COVID-19: Review of Data Analysis

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Abstract - **The first infection caused by Covid-19 appeared in December 2019 and has infected about 250 million people since. In pandemics, it is essential to model propagation so that it is possible to know how to act to avoid a significant public health problem. Since the appearance of Covid-19, mathematicians, scientists, physicians, and engineers have cooperated in data analysis. This study aims to understand which mathematical models are more relevant and used in this context. Based on Preferred Reporting Items for Systematic Reviews and Meta-Analyses (*PRISMA)* methodology, we will analyse Covid-19 related articles, meeting the results in predicting this pandemic in Portugal and worldwide. All the articles chosen use models or algorithms to perform *prediction*, and we conclude that the Susceptible-Infected-Recovered (SIR) model was the most appropriate and the most used. All the articles have been published up to April 2021.**

Keywords – PRISMA; literature review; Covid-19; prediction; SIR.

I. INTRODUCTION

Humans have been affected by infectious diseases since human behaviours allowed for their spread and, according to [1], there have been reports of episodes of infectious diseases since antiquity. According to [2], an epidemic is the spread of an infectious and contagious disease that develops in a place or region, quickly, causing many victims in a short period of time. A pandemic is an infectious disease that spreads worldwide and attacks at the same time numerous people in many countries.

The Coronavirus that existed before the onset of SARS-CoV also represented a significant public health problem, despite being responsible for only mild respiratory illnesses limited to the upper respiratory tract, such as the common flu. One of the most significant pandemics was the Spanish flu, between 1918 and 1920, in which about 50 million people died. Currently, the world is being affected by the Coronavirus (SARS–CoV–2). Covid-19 is the name attributed by the World Health Organization to the disease caused by the new Coronavirus SARS-COV-2, which can cause severe respiratory infections such as pneumonia. This virus was first identified in humans in late 2019 in the Chinese city of Wuhan. "Being based in more than 100 countries and territories on five continents" [3], it has become one of the biggest challenges of the 21st century. Because the Covid-19 virus has only been present in everyday life since 2019, knowledge about it is still limited. Because it is an acute respiratory infection, SARS-CoV-2 is spread through droplets, respiratory secretions, and direct contact with infected patients. Given this information, all individuals should be considered potential disseminators of the infection, and social distancing and the use of masks should be considered for all as prevention measures. It should be seen that, when there is transmission of the virus, it has an incubation period of 2 to 14 days, verifying the existence of viral excretion about 2 to 3 days before the beginning of symptoms. Even asymptomatic individuals may transmit the virus, although transmission of the infection is unusual. When symptoms are reported, the status of the infected individual must be taken into care, and the most common symptoms may be fever, dry cough, and fatigue. There are also less common symptoms to consider, such as high blood pressure and muscle pain, sore throat, diarrhea, conjunctivitis, headache, loss of taste or smell, skin irritations or discolouration of the fingers or toes. Moreover, in more severe states, patients infected with SARS-CoV-2 may present with difficulty breathing or shortness of breath, chest pressure or pain, speech loss or loss of motor capacity.

For a person to be considered infected, only the symptoms are not enough, and it is necessary to make a positive diagnosis of Covid-19; this is usually done through a molecular test of respiratory secretions. Since the pandemic's beginning, the international scientific community has unified efforts to produce an antiviral treatment that demonstrates positive results; practically every day, numerous methodology articles are published to be developed and potential medicines to combat this virus. At first, due to the lack of a specific and effective treatment against Covid-19, the process was based on symptomatic control and ventilatory support to more acute cases.

More than a year after the SARS-CoV-2 virus was identified, vaccines began to develop in various parts of the world. More than 200 vaccines have been developed, of which 90 have progressed to clinical trials. There are currently four authorised vaccines. Also, in 2020, the vaccination system began, and the entire vaccination process data was housed in the country's

existing infrastructure of the Electronic Health Registry. Despite current uncertainty regarding the efficacy and safety of vaccines, studies indicate that they are effective in preventing Covid-19 and in preventing severe disease and death. There is still no certainty about the period of protection they offer or the effectiveness of the various variants.

However, early on, technological tools became great allies for determining preventive measures and for the medical community, as well as for society in general, as these have helped and still help in the detection, prevention, and response against the virus. This pandemic promotes the need for new approaches and technologies. Machine Learning (ML) and Artificial Intelligence (AI) are solutions suitable to the world full of data, contributing to "technological evolution that revolutionises the lives and businesses of all of us" [4]. According to the Organization for Economic Co-operation and Development [5], before the world was even aware of the threat that coronavirus represents, "AI systems had already noticed the outbreak of an unknown type of pneumonia in China", since artificial intelligence is a system that tries to perceive the study environment and takes measures that maximize the chances of success. This tool was used in the management of all stages of the crisis: detection, prevention, response and recovery." These tools have become an indispensable ally in the fight against the pandemic, accelerating the research on treatments, analysing data and other functions like planning, implementing, and evaluating prevention programs.

By analysing articles and work developed by several authors, several epidemiological models have been published to predict its dissemination over the last years of the SARS–CoV–2 pandemic, but there are still uncertainties as to accuracy. The present study will try to understand the characteristics of the most popular models for predicting the evolution of the pandemic. We aim to analyse scientific articles to identify the most used prediction models in a pandemic situation.

This paper is organised as follows. Section 2 presents the details of the methodology of the systematic literature review. Section 3 presents the conclusions and directions for future work.

II. METHODOLOGY

This section presents a systematic review of studies that addressed the use of predictions methods for Covid-19 evolution. The review is reported according to the PRISMA statement [6]. It includes the following topics: Research questions (Section A); Inclusion criteria (Section B); Search strategy (Section C); Results (Section D); Data Extraction and Data Analysis (Section E); Discussion (Section F).

A. Research questions

The research questions are as follows: (Q1): What are the existing models/algorithms for the Covid-19 forecast? (Q2):

How to make a prediction in an application (web or mobile) for Covid-19? (Q3): What parameters are used for the creation of a Covid-19 forecasting model? (Q4): What advantages do these algorithms bring to the health area and the population?

B. Inclusion criteria

The inclusion criteria of studies and evaluation methods for this review were: (C1): Studies where algorithms applied to data related to Covid-19 are present; (C2): Studies that have calculated formulations applied to data resulting from studies on the theme of Covid-19; (C3): Studies seeking to predict the evolution of the pandemic; (C4): Studies showing assertiveness results of prediction algorithms related to the theme of Covid-19; (C5): Studies that consider the country Portugal; (C6): Studies between 2019 and 2021.

C. Search strategy

Through research and survey of scientific articles in PubMed, ScienceDirect and MedRvix databases, a study was conducted on Covid-19 and the corresponding aspects of this disease. This study made it possible to understand the best practices about data processing, algorithms to be implemented, and the best ways to select the best model. The articles included were published between 2019 - 2021 and selected according to relevance to the proposal of this review. The research terms used to perform this systematic review were: "Covid", "Algorithm", "Forecast", "Portugal", which were chosen and analysed to identify the different types of Covid-19 prediction algorithms that are being used in Portugal. This survey was conducted in April 2021.

D. Results

After the literature search, 136 studies were obtained (after removing five duplicates) and, after applying the inclusion criteria identified in Section 2.2, 49 studies were excluded, resulting in 82 studies. These studies were evaluated in terms of title and abstract, resulting in the exclusion of 28 studies. The full-text evaluation of the remaining 54 studies was performed, excluding 36 studies that did not match the defined inclusion criteria, did not present sufficient information about the algorithm used, or lacked an outcome. The remaining 18 studies are presented in the qualitative and quantitative synthesis.

E. Data Extraction and Data Analysis

Data were extracted from all identified studies using a predefined data format that included: study name, authors, year of publication, date, methods/algorithm, programming language/platforms. Two reviewers extracted the information, and any disagreements were resolved via

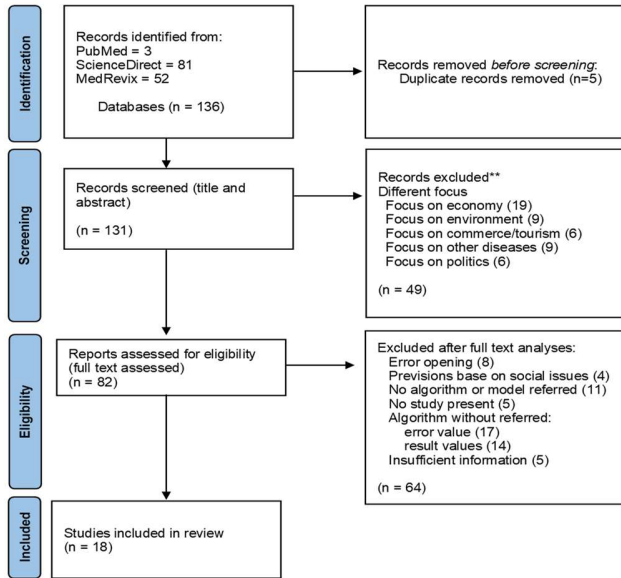discussion. Table I shows the extracted data. The characteristics of the included studies are summarized next.

Figure 1. Flow diagram for new systematic reviews (adapted from [6])

TABLE I. EXTRACTED DATA.

Article Name	Method/ Algorithm	Programming Language
Tracking R of COVID-19: A New Real-Time Estimation Using the Kalman Filter [7]	SIR	R
A Novel Smart City Based Framework on Perspectives for application of Machine Learning in combatting Covid-19 [8]	SIR Random Forest	NA
Extension of a SIR modelling the propagation of Covid-19 in several countries [9]	SIR	R
COVID 19 in Portugal: predictability of hospitalization, ICU and respiratory-assistance needs [10]	Random Forest Decision Tree	Python
Estimation of COVID-19 spread curves integrating global data and borrowing information [11]	SEIR	NA
Data-driven inference of the reproduction number for COVID-19 before and after interventions for 51 European countries [12]	SIR	Python C++
Simplified model of Covid-19 epidemic prognosis under quarantine and estimation of quarantine effectiveness [13]	SIR	R
Covid-19 trajectories Monitoring pandemic in the worldwide context [14]	SIR	R
Estimating the parameters of SIR model of COVID-19 cases in India during lock down periods [15]	SIR	Python

Article Name	Method/ Algorithm	Programming Language
The current COVID-19 wave will likely in the second-line European countries [16]	Random Forest Logistic Regression Bayesian	R
A new fractional mathematical modelling of COVID-19 with the availability of vaccine [17]	SIR SEIR	MATLAB
Data-Driven Mean-Field-Type Game Perspective [18]	SIR SEIR	C++ MATLAB
A computational tool for trend analysis and forecast of the COVID-19 pandemic [19]	Mathematical functions	MATLAB
Forecasting COVID-19 cases based on a parameter-varying stochastic SIR model [20]	SIR	R
When will the Covid-19 pandemic peak? [21]	SIR Linear Regression	R
Sociodemographic predictors of COVID-19 vaccine acceptance: a nationwide US-based survey study [22]	Logistic Regression Artificial Neural Network	NA
Time series forecasting of new cases and new deaths rate for COVID-19 using deep learning methods [23]	Artificial Neural Network	NA
Modelling the impact of SARS-CoV-2 variants and vaccines on the spread of COVID-19 [24]	SIR	MATLAB

The articles in Table I were analyzed, where the prediction methods were identified as well as the programming languages for the development of these methods. This information served as a basis for answering the formulated research questions.

F. Discussion

Over this time, several epidemiological models have been published predicting the spread of the Covid-19 virus, but there are still ambiguities as to accuracy in many cases. One of the most critical aspects of these articles is the development of models designed to help the entire population understand the importance of prevention. Some of the studies contributed to the prediction of the evolution of the pandemic and helped in decision-making. At an early stage of the pandemic, the articles helped to understand how the virus could develop and how important it was for countries to quarantine or not. With all the discoveries made, it is possible to identify trends concerning vaccines and how the pandemic may develop going forward. When analysing the eighteen selected articles, it can be said that the time interval of the studies occurs from 2020 to 2021, as indicated in Figure 2. The most used method was the SIR, consisting of twelve (12) articles; meanwhile, three (3) of the articles chose to use the SEIR, and the same number (3) used the Random Forest method; two (2) articles use logistic regression and Artificial Neural Network, and

finally, (1) article used Linear Regression and fminCon, as shown in the graph in Figure 3. The results were obtained with consideration that there may be more than one model in each article. Table II presents the results obtained for models and programming languages used by the authors. Then, with the help of this research, it was possible to realise that many mathematical models can be used to predict epidemiology. These can be Statistical Learning (SL), ML, or Deep Learning (DL). The most significant difference between SL and ML is the purpose. The SL is designed for the different relationships between the variables, while the ML is designed to make predictions as accurate as possible. The DL is an SL method that extracts resources or attributes from raw data. However, information is limited mainly by the fact that Covid-19 is recent. In many of the studies analysed, only pandemic prevention means are indicated, or specific/discrete values, for example, daily cases and not given for a prediction of the evolution of Covid-19, which is the factor that analytical work.
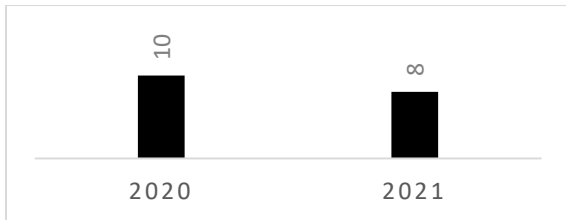

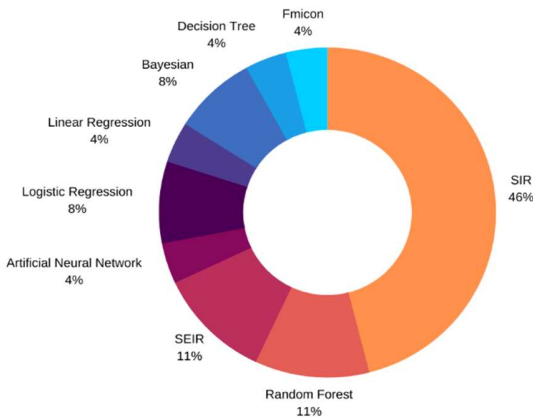Figure 2. Date of publication of the articles

Figure 3. Models/Algorithms

TABLE II. COMPARISON OF ARTICLES RESULTS.

	SIR	Random Forest	Decision Tree	SEIR	Logistic Regression	Bayesian	FmiCon	Linear Regression	Artificial Neural Network
R	6	1			1	1		1	1
Phyton	2	1	1						
MATLAB	3			2			1		1
C++	2			1					
Total	13	2	1	3	1	1	1	1	2

Based on the information acquired, the answers to the research questions are:

Question 1: What are the existing models/algorithms for the Covid-19 forecast? Practically, every day around the world, new algorithms are used or even generated and may be based on or not existing mathematical models. Regarding the articles that were studied, the SIR model was referenced in the articles [7]-[9][12]-[15][17][18][20][21][24]; in relation to the Random Forest algorithm, it was mentioned in the articles [8][10][16]; the Decision Tree algorithm was exclusively referenced in the article [10]; the variant of the SEIR model appears in the articles [11][17][18]; Logistic Regression is present in the articles [16][22]; Linear Regression was alluded only in the article [21]; the Artificial Neural Network was referenced in the articles [22][23]; finally the Fmincon algorithm in the article [19].

Question 2: How to make a prediction in an application (web or mobile) for Covid-19? A prediction can be made through programs such as MATLAB, which was used to make the predictions in the articles [17]-[19][24]. R was used by the authors of the articles [7][9][13][14][16][20][21]; the articles [10][12][15] use Phyton for prediction, C++ is used in the articles [12][18]. Subsequently, the results obtained are shared and can be implemented in a computerized application content.

Question 3: What parameters are used for the creation of a Covid-19 forecasting model? In a forecast model for Covid-19, the parameters are usually generalised, differentiating between the content with which the treatment is carried out. For their calculations, it is necessary to inform the number of the global population (Susceptible), the number of cases that manifest having the disease (Infected) and the number of the entire population that has managed to overcome so far (Recovered), this information is contained in all eighteen (18) articles analyzed.

Question 4: What advantages do these algorithms bring to the health area and the population? The predictor algorithms emerge in the connection between pure statistics with the computer media of ML. Health benefits from them in collecting more accurate data because this significant advance in data analysis allows a pleasant and symbiotic visualization, contributing to a more effective approach by health professionals [19]. For researchers in this area, these algorithms help them have the means for future analysis of a new eventual pandemic [17] and the population now has access to information.

The articles analyzed stated that the deterministic model most implemented in the case studies was the SIR and will be used for future work. This model [25][26] has different dependencies, which are generally called capital letters such as "S", "I", and "R". In the "SIR" model, "S" represents the group of the population likely to contract the disease, "I" represents the group of the population that contracted the disease and that can transmit it to another individual, infectious group, and the "R" represents the group of the population that recovered from the disease.

The transition rates of individuals between different groups are expressed through derivatives; deterministic models are formulated in terms of systems of differential equations. To make the model more realistic, it is usual to increase the number of compartments to characterize more stages of the disease. For example, in a study on the effect of quarantine on the transmission of infectious disease, the authors introduced to this model the quarantine compartment, "Q", if all infected individuals should pass through the compartment before returning to the compartment of susceptible "S" or recovered "R".

When performing the analysis of articles, several questions arise regarding this model, such as:
• What if the dataset changes regularly?

For this question and looking at the case of Portugal, data is provided by DGS every day, but Rt (Recovered by time) is updated weekly. To combat the fact that data changes regularly, the estimate will be developed weekly, with the preceding; this is the most appropriate solution to understand the data trend. The monthly, or even long-term, estimate for the study object in question is not recommended.

For the prediction of the SIR data-based model, some pros and cons are obtained, which are them:
• Pros: It is a simple model; It is compartment-based; It is based on a dataset during a time window; It is a deterministic model; You do not need many iterations to achieve the desired accuracy.
• Cons: When using the standard SIR model, the "N" corresponds to the total population, being a fixed and global value; Age groups are not distinguished.

It is concluded that a model stands out for the number of times it is mentioned in the articles analysed.

III. CONCLUSION

Through what was addressed in the previous sections, it is concluded that research is one of the most critical phases of this work because it shows the relevance of mathematical modelling in the study of epidemics, the same starting point for the evolution of this study.

To obtain the results of the realised studies, it should be considered that *Covid-19* is recent and, although there is information about the viruses in this family, there is no information on how the virus will grow. As cited earlier, the pandemic is recent and constantly updated, making it challenging to obtain a detailed response or an approximation of great perceptibility of the predicted results in relation to the actual data. Consequently, the analyst's work is challenging, requiring comparing accurate data with the predicted periods to confirm the forecast's success rate. That is why it is vital that the combinations of virologists' knowledge with ML can help create frameworks to combat Covid-19 and provide better automated solutions to fight against Covid-19. In the processing of data, a segmentation of the research was to be accomplished to carry out a collection of mathematical models that meet the proposed needs, understand the evolution and its factors, and make predictions within the scope of Covid-19. The models used in the articles analysed were systematically organised, considering their characteristics. In general, the analysed models can be accurate and have a minimum error rate. However, they cannot accurately predict what will happen in each situation, as it is theoretically impossible to determine how individuals will adapt their behaviour in the community. Using modelling, it is possible to simulate the propagation, in this case of Covid-19, in each population to estimate the total number of affected individuals.

In the analysed studies, several epidemiological models were published to predict the spread of the pandemic, and there are still uncertainties as to their accuracy. Regarding the mathematical models used, it can be stowed that the authors selected the SIR model, the Random Forest, Decision Tree, Logistic Regression, Linear Regression, Artificial Neural Networks, Fmicon, Bayesian and the SEIR model to carry their studies.

The adoption of preventive measures of public health was essential to reducing the outbreak of this contagious disease. Initially, quarantine was the best preventive measure; studies show that without other resources such as masks or gel alcohol, more than four quarantines were required until a reasonable amount of group immunity was arrived at. With the arrival of vaccines, the picture has changed and, as a result, the number of quarantines has been reduced, and a higher number of immune persons is achieved in a smaller period.

After the research and analysis phase, choosing the most appropriate model to simulate the epidemic outbreak is initiated according to the characteristics of the virus under analysis. The transmission and contagion period are the two characteristics being modelled through their rates, and the values of these characteristics are decisive in the analysis of the outbreak's evolution. These characteristics were best represented by the SIR model, which was the most referred by the authors.

After the analysis of scientific articles and the preference of the method to be implemented, it is concluded that it is essential to understand more about the virus and its history.

For future work, it will be interesting to use the SIR method with the addition of new parameters, such as vaccination.

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