA, RNA and proteins, usually in text format); (ii) structures (biological and chemical molecules, such as structural proteins and enzymes involved in pathways, in image format); (iii) gene expression profiles (measurement of gene activity, in numerical and image formats); (iv) biochemical pathways (in text or image format); (v) chromosome mapping (in text or image format); (vi) Single Nucleotide Polymorphisms (in text format); and (vii) phylogenetic data (in text or image format). It is also important to note that biological data present some interferences resulting from the wide variety of equipment and protocols used in a given experiment. This is known as the "batch effect," which is the result of laboratory variables, such as reagents, machines, human error, among other factors that can interfere with an experiment. When dealing with large amounts of data and high-throughput data, batch effects can be the source of misleading results [30].

In addition, ethical concerns are highlighted. As highlighted by the authors of [31], the quality of the data provided to artificial intelligence systems will impact the results, as the data are collected from a society full of inequalities, exclusions, and discrimination. Corroborating the authors of [32], machine learning can validate discriminatory norms because, if such norms were discovered in a database of data, an accurate classification algorithm will reproduce those.

2.5.2 Machine Learning Algorithms

After preprocessing, artificial intelligence algorithms are applied to the data. This is a process of excavating largevolume data sets, which are analyzed, and information, patterns, trends, among others, are extracted from them [33]. The amount of data currently collected and available for analysis is significant; however, choosing the correct method that can cover this amount of information does not always translate into more knowledge. To this end, the

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use of data mining to extract information and knowledge is recommended because it can handle a huge volume of data, minimizing the noise coming from it [33].

The objective of artificial intelligence is to mathematically model classification, analysis, and prediction and manipulation tasks to build intelligent systems [34]. To this end, artificial intelligence uses a set of principles, models, and tools in different subdomains, such as logic, reasoning under uncertainty, intelligent agents, and machine learning [35]. Machine learning (or ML) can occur in different ways, such as supervised, unsupervised, reinforcement, or transfer learning.

Supervised machine learning occurs by training an algorithm based on a set of data with examples and expected responses. In this case, the database has numerical or textual values that are used by the algorithms to infer the responses. Examples of supervised ML use cases include regression algorithms, whose target response is a numerical value, or a classification algorithm, whose target response is a qualitative variable, such as a class or label [36].

On the other hand, unsupervised machine learning occurs from unlabeled data, without any associated response. In this case, patterns are determined based on the similarity of the data. This type of algorithm tends to structure data considering characteristics that represent a class or a new series of uncorrelated values, which can be used to group data, such as grouping customers into different categories or detecting fraud/anomalies in financial transactions [36], [37].

Reinforcement learning occurs when the algorithm is provided with examples that do not contain labels, as is also done in unsupervised learning. However, an example may be accompanied by a positive or negative return, depending on the solution suggested by the algorithm. In this case, errors aid in learning, as they bring a penalty, teaching the algorithm which decisions have the least penalties, maximizing the reward received throughout its execution [36], [37].

Transfer learning (TL) refers to a collection of models in which the knowledge acquired by another model when solving a problem is saved and then transferred to another model in charge of solving a comparable problem. This transfer reduces or eliminates the need to train new models, in addition to allowing the advancement of this knowledge [37]. As discussed in more detail by the authors of [38], TL is a learning framework that relaxes the assumption of supervised learning algorithms that training and testing data must be independent and identically distributed, represented by the same features and demonstrated by the same generator. This relaxation addresses the issue of having insufficient data to train some machine learning algorithms, especially those that focus on deep learning. In Deep Learning, the success of extracting hidden patterns and features is directly related to training with large volumes of data. In this situation, transfer learning enables the reuse of principles learned in another domain, reducing data requirements and accelerating model convergence [39].

The main machine learning models used in each of these categories and their intended uses are summarized in Table 1.

Category	Models
Supervised	Linear regression, logistic regression, support vector machines (SVM), Bayesian classifier, decision
-	trees, linear discriminant analysis, k-Nearest Neighbors (KNN), neural networks.
Unsupervised	Clustering, anomaly detection, neural networks, latent variable models.
Reinforcement	Markov models, Monte Carlo methods, temporal differences, recurrent neural networks (RNN),
	convolutional neural networks (CNN).
Transfer	Inception-v3, ResNet, AlexNet, other convolutional neural network (CNN)-based models.
Learning	
Deep Learning	Recurrent neural networks (RNN), convolutional neural networks (CNN), generative models
	(Boltzmann, GAN, deep belief).

Table 1: Category of Machine Learning Models [37]

2.5.3 Algorithm Evaluation and Validation

Evaluation and validation of results are important concepts in the field of statistics and refer to the process of assessing the performance and reliability of statistical models and methods. Evaluation is the process of verifying

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the quality or effectiveness of a statistical model or method. This can be done in a variety of ways, such as through the use of evaluation metrics, which are quantitative measures used to assess the performance of a model. Some common evaluation metrics include accuracy, sensitivity, precision, F1-Score, and specificity. Evaluation can also be performed through the use of visualizations, such as plots or graphs, which can help identify patterns or trends in the data that may not be immediately apparent in the raw data [40].

Validation is the process of verifying that a statistical model or method is accurate and reliable. This can be done through the use of cross-validation, which is a resampling procedure that involves partitioning the data into a training set and a test set, training the model on the training set, and evaluating the model on the test set. Validation can also be accomplished through the use of external data sources, such as historical data or independent data sets, which can be used to verify the accuracy and reliability of the model [40].

Cross-validation is a resampling procedure used to evaluate the performance of a machine learning model. It involves partitioning the data into a training set, which is used to train the model, and a test set, which is used to evaluate the model. Cross-validation is an important technique because it allows us to evaluate the performance of the model on unseen data, which can help identify overfitting and underfitting that may have occurred during training [41].

There are different types of cross-validation, but a common method is k-fold cross-validation. In k-fold cross-validation, the data is partitioned into k equally sized subsets and the model is trained and evaluated k times, with a different subset of data used as the test set in each iteration. The final performance of the model is then calculated as the average of the performance over each of the k iterations, as illustrated in Figure 4 [41].



Figure 4: Cross-validation

A confusion matrix is a table used to evaluate the performance of a classification model. It displays the number of true positive, true negative, false positive, and false negative predictions made by the model and can be used in conjunction with cross-validation to assess the stability and generalizability of the model [42], illustrated in Figure 5.

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Figure 5: Confusion matrix

The entries in the confusion matrix can be used to calculate a variety of evaluation metrics, such as accuracy, which is the number of true positive predictions made by the model divided by the total number of positive predictions made by the model [42]. The following are the main metrics for evaluating models. These are accuracy, sensitivity, precision, F1 score, specificity and, finally, the ROC curve [43].

Accuracy is the degree to which a binary classification identifies or excludes a class, that is, the proportion of correct predictions (true positives and true negatives) among the total number of observations. Its calculation is achieved through the equation:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN}$$
(1)

Sensitivity (Recall) determines the number of real positives captured and labeled as TP by the model. High rates of true positives and low rates of false positives contribute to this metric. Its calculation is done by the equation:

$$Recall = \frac{TP}{TP + FN}$$
(2)

Precision calculates how many of the classes classified as positive are actually positive. The cost of false positives is high when calculating precision through its formula, explained by the equation:

$$Precision = \frac{TP}{TP + FP}$$
(3)

The F1 Score strikes a balance between Precision and Recall. The metric is used for any classification where there is a considerable difference between Precision and Recall. Instead of using the arithmetic mean, the F1 Score uses the harmonic mean, being a function of two variables (Precision and Recall) at the same time and penalizing extreme values. Its calculation follows the equation:

$$F1 Score = 2 \times \frac{Recall \times Precision}{Recall + Precision}$$
(4)

Specificity measures the detection rate of TNs among the data set. It is penalized for high numbers of false positives. Specificity is calculated using the equation:

$$Specificity = \frac{IN}{TN + FN}$$

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Another derivation of a confusion matrix is the ROC (Receiver Operating Characteristic) curve, which is a performance measure for classification problems under different thresholds. Machine learning applications, such as ANN (artificial neural networks), are able to predict membership in a given class. The decision to classify an observation is given by a parameter called the decision threshold. Additionally, ROC can also be used to calculate the Area Under the Curve (AUC), which measures the degree of separation between the boundaries of the same classification method, as well as the performance comparison of different classification techniques (e.g., linear regression versus ANN). The higher the AUC, the better the model predicted a certain class [44].

ROC curves can be calculated from any metric derived from a confusion matrix [45]. A common calculation derives from two competing metrics: recall (also known as sensitivity), which measures the true positive rate (TPR); and false positive rate (FPR), which is estimated by 1 - specificity. This relationship is calculated such that the higher the TPR, the lower the FPR, as described in the equation below, where FPR measures the false positive rate on a scale from 0 to 1 [46].

$$FPR = \frac{FP}{FP + TN}$$

(6)

(5)

It is important to note that different evaluation metrics may be more or less appropriate for a given problem, depending on the relative costs and benefits of different types of errors. For example, in a medical diagnostic task, it may be more important to minimize false negatives (failure to detect a positive case) than to increase false positives (incorrectly detecting a positive case), since the consequences of missed diagnoses may be more serious than those of incorrect diagnoses [47].

2.6 Applications of Data Mining In Covid-19

In the context of the COVID-19 pandemic, data mining has been used as a tool to support the diagnosis of the disease, development of prevention models, clinical research, pharmaceutical research, epidemiology of the virus, support for decision-making, and actions to combat the pandemic. Thus, this section reviews the works that use data mining and artificial intelligence in the COVID-19 pandemic, exemplifying their applications.

2.6.1 Diagnosis, Hospital Triage

Hospital triage plays a critical role in controlling the spread of COVID-19, as this process helps in the early identification of infected patients, contributing to the treatment and effective allocation of hospital resources [48]. In this sense, studies show the applicability of artificial intelligence in patient triage and diagnosis.

COVID-19 has brought many patients to medical care in a short period of time for treatment of a previously undescribed disease, challenging health services to provide urgent interventions in difficult circumstances. Since the first cases of COVID-19 were documented in China in late December 2019, the epidemiological focus has been primarily on establishing disease severity and outcomes among critically ill patients. Considering risk factors for COVID-19, an analysis of the relationship between obesity and COVID-19 infection in adult outpatients was conducted [49]. A total of 1,050 participants were screened in two emergency departments of hospitals (public and private) in the southern region of Brazil. Of these patients, 297 were diagnosed with COVID-19 by RT-PCR (Reverse transcription–polymerase chain reaction) and completed the 28-day follow-up, which was conducted by telephone contact on days 7, 14, and 28 after inclusion in the study. Ninety-five (32.0% of the sample) individuals were obese, and 233 (78.5% of the sample) had no previous medical condition. Twenty-three participants (7.7% of the sample) had no previous medical condition. Twenty-three participants (7.7% of the sample) required hospitalization during the follow-up period. Multivariate logistic regression models were used to explore the association between obesity and other potential predictors of hospitalization. After model adjustment, obesity (BMI \ge 30.0 kg/m²) (OR = 2.69, 95% CI 1.63-4.83, P < 0.001) and older age (OR = 1.05, 95% CI 1.01-1.09, P < 0.001) were significantly associated with higher risks of hospitalization.

Aiming at a large-scale population screening and rapid, noninvasive diagnostic strategy to ensure patient comfort, surface-enhanced Raman scattering (SERS) as a diagnostic modality for label-free discrimination of SARS-CoV-2 infection from saliva samples was described [50]. To this end, the analysis of the saliva of patients infected and recovered from COVID-19 was performed using a portable Raman spectrophotometer, which mixed the sample with gold nanoparticles (AuNPs) to evaluate the enhanced Raman peaks. These data were encoded, segregated, and managed with the aid of support vector machine learning (SVM) algorithms. The constructed classification

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models achieved an accuracy of 95% and an F1-score of 94.73% for healthy patients and 95.28% accuracy for patients infected with COVID-19. The approach presented is capable of identifying patients infected with SARS-CoV-2 from healthy patients and differentiating the stages of patient recovery. Thus, the portable Raman spectrophotometer and saliva as a sample present a rapid and non-invasive screening and diagnostic strategy.

Using immunological biomarker data, an analysis was conducted on data from 28 different biomarkers in two cohorts of COVID-19 patients (totaling 95 patients) to systematically capture, quantify, and program how immunological signals may be associated with the clinical outcome of COVID-19 [51]. These data were used as input for different artificial intelligence techniques, including artificial neural network, random forest, classification and regression trees, k-means, and support vector machines. The study presented five immunological biomarkers related to the severity of COVID-19 and suggested that screening for such biomarkers may help in understanding the immune response underlying inflammatory diseases, since the differentiated concentration of immunological biomarkers plays a fundamental role in regulating the host response against pathogens. The methodology used presented values of 94% accuracy, 96.6% precision, 91.6% recall, and 95% specificity in the test data. The validity of these values was corroborated by using the model to predict 83% and 87% (recovered and deceased) of unseen data.

Regarding image-based diagnosis, a consolidated approach within several areas of knowledge was described, searching for articles in the health area using diagnosis based on X-ray images and computed tomography scans for diagnosing respiratory infections and other outcomes associated with COVID-19 [52]. The authors found articles in which X-ray and computed tomography image analyses were performed using deep learning, and most of the articles used Convolutional Neural Networks to identify specific patterns in the images, such as signs of tumors, regions with different colors, deviations of tissues, and arteries. Several studies and authors were cited in this systematic review. The proposal of a protocol for the clinical diagnosis of COVID-19-positive patients, based on computed tomography (CT) results using the neural network approach with deep learning, was presented [53]. The model construction employed 800, 170, and 171 image pairs for the training, testing, and external validation set stages, respectively. The results were evaluated using quantitative evaluation metrics such as root-mean-square error (RMSE), structural similarity index measure (SSIM), and peak signal-to-noise ratio (PSNR).

An AI-assisted X-ray analysis with deep learning neural networks was performed [54], based on the argument that chest radiography (CXR), despite being one of the most common investigations performed worldwide, was not considered a sensitive or specific examination for COVID-19-related changes. The authors developed and validated an algorithm that could differentiate the X-rays of COVID-19 positive patients from COVID-19 negative patients, with the accuracy of radiologists improving from 65.9% to 81.9% and the sensitivity improving from 17.5% to 71.75% when provided with AI assistance. The authors argue that the implementation of this tool can improve the sensitivity and accuracy of radiologists in identifying COVID-positive patients in routine clinical practice.

Regarding pediatric diagnosis, an analysis was performed to assess the difference in cellular or humoral immune responses of pediatric and adult patients with COVID-19 to verify whether these factors contribute to disease severity [55]. The authors suggested that children produce a strong but differentiated immune response when compared to adults, which is associated with the mild manifestation of pediatric COVID-19.

In summary, rapid screening and diagnosis are essential tools for combating COVID-19, as they help in the early identification and isolation of infected individuals, thus reducing the number of new cases and the spread of the virus.

2.6.2 Genomic Analysis and Drug Research

One application of artificial intelligence in genomics is the identification of potential drug targets. By analyzing genomic and disease-related data, AI algorithms can identify genes, metabolic pathways, and patient data that are involved in the development of a specific disease. This information can then be used to identify compounds that may be effective in treating the disease.

As described by the authors of [56], one of the main objectives of genomic analyses is to develop genomic medicines, fostering the description and interpretation of diseases and medicines associated with genetic

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modifications. In support of this objective, efforts have been made to combine population-level sequence data and genomic data with phenotypic knowledge, clinical reports, and other types of multi-omics datasets (e.g., transcriptomics, proteomics, and metabolomics) [57]. In this way, complex scientific and computational demands have been created for researchers, health specialists, and clinical services [56]. Thus, the need arises for computational techniques that enable the evaluation of heterogeneous and high-dimensional data and systems that provide easier, cheaper, more extensible, and comprehensive experimental and analytical solutions [56]. Supporting the needs described above, the use of data mining and related technologies, including data analytics, machine learning, and deep learning, can accelerate the process of identifying insights and also lead to a better response to scientific and computational demands. Artificial intelligence has been dedicated to significant incremental developments in clinical genome analysis, such as phenotyping in rare syndromes and cancer. Although, mainly, artificial intelligence-based work in the field of genomics is in the research phase, the demand for machine learning and deep learning techniques for functional genomic analysis is increasing. Now, improvements in computing, artificial intelligence, and the increase in biomedical datasets allow advances in existing service fields. Simultaneously, these advances in open-access research and open-source tools make the use of artificial intelligence thriving in various types of genome studies [56]. Based on the needs described above and the advancement of artificial intelligence in genome sequence analysis, the authors of [56] aim in their work to present an artificial intelligence-based system for analyzing the genome sequence of SARS-CoV and similar viruses, including SARS, MERS, and Ebola. We performed comparative analyses to study the basic patterns of the genome sequence of these viruses and also used a machine learning algorithm for classification [56].

For comparative analysis of genome sequences, the authors of [56] used Biopython. Genome sequence analysis has often become an essential tool for studying disease outbreaks. SARS-CoV and other viruses, including SARS, MERS, and Ebola genomes, were used in this study. The authors began their analyses by reading the DNA sequence; by doing so, they extracted the nucleotide information or the length of the genome sequence. The length of the SARS-CoV genome sequence is 29,903, the SARS genome sequence is 2975, the MERS genome sequence is 30,119, and the length of the Ebola genome sequence is 18,959 [56].

For the classification of different genome sequences, the authors of [56] used linear SVM. The dataset consisted of genome sequences of all four types of viruses. Beforehand, they performed preprocessing by assigning the class labels manually and extracted useful features provided to the SVM classifiers. Subsequently, the data were randomly split, and the genome coding sequences were collected into training and testing samples at a ratio of 80% and 20%, respectively [56]. Finally, the researchers calculated the accuracy, recall, precision, and F1-score. The SVM classifier achieved good classification accuracy results for all types of genomic sequences, including COVID-19 with 97%, SARS with 96%, MERS and Ebola with 95%, respectively. The precision, recall, and F1-Score are 96%, 77%, 96% for COVID-19, 96%, 74%, and 96% for SARS, 95%, 74%, and 95% for MERS, and 95%, 74%, and 95% for Ebola, respectively [56].

The results of the technique applied by the authors of [56] provide support for understanding the origin, behavior, and structure of the virus, which can help in the development of vaccines, antiviral drugs, and efficient preventive strategies. The authors of [57] contextualize that we live in a world in which a massive amount of data is generated in almost all sectors. In order for us to make more efficient use of this data, AI provides us with resources to handle this data. Contextualizing AI within the pharmaceutical sciences, AI provides the best approach for a better health system. For this to become a reality, AI and ML require a large amount of data, and most pharmaceutical and healthcare sectors have extensive data. The authors of [58] comment that artificial intelligence and machine learning help to use resources in the best options for doctors, consumers, insurers, and regulators. To make these decisions, data is generated from different sources, such as academia, organizations and research and development, industrial units, pharmacies, and community centers. Additionally, the use of AI and ML is already being used in the pharmaceutical industry in several sectors, such as the discovery of new drugs, evaluation of active compounds, drug repurposing, disease diagnosis, clinical trials, and electronic health records [57].

The development of a new molecule takes approximately 13.5 years to reach the point of approval. Regarding research and development costs, they are estimated at US\$2.6 billion [59]. In this context, the development of AI has a major impact on the discovery and development of new drugs, bringing advantages such as reducing the time in protocols that would take a long time without the use of AI, through better use of available resources [57].

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If mind and machine work together, the processes of drug design, chemical synthesis, and biological test analysis would be more efficient. There are four main steps in the process of building an AI model for drug discovery. The first is to define the problem, which should be specific or broad. Then, choosing the appropriate AI algorithm and setting the initial values for hyperparameters to provide the appropriate AI architecture. Third, the input data should be prepared in a satisfactory way in terms of quality, quantity, and characteristics. Finally, the model is selected for training and evaluation. This includes training algorithms, optimization strategies, evaluation mechanisms, and hyperparameter tuning algorithms [57]. Several common algorithm models can be used in the first and second stages of model building. These models include random forest, artificial neural network, deep Boltzmann machine, deep belief network, generative adversarial network, variational autoencoder, adversarial autoencoder, symbolic learning, and meta-learning. Due to its use in quantitative structure-activity relationships and virtual screening, artificial neural network has become one of the most powerful nonlinear data models. This has increased significantly in the last twenty years. At the same time, generative adversarial network technique has helped in medicinal chemistry by creating molecular models and in biochemistry by creating peptides and proteins by reducing the dimension of single-cell data in preclinical development [57].

The authors of [57] concluded that the use of artificial intelligence in the healthcare system has gradually increased, covering a range of applications in the fields of pharmacology. Emphasizing that AI technologies are used in all stages of the drug development process, which avoids risks associated with preclinical and clinical trials, also significantly reducing costs. Another point highlighted by the authors is the potential to improve patient care, assisting in the diagnosis of diseases. Highlighting some limitations of AI, the authors describe the high cost and security breaches in relation to data privacy. They also comment on the issue that AI cannot compensate for in vivo studies in the drug discovery process. Evidencing that in vivo experiments are necessary in the drug development process to confirm the safety and efficacy of drugs [57].

2.7 Possible Use of AI in the Indian Context

The COVID-19 pandemic posed significant challenges to the Indian healthcare system, particularly in Primary Health Care (PHC) and the National Health Mission (NHM), which includes the flagship Family Health Program (FHP) [60]; [61]. In these contexts, artificial intelligence (AI) can play a pivotal role in addressing these challenges by optimizing healthcare processes, enhancing health promotion, and combating the spread of misinformation. As discussed by the authors of [60], during the crisis, FHP teams were crucial in health promotion initiatives, focusing on measures such as vaccination, hygiene practices, and social distancing. From this perspective, AI can expand the reach of these actions by facilitating access to information and adapting health content for different demographics. One potential use of AI could be in the development of more targeted awareness campaigns, tailored to the specific needs and characteristics of different communities, thereby improving the impact of preventive measures, such as vaccination and hygiene practices.

The pandemic also required a rapid reorganization of healthcare professionals' work, as they had to manage a high volume of suspected and confirmed cases while also facing shortages in Personal Protective Equipment (PPE) [60]. In this scenario, AI could have been used to streamline patient triage, quickly identifying individuals at the highest risk of severe complications. Furthermore, intelligent systems could help optimize resource allocation, ensuring that areas with the most urgent need receive PPE and medical supplies efficiently.

The authors of [61] highlight that, in addition to physical health challenges, mental health was also significantly affected during the pandemic, particularly among students, healthcare workers, and migrant laborers. Anxiety, depression, and stress levels increased significantly across these groups. In this context, AI could be employed as a tool to identify individuals at risk, analyzing mental health data on a large scale to enable more personalized and effective interventions. This approach could help improve the mental well-being of these groups by actively monitoring their mental health and providing early interventions to prevent mental health crises.

This section briefly explores the potential applications of AI, particularly in patient screening, health promotion, and mental health support. There are still many opportunities to expand the use of these technologies, especially in personalizing healthcare and supporting mental health initiatives. By leveraging AI, India can better prepare for future health crises, improving its healthcare infrastructure and resilience.

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3. CONCLUSION

Artificial intelligence (AI) has revolutionized healthcare research, offering significant advancements in diagnostics, patient screening, and drug development. By optimizing processes and enhancing data analysis capabilities, AI has proven invaluable in managing healthcare challenges during the COVID-19 pandemic. It enabled rapid epidemiological predictions, facilitated vaccine development, and improved patient triage and resource allocation. Despite its successes, AI implementation revealed challenges, particularly regarding data quality, biases, and infrastructure disparities. The reliance on high-quality datasets often excludes resource-limited settings, highlighting the need for more adaptable and inclusive AI models. Furthermore, variations in data formats and quality introduce inconsistencies, limiting AI's broader applicability. To overcome these challenges, future research should prioritize developing robust, scalable AI frameworks capable of handling diverse datasets, especially in under-resourced regions. Expanding AI applications to include mental health and socioeconomic data can enhance predictive accuracy and crisis preparedness. Additionally, advancements in deep learning and algorithmic fairness are crucial to reducing biases and ensuring equitable AI deployment. In conclusion, AI has demonstrated its transformative potential during the COVID-19 crisis. Continued research and refinement will be essential to harnessing AI's full capabilities, making healthcare systems more resilient and responsive to future global health emergencies.

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